

SEQUENCE LISTING

<110> Dumas Milne Edwards, J.B.
Duclert A.
Giordano, J.Y.

<120> Expressed Sequence Tags and Encoded Human Proteins.

<130> GENSET.054A

<150> US 60/122,487

<151> 1999-02-26

<160> 36681

<170> Patent.pm

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<221> sig_peptide
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ctcaaacggc ctagtgttc gcgcttcgg agaaaatcag cgggtctaatt aattcctctg 180
gtttgttgaa gcagttacca agaattctca accctttccc acaaaagcta attgagtaca 240
cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg 300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt 357
Met Trp Trp Phe
-20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct 405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
-15 -10 -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata 453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
1 5 10 15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa 501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
20 25 30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa 549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
35 40 45
aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaa 602

Lys
ctcttcaraa acatgtcttt acaagcatat ctcttgatt gctttctaca ctgttgaatt 662
gtctggcaat atttctgcag tggaaaattt gattarmta gttcttgact gataaatatg 722
gtaagggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw 782
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa 822

<210> 2
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<213> Homo Sapiens

<220>
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score 5.5
seq SFLPSALVIWTS/AF

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1 5 10 15
Ile Trp Thr Ser Ala
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<222> 90..344

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Met Lys Lys Val Leu Leu Leu Ile
-15 -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag 161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
-5 1 5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr 209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
10 15 20
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att 257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
25 30 35
cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata 305

004220" 666E7550

Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
 40 45 50 55
 cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa 354
 Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
 60 65
 ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat 414
 caaaatttcct gttaataaaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta 474
 gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa 526

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 ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat 100
 Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
 -5 1 5
 gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca 148
 Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
 10 15 20 25
 tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct 196
 Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
 30 35 40

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ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat      244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
      45                      50                      55
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt      292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
      60                      65                      70
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca      340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
      75                      80                      85
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat      388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
      90                      95                      100                      105
gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc      436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
      110                      115                      120
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt      484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe
      125                      130                      135
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg      532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp
      140                      145                      150
caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa      580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu
      155                      160                      165
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat      628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp
      170                      175                      180                      185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag      676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu
      190                      195                      200
gat gag agg ctc acc cct ctc tgaagggtg ttgttctgct tcctcaaraa      727
Asp Glu Arg Leu Thr Pro Leu
      205
attaaacatt tgtttctgtg tgactgctga gcacccctgaa ataccaagag cagatcatat      787
wttttgtttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa      847
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<210> 7
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 <213> Homo sapiens

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<221> sig_peptide
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 Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser
 -10 -5 1 5
 ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag 146
 Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln
 10 15 20
 ggc ctt gaa gtt ttc tac cca gag ttg ggg aac att ggc tgc aag gtt 194
 Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
 25 30 35
 gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag 242
 Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
 40 45 50
 ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg 290
 Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
 55 60 65 70
 gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga 338
 Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
 75 80 85
 ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag 386
 Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
 90 95 100
 aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc 434
 Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
 105 110 115
 cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt 482
 Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
 120 125 130
 cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga 530
 Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
 135 140 145 150
 ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa 578
 Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
 155 160 165
 cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca 626
 Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro

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acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac      674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
          185          190          195
cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt      725
Gln Ala Glu Ile Ala Ala Cys
          200          205
ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaaccct      785
tcttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a      826

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<210> 8
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 <213> Homo sapiens

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 <222> -22..-1
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          -5          1          5          10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
          15          20          25
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
          30          35          40
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
          45          50          55
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
          60          65          70
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
          75          80          85          90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
          95          100          105
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
          110          115          120
Ser Gly Phe His Arg Tyr Gln Phe Val Tyr Leu Gln Glu Gly Lys
          125          130          135
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
          140          145          150
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
          155          160          165          170
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
          175          180          185
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
          190          195          200
Ala Ala Cys
          205

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 ctggacaagg attaagaatg tggatcaagc aggttttttaa atcaagattt aacattccaa 180
 cacataaaaa ttatttatcc aacagctcct cccagatcat atactcct atg aaa gga 237
 Met Lys Gly
 gga atc tcc aat gta tgg ttt gac aga ttt aaa ata acc aat gac tgc 285
 Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr Asn Asp Cys
 -85 -80 -75 -70
 cca gaa cac ctt gaa tca att gat gtc atg tgt caa gtg ctt act gat 333
 Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val Leu Thr Asp
 -65 -60 -55
 ttg att gat gaa gaa gta aaa agt ggc atc aag aag aac agg ata tta 381
 Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn Arg Ile Leu
 -50 -45 -40
 ata gga gga ttc tct atg gga gga tgc atg gca atg cat tta gca tat 429
 Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His Leu Ala Tyr
 -35 -30 -25
 aga aat cat caa gat gtg gca gga gta ttt gct ctt tct agt ttt ctg 477
 Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser Ser Phe Leu
 -20 -15 -10
 aat aaa gca tct gct gtt tac cag gct ctt cag aag agt aat ggt gta 525
 Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser Asn Gly Val
 -5 1 5 10
 ctt cct gaa tta ttt cag tgt cat ggt act gca gat gag tta gtt ctt 573
 Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu Leu Val Leu
 15 20 25
 cat tct tgg gca gaa gag aca aac tca atg tta aaa tct cta gga gtg 621
 His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser Leu Gly Val
 30 35 40
 acc acg aag ttt cat agt ttt cca aat gtt tac cat gag cta agc aaa 669
 Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu Leu Ser Lys
 45 50 55
 act gag tta gac ata ttg aag tta tgg att ctt aca aag ctg cca gga 717
 Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys Leu Pro Gly
 60 65 70 75
 gaa atg gaa aaa caa aaa tgaatgaatc aagagtgatt tgttaatgta 765
 Glu Met Glu Lys Gln Lys
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taagaaatag caaaaaaaaa aaaaaaa

825
852

<210> 10
<211> 507
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<213> Homo sapiens

<220>
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 -70 -65 -60
Leu Thr Asp Leu Ile Asp Glu Val Lys Ser Gly Ile Lys Lys Asn
 -55 -50 -45
Arg Ile Leu Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His
 -40 -35 -30 -25
Leu Ala Tyr Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser
 -20 -15 -10
Ser Phe Leu Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser
 -5 1 5
Asn Gly Val Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu
 10 15 20
Leu Val Leu His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser
 25 30 35 40
Leu Gly Val Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu
 45 50 55
Leu Ser Lys Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys
 60 65 70
Leu Pro Gly Glu Met Glu Lys Gln Lys
 75 80

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<212> DNA
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<220>
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Leu Pro Trp Glu Asp Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro	
-35 -30 -25	
cgg aag tgt tcc gtc ttc cac ctg ttc gtg gcc tgc ctc tcg ctg ggc	149
Arg Lys Cys Ser Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly	
-20 -15 -10	
ttc ttc tcc cta ctc tgg ctg cag ctc agc tgc tct ggg gac gtg gcc	197
Phe Phe Ser Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala	
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cgg gca gtc agg gga caa ggg cag gag acc tcg ggc cct ccc cgt gcc	245
Arg Ala Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala	
10 15 20 25	
tgc ccc cca gag ccg ccc cct gag cac tgg gaa gaa gac gca tcc tgg	293
Cys Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp	
30 35 40	
ggc ccc cac cgc ctg gca gtg ctg gtg ccc ttc cgc gaa cgc ttc gag	341
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe Glu	
45 50 55	
gag ctc ctg gtc ttc gtg ccc cac atg cgc cgc ttc ctg agc agg aag	389
Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser Arg Lys	
60 65 70	
aag atc cgg cac cac atc tac gtg ctc aac cag gtg gac cac ttc agg	437
Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp His Phe Arg	
75 80 85	
ttc aac cgg gca gcg ctc atc aac gtg ggc ttc ctg gag agc agc aac	485
Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu Glu Ser Ser Asn	
90 95 100 105	
agc acg gac tac att gcc atg cac gac gtt gac ctg ctc cct ctc aac	533
Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp Leu Leu Pro Leu Asn	
110 115 120	
gag gag ctg gac tat ggc ttt cct gag gct ggg ccc ttc cac gtg gcc	581
Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala Gly Pro Phe His Val Ala	
125 130 135	
tcc ccg gag ctc cac cct ctc tac cac tac aag acc tat gtc ggc ggc	629
Ser Pro Glu Leu His Pro Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly	
140 145 150	
atc ctg ctg ctc tcc aag cag cac tac cgg ctg tgc aat ggg atg tcc	677
Ile Leu Leu Leu Ser Lys Gln His Tyr Arg Leu Cys Asn Gly Met Ser	
155 160 165	
aac cgc ttc tgg ggc tgg ggc cgc gag gac gag gag ttc tac cgg cgc	725
Asn Arg Phe Trp Gly Trp Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg	
170 175 180 185	
att aag gga gct ggg ctc cag ctt ttc cgc ccc tcg gga atc aca act	773
Ile Lys Gly Ala Gly Leu Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr	
190 195 200	
ggg tac aag aca ttt cgc cac ctg cat gac cca gcc tgg cgg aag agg	821
Gly Tyr Lys Thr Phe Arg His Leu His Asp Pro Ala Trp Arg Lys Arg	
205 210 215	
gac cag aag cgc atc gca gct caa aaa cag gag cag ttc aag gtg gac	869
Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp	

220	225	230	
agg gag gga ggc ctg aac act gtg aag tac cat gtg gct tcc cgc act			917
Arg Glu Gly Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr			
235	240	245	
gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc ctc aac atc atg ttg			965
Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu			
250	255	260	265
gac tgt gac aag acc gcc aca ccc tgg tgc aca ttc agc tgagctggat			1014
Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser			
270	275		
ggacagtgag gaagcctgta cctacaggcc atattgctca ggctcaggac aaggcctcag			1074
gtcgtggggc cagctctgac aggatgtgga gtggccagga ccaagacagc aagctacgca			1134
attgcagcca cccggccgcc aaggcaggct tgggctgggc caggacacgt ggggtgcctg			1194
ggacgtgtct tgccatgcac agtgatcaga gagaggctgg ggtgtgtcct gtccgggacc			1254
ccccctgcct tctgtctcac cctactctga cctccttcac gtgcccaggc ctgtgggtag			1314
tggggagggc tgaacaggac aacctctcat caccctcact tttgttcctt cctgctgggc			1374
tgcctcgtgc agagacacag tgtagggggc atgcagctgg cgtaggtggc agttgggcct			1434
ggtgaggggtt aggacttcag aaaccagagc acaagcccca cagaggggga acagccagca			1494
ccgctctagc tggttgttgc catgccggaa tgtgggccta gtgttgccag atcttctgat			1554
ttttcgaaag aaactagaat gctggattct caaaaaaaaa aaaaaaaaa			1602

<210> 12
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<220>
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 <222> -49...-1
 <223> score 5.6
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 -30 -25 -20
 His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
 -15 -10 -5
 Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
 1 5 10 15
 Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
 20 25 30
 Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
 35 40 45
 Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
 50 55 60
 Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
 65 70 75
 Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
 80 85 90 95
 Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
 100 105 110


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Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
      115                      120                      125
Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
      130                      135                      140
Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
      145                      150                      155
Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
      160                      165                      170                      175
Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
      180                      185                      190
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
      195                      200                      205
His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
      210                      215                      220
Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
      225                      230                      235
Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
      240                      245                      250                      255
Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
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Thr Pro Trp Cys Thr Phe Ser
      275

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<210> 13
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 <223> score 4.4
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ttcagaacag aagc atg gat ctc gga atc cct gac ctg ctg gac gcg tgg      110
      Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp
      -310                      -305                      -300
ctg gag ccc cca gag gat atc ttc tcg aca gga tcc gtc ctg gag ctg      158
Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu
      -295                      -290                      -285
gga ctc cac tgc ccc cct cca gag gtt ccg gta act agg cta cag gaa      206
Gly Leu His Cys Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu
      -280                      -275                      -270
cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc tgt ggc ctt      254
Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu
      -265                      -260                      -255
caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att gat ccc aat      302
Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn

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-250	-245	-240	-235	
gag gtg tac tgc tca gaa gca tct cct ggc agt gac agt ggc atc tct				350
Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser				
-230	-225	-220		
gag gac tcc tgc cat cca gac agt ccc cct gcc ccc agg gca acc agt				398
Glu Asp Ser Cys His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser				
-215	-210	-205		
tct cct atg ctc tat gag gtt gtc tat gag gca ggg gcc ctg gag agg				446
Ser Pro Met Leu Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg				
-200	-195	-190		
atg cag ggg gaa act ggg cca aat gta ggc ctt atc tcc atc cag cta				494
Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu				
-185	-180	-175		
gat cag tgg agc cca gca ttt atg gtg cct gat tcc tgc atg gtc agt				542
Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser				
-170	-165	-160	-155	
gag ctg ccc ttt gat gct cat gcc cac atc ctg ccc aga gca ggc acc				590
Glu Leu Pro Phe Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr				
-150	-145	-140		
gta gcc cca gtg ccc tgt aca acc ctg ctg ccc tgt caa acc ctg ttc				638
Val Ala Pro Val Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe				
-135	-130	-125		
ctg acc gat gag gag aag cgt ctg ctg ggg cag gaa ggg gtt tcc ctg				686
Leu Thr Asp Glu Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu				
-120	-115	-110		
ccc tct cac ctg ccc ctc acc aag gca gag gag agg gtc ctc aag aag				734
Pro Ser His Leu Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys				
-105	-100	-95		
gtc agg agg aaa atc cgt aac aag cag tca gct cag gac agt cgg cgg				782
Val Arg Arg Lys Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg				
-90	-85	-80	-75	
cgg aag aag gag tac att gat ggg ctg gag agc agg gtg gca gcc tgt				830
Arg Lys Lys Glu Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys				
-70	-65	-60		
tct gca cag aac caa gaa tta cag aaa aaa gtc cag gag ctg gag agg				878
Ser Ala Gln Asn Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg				
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cac aac atc tcc ttg gta gct cag ctc cgc cag ctg cag acg cta att				926
His Asn Ile Ser Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile				
-40	-35	-30		
gct caa act tcc aac aaa gct gcc cag acc agc act tgt gtt ttg att				974
Ala Gln Thr Ser Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile				
-25	-20	-15		
ctt ctt ttt tcc ctg gct ctc atc atc ctg ccc agc ttc agt cca ttc				1022
Leu Leu Phe Ser Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe				
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cag agt cga cca gaa gct ggg tct gag gat tac cag cct cac gga gtg				1070
Gln Ser Arg Pro Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val				
10	15	20		
act tcc aga aat atc ctg acc cac aag gac gta aca gaa aat ctg gag				1118
Thr Ser Arg Asn Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu				
25	30	35		
acc caa gtg gta gag tcc aga ctg agg gag cca cct gga gcc aag gat				1166
Thr Gln Val Val Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp				

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gca aat ggc tca aca agg aca ctg ctt gag aag atg gga ggg aag cca			1214
Ala Asn Gly Ser Thr Arg Thr Leu Leu Glu Lys Met Gly Gly Lys Pro			
55	60	65	70
aga ccc agt ggg cgc atc cgg tcc gtg ctg cat gca gat gag atg			1259
Arg Pro Ser Gly Arg Ile Arg Ser Val Leu His Ala Asp Glu Met			
75	80	85	
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tggcttttctt cccactggga ttctactta ggtgtctgcc ctcaggggtc caaatcactt			1379
caggacaccc caagagatgt ccttttagtct ctgcctgagg cctagtctgc atttgtttgc			1439
atatatgaga gggtacctca aatacttctg ttatgtatct gtgattttat ttcttctttg			1499
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aaaaaaaa			1568

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 -290 -285 -280
 Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln
 -275 -270 -265
 Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu
 -260 -255 -250
 Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys
 -245 -240 -235
 Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Ser Cys
 -230 -225 -220 -215
 His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu
 -210 -205 -200
 Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu
 -195 -190 -185
 Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser
 -180 -175 -170
 Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe
 -165 -160 -155
 Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val
 -150 -145 -140 -135
 Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu
 -130 -125 -120
 Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu
 -115 -110 -105
 Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys Val Arg Arg Lys

<223> matinspector prediction
name CMYB_01
score 0.983
sequence tgtcagttg

<221> protein_bind
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name MYOD_Q6
score 0.961
sequence cccaactgac

<221> protein_bind
<222> complement(75..85)
<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag

<221> protein_bind
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<223> matinspector prediction
name S8_01
score 0.966
sequence aactaaattag

<221> protein_bind
<222> complement(129..139)
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name DELTAEF1_01
score 0.960
sequence gcacacctcag

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name GATA_C
score 0.964
sequence agataaatcca

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score 0.959
sequence ttgtagataggaca

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name GATA_C
score 0.953
sequence agataggacat

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score 0.973
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<221> protein_bind
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score 0.983
sequence cataacagatggtaag

<221> protein_bind
<222> 284..299
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name TAL1BETAITF2_01
score 0.978
sequence cataacagatggtaag

<221> protein_bind
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name MYOD_Q6
score 0.954
sequence accatctggt

<221> protein_bind
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name GATA1_04
score 0.953
sequence tcaagataaagta

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name IK1_01
score 0.963
sequence agttgggaattcc

<221> protein_bind
<222> 393..404
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name IK2_01
score 0.985

sequence agttgggaattc

<221> protein_bind
<222> 396..405
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name CREL_01
score 0.962
sequence tgggaattcc

<221> protein_bind
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score 0.950
sequence tcagtgatatggca

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name SRY_02
score 0.951
sequence taaaacaaaaca

<221> protein_bind
<222> 486..493
<223> matinspector prediction
name E2F_02
score 0.957
sequence tttagcgc

<221> protein_bind
<222> complement(514..521)
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name MZF1_01
score 0.975
sequence tgagggga

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gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta 180
gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa 240
atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg 300
atactttatc ttgagtagga gagccttcct gtggcaacgt ggagaaggga agaggtcgta 360
gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag 420
catcagtgat atggcaaatg tgggactaag ggtagtgatc agaggggttaa aattgtgtgt 480
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cttcat 546

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23

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<400> 19
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24

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score 0.956
sequence ggaccaatcat

<221> protein_bind
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name MZF1_01
score 0.962
sequence cctgggga

<221> protein_bind
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name CMYB_01
score 0.994
sequence tgaccgttg

<221> protein_bind
<222> complement(126..134)
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name VMYB_02
score 0.985
sequence tccaacggt

<221> protein_bind
<222> 135..143

<223> matinspector prediction
name STAT_01
score 0.968
sequence ttcctggaa

<221> protein_bind
<222> complement(135..143)
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name STAT_01
score 0.951
sequence ttccaggaa

<221> protein_bind
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name MZF1_01
score 0.956
sequence ttggggga

<221> protein_bind
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name IK2_01
score 0.965
sequence gaatgggatttc

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score 0.986
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name SRY_02
score 0.955
sequence gaaaacaaaaca

<221> protein_bind
<222> 592..599
<223> matinspector prediction
name MZF1_01
score 0.960
sequence gaagggga

<221> protein_bind
<222> 618..627
<223> matinspector prediction
name MYOD_Q6
score 0.981
sequence agcatctgcc

<221> protein_bind
 <222> 632..642
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 name DELTAEF1_01
 score 0.958
 sequence tcccaccttcc

<221> protein_bind
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 <223> matinspector prediction
 name S8_01
 score 0.992
 sequence gaggaattat

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 name MZF1_01
 score 0.986
 sequence agagggga

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tgattggtcc	ctggggaagg	tctggctggc	tccagcacag	tgaggcattt	aggtatctct		120
cggtagccgt	tggattcctg	gaagcagtag	ctgttctggt	tggatctggt	agggacaggg		180
ctcagagggc	taggcacgag	ggaaggtcag	aggagaaggs	aggsarggcc	cagtgagarg		240
ggagcatgcc	ttcccccaac	cctggcttsc	ycttggyam	agggcgkty	tgggmacttr		300
aaytcagggc	ccaascagaa	scacaggccc	aktcntggct	smaagcacia	tagcctgaat		360
gggatttcag	gttagncagg	gtgagagggg	aggctctctg	gcttagtttt	gttttgtttt		420
ccaaatcaag	gtaacttgct	cccttctgct	acgggccttg	gtcttggttt	gtcctcacc		480
agtcggaact	ccctaccact	ttcaggagag	tggtttttag	cccgtggggc	tgttctgttc		540
caagcagtgt	gagaacatgg	ctggtagagg	ctctagctgt	gtgcggggcc	tgaaggggag		600
tgggttctcg	cccaaagagc	atctgccc	ttcccacctt	cccttctccc	accagaagct		660
tgctgagct	gtttggacaa	aaatccaaac	cccacttggc	tactctggcc	tggcttcagc		720
ttggaacca	atacctaggg	ttacaggcca	tcttgagcca	ggggcctctg	gaaattctct		780
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<400> 21		
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<210> 22
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<400> 22		
gagaccacac	agctagacaa	20

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<210> 23
<211> 555
<212> DNA
<213> Homo Sapiens

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<222> 501

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<222> 191..206
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      score 0.964
      sequence ggactcacgtgctgct

<221> protein_bind
<222> 193..204
<223> matinspector prediction
      name NMYC_01
      score 0.965
      sequence actcacgtgctg

<221> protein_bind
<222> 193..204
<223> matinspector prediction
      name USF_01
      score 0.985
      sequence actcacgtgctg

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name USF_01
      score 0.985
      sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name NMYC_01
      score 0.956
      sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
      name MYCMAX_02
      score 0.972
      sequence cagcacgtgagt

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name USF_C
score 0.997
sequence tcacgtgc

<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
name USF_C
score 0.991
sequence gcacgtga

<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
name MZF1_01
score 0.968
sequence catgggga

<221> protein_bind
<222> 397..410
<223> matinspector prediction
name ELK1_02
score 0.963
sequence ctctccggaagcct

<221> protein_bind
<222> 400..409
<223> matinspector prediction
name CETS1P54_01
score 0.974
sequence tccggaagcc

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1_Q4
score 0.963
sequence agtgactgaac

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
name AP1FJ_Q2
score 0.961
sequence agtgactgaac

<221> protein_bind
<222> 547..555
<223> matinspector prediction
name PADS_C

score 1.000
sequence tgtgtctc

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kawaagctca gcaccgggtg ccatacacagg gccggcagca cacacatccc attactcaga 180
aggaactgac ggactcacgt gctgtctcgt ccccatgagc tcagtggacc tgtctatgta 240
gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaatcc aagtgattgt 300
cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag 360
gttgctctgc ccattgggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc 420
cgtgtcttct gcctgtctccc gctcacatcc cacacttggtg ttcagtcact gagttacaga 480
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<213> Homo sapiens

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<222> 108..389

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<222> 108..167
<223> score 5
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Met Phe Ser
-20
aaa cta gca cat ttg cag agg ttt gct gta ctt agt cgc gga gtt cat 164
Lys Leu Ala His Leu Gln Arg Phe Ala Val Leu Ser Arg Gly Val His
-15 -10 -5
tct tca gtg gct tct gct aca tct gtt gca act aaa aaa aca gtc caa 212
Ser Ser Val Ala Ser Ala Thr Ser Val Ala Thr Lys Lys Thr Val Gln
1 5 10 15
ggc cct cca acc tct gat gac att ttt gaa agg gaa tat aag tat ggt 260
Gly Pro Pro Thr Ser Asp Asp Ile Phe Glu Arg Glu Tyr Lys Tyr Gly
20 25 30
gca cac aac tac crt cct tta cct gta gcc ctg gag aga gga aaa ggt 308
Ala His Asn Tyr Xaa Pro Leu Pro Val Ala Leu Glu Arg Gly Lys Gly
35 40 45
att tac tta tgg gat gta gaa ggc aga aaa tat ttt gac ttc ctg agt 356
Ile Tyr Leu Trp Asp Val Glu Gly Arg Lys Tyr Phe Asp Phe Leu Ser
50 55 60
tct tac agt gct gtc aac caa ggg cat tgt cac cc 391
Ser Tyr Ser Ala Val Asn Gln Gly His Cys His
65 70

<210> 25
 <211> 295
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 82..294

<221> sig_peptide
 <222> 82..141
 <223> score 3.5
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 agcatcccag aagactgcgc c atg ggg ctc agc gac ggg gaa tgg cag ttg 111
 Met Gly Leu Ser Asp Gly Glu Trp Gln Leu
 -20 -15
 gtg ctg aac gtc tgg ggg aag gtg gag gct gac atc cca ggc cat ggg 159
 Val Leu Asn Val Trp Gly Lys Val Glu Ala Asp Ile Pro Gly His Gly
 -10 -5 1 5
 cag gaa gtc ctc atc agg ctc ttt aag ggt cac cca gag act ctg gag 207
 Gln Glu Val Leu Ile Arg Leu Phe Lys Gly His Pro Glu Thr Leu Glu
 10 15 20
 aag ttt gac aag ttc aag cac ctg aag tca gag gac gag atg aag gca 255
 Lys Phe Asp Lys Phe Lys His Leu Lys Ser Glu Asp Glu Met Lys Ala
 25 30 35
 tct gag gac tta aag aag cat ggt gcc act gtg ctc acc g 295
 Ser Glu Asp Leu Lys Lys His Gly Ala Thr Val Leu Thr
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<210> 26
 <211> 449
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 110..448

<221> sig_peptide
 <222> 110..169
 <223> score 3.5
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 Met Gly Leu
 -20

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agc gac ggg gaa tgg cag ttg gtg ctg aac gtc tgg ggg aag gtg gag      166
Ser Asp Gly Glu Trp Gln Leu Val Leu Asn Val Trp Gly Lys Val Glu
      -15                      -10                      -5
gct gac atc cca ggc cat ggg cag gaa gtc ctc atc agg ctc ttt aag      214
Ala Asp Ile Pro Gly His Gly Gln Glu Val Leu Ile Arg Leu Phe Lys
      1                      5                      10                      15
ggg cac cca gag act ctg gag aag ttt gac aag ttc aag cac ctg aag      262
Gly His Pro Glu Thr Leu Glu Lys Phe Asp Lys Phe Lys His Leu Lys
      20                      25                      30
tca gag gac gag atg aag gca tct gag gac tta aag aag cat ggt gcc      310
Ser Glu Asp Glu Met Lys Ala Ser Glu Asp Leu Lys Lys His Gly Ala
      35                      40                      45
acy gtg ctc acc gcc ctg ggt ggc atc ctt aag aag aag ggg cat cat      358
Thr Val Leu Thr Ala Leu Gly Gly Ile Leu Lys Lys Lys Gly His His
      50                      55                      60
gag gca gag att aag ccc ctg gca cag tcg cat gcc acc aag cac aag      406
Glu Ala Glu Ile Lys Pro Leu Ala Gln Ser His Ala Thr Lys His Lys
      65                      70                      75
atc ccc gtg aaa ntn mct gga gtt cat ctc gga atg cat cat c      449
Ile Pro Val Lys Xaa Xaa Gly Val His Leu Gly Met His His
      80                      85                      90

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<210> 27
 <211> 382
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 58..381

<221> sig_peptide
 <222> 58..159
 <223> score 3.8
 seq TLFVFISXGSALG/FK

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<400> 27
agctctcaga gggaattgag caccggcag cggtctcagg ccaagccccc tgccagc      57
atg gcc agc gag ttc aag aag aag ctc ttc tgg agg gca gtg gtg gcc      105
Met Ala Ser Glu Phe Lys Lys Lys Leu Phe Trp Arg Ala Val Val Ala
      -30                      -25                      -20
gag ttc ctg gcc acg acc ctc ttt gtc ttc atc agc anc ggt tct gcc      153
Glu Phe Leu Ala Thr Thr Leu Phe Val Phe Ile Ser Xaa Gly Ser Ala
      -15                      -10                      -5
ctg ggc ttc aaa tac ccg gtg ggg mac aac cag acg gcg gtc cag gac      201
Leu Gly Phe Lys Tyr Pro Val Gly Xaa Asn Gln Thr Ala Val Gln Asp
      1                      5                      10
aac gtg aag gtg tcg ctg gcc ttc ggg ctg agc atc gcc acg ctg gcg      249
Asn Val Lys Val Ser Leu Ala Phe Gly Leu Ser Ile Ala Thr Leu Ala
      15                      20                      25                      30
cag agt gtg ggc cac atc agc ggc gcc cac ctc aac ccg gct gtc aca      297
Gln Ser Val Gly His Ile Ser Gly Ala His Leu Asn Pro Ala Val Thr
      35                      40                      45

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ctg ggg ctg ctg ctc agc tgc cag atc agc atc ttc cgn nnn tca tgt 345
 Leu Gly Leu Leu Leu Ser Cys Gln Ile Ser Ile Phe Arg Xaa Ser Cys
 50 55 60
 aca tca tcg ccc agt gcg tgg ggg cca tcg tcg cca c 382
 Thr Ser Ser Pro Ser Ala Trp Gly Pro Ser Ser Pro
 65 70

<210> 28
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 147..494

<221> sig_peptide
 <222> 147..278
 <223> score 5.5
 seq ILFFTGWIMIDA/AV

<400> 28
 gctccccggg ctgaggtgga gccgcgggac gccggcaggg ttgtggcgca sagtctcctt 60
 cctgcgcgcg cgcctgaagt cggcgtgggc gtttgaggaa gctggratwc agcatttaat 120
 gaaaaattta tgcttaagaa gtaaaa atg gca ggc ttc cta gat aat ttt cgt 173
 Met Ala Gly Phe Leu Asp Asn Phe Arg
 -40
 tgg cca gaa tgt gaa tgt att gac tgg agt gag aga aga aat gct gtg 221
 Trp Pro Glu Cys Glu Cys Ile Asp Trp Ser Glu Arg Arg Asn Ala Val
 -35 -30 -25 -20
 gca tct gtt gtc gca ggt ata ttg ttt ttt aca ggc tgg tgg ata atg 269
 Ala Ser Val Val Ala Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met
 -15 -10 -5
 att gat gca gct gtg gtg tat cct aag cca gaa cag ttg aac cat gcc 317
 Ile Asp Ala Ala Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala
 1 5 10
 ttt cac aca tgt ggt gta ttt tcc aca ttg gct ttc ttc atg ata aat 365
 Phe His Thr Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn
 15 20 25
 gct gta tcc aat gct cag gtg aga ggt gat agc tat gaa agc ggc tgt 413
 Ala Val Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys
 30 35 40 45
 tta gga aga aca ggt gct cga gtt tkg ctt ttc att ggt ttc atg ttg 461
 Leu Gly Arg Thr Gly Ala Arg Val Xaa Leu Phe Ile Gly Phe Met Leu
 50 55 60
 atg ttt ggg tca ctt att gct tcc atg tgg att c 495
 Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile
 65 70

<210> 29
 <211> 379
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..379
 <221> sig_peptide
 <222> 80..136
 <223> score 6.2
 seq WXFLVAIIKGVQC/XX

<400> 29
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 tgaacacaga ggactcacc atg gag ttt ggg ctg asc tgg stt ttc ctt gtt 112
 Met Glu Phe Gly Leu Xaa Trp Xaa Phe Leu Val
 -15 -10
 gct att ata aaa ggt gtc cag tgt cak gyg can ctg gtg gag tct ggg 160
 Ala Ile Ile Lys Gly Val Gln Cys Xaa Xaa Xaa Leu Val Glu Ser Gly
 -5 1 5
 gga rgc ttg gtc aar yct gga ggg tcc ctg aga ctc tcc tgt gca gcc 208
 Gly Xaa Leu Val Lys Xaa Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
 10 15 20
 tct gga ttc acc ttc agt gac twc tac atg arc tgg atc cgc cag gct 256
 Ser Gly Phe Thr Phe Ser Asp Xaa Tyr Met Xaa Trp Ile Arg Gln Ala
 25 30 35 40
 cca ggg aag ggg ctg gar tgg gtt tca tac att agt agc ggt ggw taw 304
 Pro Gly Lys Gly Leu Glu Trp Val Ser Tyr Ile Ser Ser Gly Gly Xaa
 45 50 55
 tac aca aac tac gca gac tct gan rag ggn cgm wtc amc atc tcc aga 352
 Tyr Thr Asn Tyr Ala Asp Ser Xaa Xaa Gly Arg Xaa Xaa Ile Ser Arg
 60 65 70
 gay aac gcc aag aac tca ctg tat ctg 379
 Asp Asn Ala Lys Asn Ser Leu Tyr Leu
 75 80

<210> 30
 <211> 442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..442
 <221> sig_peptide
 <222> 65..121
 <223> score 11.7
 seq VFCLLAVAPGAHS/QV

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 cacc atg gac tgg acc tgg agg gtc ttc tgc ttg ctg gct gta gct cca 109
 Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro

	-15	-10	-5	
ggt gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag				157
Gly Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys				
	1	5	10	
aag cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc				205
Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr				
	15	20	25	
ttc acc agc yac tat atg cac tgg gtg cga cag gcc cct gga caa ggg				253
Phe Thr Ser Xaa Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly				
	30	35	40	
ytt gag tgg atg gga ata atc aac cct agt grt ggy agc acn aas tac				301
Xaa Glu Trp Met Gly Ile Ile Asn Pro Ser Xaa Gly Ser Thr Xaa Tyr				
	45	50	55	60
gca cag aag ttc cag ggc aga gtc acc atg acy agg gac acg tcc acg				349
Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr				
	65	70	75	
agc aca gtc tac atg sag ctg agc agc ctg asa tct gas gac acg gcc				397
Ser Thr Val Tyr Met Xaa Leu Ser Ser Leu Xaa Ser Xaa Asp Thr Ala				
	80	85	90	
gtg tat yay tgt gck aga gak gcg tat agy agc tac cgc ttt gac				442
Val Tyr Xaa Cys Ala Arg Xaa Ala Tyr Ser Ser Tyr Arg Phe Asp				
	95	100	105	

<210> 31
 <211> 400
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..400
 <221> sig_peptide
 <222> 20..76
 <223> score 11
 seq TLLLLTVPSWVLS/QV

<400> 31	
gtgaatcctg ctctccacc atg gac ata ctt tgt tcc acg ctc ctg cta ctg	52
Met Asp Ile Leu Cys Ser Thr Leu Leu Leu	
	-15 -10
act gtc ccg tcc tgg gtc tta tcc cag gtc acc ttg agg gag tct ggt	100
Thr Val Pro Ser Trp Val Leu Ser Gln Val Thr Leu Arg Glu Ser Gly	
	-5 1 5
cct gcg ctg gtg aaa ccc aca cag acc ctc aca ctg acc tgc acc ttc	148
Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr Cys Thr Phe	
	10 15 20
tct ggg ttc tcr ctc asc act agt gga atg tst gtg agy tgg atc cgt	196
Ser Gly Phe Ser Leu Xaa Thr Ser Gly Met Xaa Val Ser Trp Ile Arg	
	25 30 35 40
cag scc cca ggg aag gsc ctg gag tgg ctt gca ytc att gat tgg sar	244
Gln Xaa Pro Gly Lys Xaa Leu Glu Trp Leu Ala Xaa Ile Asp Trp Xaa	
	45 50 55

gat gat aar was tac agc aca tct ctg aag aac aga ctc acc atc tcc	292
Asp Asp Lys Xaa Tyr Ser Thr Ser Leu Lys Asn Arg Leu Thr Ile Ser	
60 65 70	
aag gac acc tcc aaa aac cag gtg gtc ctt aca ctg tcc aag atg gac	340
Lys Asp Thr Ser Lys Asn Gln Val Val Leu Thr Leu Ser Lys Met Asp	
75 80 85	
cct gtg gac aca gcc aca tat tac tgt gca cgg agt aga tta gtc cct	388
Pro Val Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Arg Leu Val Pro	
90 95 100	
cac gac cac tgg	400
His Asp His Trp	
105	

<210> 32
 <211> 283
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..283

<221> sig_peptide
 <222> 20..76
 <223> score 11
 seq TLLLLTVPSWVLS/QV

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gtgaatcctg ctctccacc atg gac ata ctt tgt tcc acg ctc ctg cta ctg	52
Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu	
-15 -10	
act gtc ccg tcc tgg gtc tta tcc cag gtc acc ttg arg gag tct ggt	100
Thr Val Pro Ser Trp Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly	
-5 1 5	
cct gcg ctg gtg aaa ccc aca gag acc ctc aca ctg acc tgc acc ctc	148
Pro Ala Leu Val Lys Pro Thr Glu Thr Leu Thr Leu Thr Cys Thr Leu	
10 15 20	
tct ggg ttc tca ctc aac gtt agt gga atg cgt atg atc tgg gtc cgt	196
Ser Gly Phe Ser Leu Asn Val Ser Gly Met Arg Met Ile Trp Val Arg	
25 30 35 40	
cag ttc cca ggg cag gcc ctg gag tgg ctt gca cgc att gat tgg gat	244
Gln Phe Pro Gly Gln Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp	
45 50 55	
gat gag aag tac ttc act tca tct ctg agg acc agg ctc	283
Asp Glu Lys Tyr Phe Thr Ser Ser Leu Arg Thr Arg Leu	
60 65	

<210> 33
 <211> 388
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 58..387

<221> sig_peptide
<222> 58..114
<223> score 10.6
seq ILFLVAAXTGAXS/QV

<400> 33
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atg gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca nca aca ggt 105
Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Xaa Thr Gly
-15 -10 -5
gcc cwc tcc cag gtt cak ctg gwg cag tct gga rgt gag gtg aag amg 153
Ala Xaa Ser Gln Val Xaa Leu Xaa Gln Ser Gly Xaa Glu Val Lys Xaa
1 5 10
cct ggg gcc tca gtg aar gtc tcc tgc aag gcy tct ggt tac ayc tty 201
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Xaa Phe
15 20 25
amc aga tay grt atc aac tgg gtk cgw cag gcc cct gga caa ggs ctt 249
Xaa Arg Tyr Xaa Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
gag tgg atg gga tgg atc agc cct tac aat gga aat aca aat tat gca 297
Glu Trp Met Gly Trp Ile Ser Pro Tyr Asn Gly Asn Thr Asn Tyr Ala
50 55 60
cag caa ttc cag gac aga gtc acc ttg acc aca gac aca tcg acg agt 345
Gln Gln Phe Gln Asp Arg Val Thr Leu Thr Thr Asp Thr Ser Thr Ser
65 70 75
aca gca ttt ctg gag ttg agg agt ctg aaa tct gac gac acg g 388
Thr Ala Phe Leu Glu Leu Arg Ser Leu Lys Ser Asp Asp Thr
80 85 90

<210> 34
<211> 419
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 58..417

<221> sig_peptide
<222> 58..114
<223> score 10.7
seq ILFLVAAATGXHS/QV

<400> 34
atcacccaaa aaccacacccc ctccttgagg gaatccccta gatcacagct cctcacc 57
atg gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca gca aca ggt 105
Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
-15 -10 -5
gyc cac tcc cag gtt car ctg gtg cag tct gga sct gag gtg aag aag 153

Gln Xaa Leu Gln Gly Arg Val Thr Met Thr Xaa Asp Thr Ser Thr Xaa
 65 70 75
 aca gcc tac atg gaa ctg agg agc ctg mga tct gac gac acg gcc rtk 393
 Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Xaa
 80 85 90
 tat tac tgt gcg cga gag atm nta gtg gna sta tgt gat gga cag ttg 441
 Tyr Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu
 95 100 105
 ggg cca ggg aac ct 455
 Gly Pro Gly Asn
 110

 <210> 36
 <211> 373
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 58..372

 <221> sig_peptide
 <222> 58..114
 <223> score 9.5
 seq ILXLVAAXTGAHS/QG

 <400> 36
 atcacccaaa aaccacaccc ctcttgga gaatccccta gatcacagct cctcacc 57
 atg gac tgg acc tgg asc atc ctt wtw ttg gtg gca gcw rca aca ggt 105
 Met Asp Trp Thr Trp Xaa Ile Leu Xaa Leu Val Ala Ala Xaa Thr Gly
 -15 -10 -5
 gcc cac tcc cag ggt cag ywg gtg cag tct gga gct gaa gtg aag aag 153
 Ala His Ser Gln Gly Gln Xaa Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 cct ggg gcc tca gtg aag gtc tcc tgc aag gmt tct ggt tac acc ttt 201
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Tyr Thr Phe
 15 20 25
 aca tac ttt ggt gtc agt wgg ttt cgg cag gcc cct gga caa ggg ctt 249
 Thr Tyr Phe Gly Val Ser Xaa Phe Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 gar tgg atg gca tgg atc agc ggt cat aat ggt gac aca aac tat gcg 297
 Glu Trp Met Ala Trp Ile Ser Gly His Asn Gly Asp Thr Asn Tyr Ala
 50 55 60
 acg gag gat cca ggg cag agt cac cct gac cac agn cac atc cac gng 345
 Thr Glu Asp Pro Gly Gln Ser His Pro Asp His Xaa His Ile His Xaa
 65 70 75
 cac agc ctn cat gga gct gng gag ccg g 373
 His Ser Leu His Gly Ala Xaa Glu Pro
 80 85

 <210> 37
 <211> 382
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 58..381

<221> sig_peptide

<222> 58..114

<223> score 9.2

seq ILFLVAAATGAHS/QL

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atg gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca gca aca ggt 105
Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
-15 -10 -5
gcc cac tcc caa ctt cag ctg gtg cag tct gga gct gag gtg aag aag 153
Ala His Ser Gln Leu Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10
cct ggg gcc tca atg aaa gtc tcc tgc cag gct tct gat tac acc ttt 201
Pro Gly Ala Ser Met Lys Val Ser Cys Gln Ala Ser Asp Tyr Thr Phe
15 20 25
ttg aac ttt ggt atc acg tgg gtg cga cag gcc cct gga caa ggg ctt 249
Leu Asn Phe Gly Ile Thr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
gag tgg atg gga tgg atc agc ttt cac agt ggt aat aca aac tat gca 297
Glu Trp Met Gly Trp Ile Ser Phe His Ser Gly Asn Thr Asn Tyr Ala
50 55 60
gag aac ttc cag ggc aga ggc gcc att agc gca gay aca tcc acg ayt 345
Glu Asn Phe Gln Gly Arg Gly Ala Ile Ser Ala Asp Thr Ser Thr Xaa
65 70 75
acs gcy tac atc gag gtg agg agc ctc aga tct gac g 382
Thr Ala Tyr Ile Glu Val Arg Ser Leu Arg Ser Asp
80 85

<210> 38

<211> 420

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 58..420

<221> sig_peptide

<222> 58..114

<223> score 10.8

seq ILFLVAAATGAHS/QV

<400> 38

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atg gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca gca aca ggt 105

Met	Asp	Trp	Thr	Trp	Ser	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Gly		
				-15					-10					-5			
gcc	cac	tcc	cag	gtt	cag	ctg	gtg	cag	tct	gga	rst	gag	gtg	aag	aag	153	
Ala	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Xaa	Glu	Val	Lys	Lys		
		1				5				10							
cct	ggg	gcc	tca	gtg	aag	gtc	tcc	tgc	aag	rcc	tct	ggt	tac	acc	ttt	201	
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Xaa	Ser	Gly	Tyr	Thr	Phe		
	15				20				25								
acc	agt	tay	gny	atc	agc	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggw	ctt	249	
Thr	Ser	Tyr	Xaa	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu		
	30			35				40						45			
gag	tgg	atg	gga	tgg	atc	agc	rst	tac	aaw	ggt	aas	aca	gay	tat	gca	297	
Glu	Trp	Met	Gly	Trp	Ile	Ser	Xaa	Tyr	Xaa	Gly	Xaa	Thr	Asp	Tyr	Ala		
			50				55						60				
cag	aar	ttc	cag	ggc	aga	stc	acc	wtg	acc	aca	gac	aca	tcc	acg	aay	345	
Gln	Lys	Phe	Gln	Gly	Arg	Xaa	Thr	Xaa	Thr	Thr	Asp	Thr	Ser	Thr	Asn		
		65			70								75				
att	gcc	tac	atg	gas	ytg	agg	aac	ctg	aga	tct	gac	gac	acg	gcc	ttc	393	
Ile	Ala	Tyr	Met	Xaa	Leu	Arg	Asn	Leu	Arg	Ser	Asp	Asp	Thr	Ala	Phe		
		80			85							90					
tat	tac	tgt	gtg	aga	ggc	cat	ctt	gga								420	
Tyr	Tyr	Cys	Val	Arg	Gly	His	Leu	Gly									
		95			100												

<210> 39
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 52..471
 <221> sig_peptide
 <222> 52..108
 <223> score 10.8
 seq ILFLVAAATGAHS/QV

<400>	39																
acccaacaac	cacatccctc	ctcagmagcc	cccagagcac	aackcctyac	c	atg	gac									57	
					Met	Asp											
tgg	acc	tgg	agg	atc	ctc	ttt	ttg	gtg	gca	gca	gcc	aca	ggt	gcc	cac	105	
Trp	Thr	Trp	Arg	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Gly	Ala	His		
		-15					-10					-5					
tcc	cag	gtc	cag	ctt	gtg	cag	tct	ggg	gct	gag	gtg	aag	aag	cct	ggg	153	
Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly		
	1			5				10						15			
gcc	tca	gtg	aag	gtt	tcc	tgc	aag	gct	tct	gga	tac	ayc	ttc	act	ary	201	
Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Xaa	Phe	Thr	Xaa		
			20				25					30					
tmt	gct	atn	cat	tgg	gtg	cgc	cag	gcc	ccc	gga	car	agr	ctt	gag	tgg	249	
Xaa	Ala	Xaa	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Arg	Leu	Glu	Trp		
		35				40						45					


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atg ggr tgg atc aac gct gcc amt ggt wam aca awa tat tca cag aas      297
Met Gly Trp Ile Asn Ala Ala Xaa Gly Xaa Thr Xaa Tyr Ser Gln Xaa
      50                      55                      60

ttc cag grc aga gtc acc wtt acc agg gac aca tcc gcg agc aca gtc      345
Phe Gln Xaa Arg Val Thr Xaa Thr Arg Asp Thr Ser Ala Ser Thr Val
      65                      70                      75

tcc atg gag ctg agc agc ctg aga tct gaa gac acg gct gtg tat ttc      393
Ser Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
      80                      85                      90                      95

tgt gcg aga gat tgg gaa att gca gta gta cca act gct ata aac tct      441
Cys Ala Arg Asp Trp Glu Ile Ala Val Val Pro Thr Ala Ile Asn Ser
      100                      105                      110

tac ggg ttc gac cct ggg gcc agg gaa cct      471
Tyr Gly Phe Asp Pro Gly Ala Arg Glu Pro
      115                      120

<210> 40
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..427

<221> sig_peptide
<222> 83..139
<223> score 13.3
      seq LALLLAVLQGVCA/EV

<400> 40
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tcattttctg tctccacca tc atg ggg tca acc gcc atc ctc gcc ctc ctc      112
      Met Gly Ser Thr Ala Ile Leu Ala Leu Leu
                        -15                      -10

ctg gct gtt ctc caa gga gtc tgt gcc gag gtg cag ctg gtg cag tct      160
Leu Ala Val Leu Gln Gly Val Cys Ala Glu Val Gln Leu Val Gln Ser
                        -5                      1                      5

gga gca gag gtg aaa aag ccc ggg gag tct ctg aag atc tcc tgt aag      208
Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys
      10                      15                      20

ggt gtt gga tac aat ttt gcc ggc tgg tgg atc ggc tgg gtg cgc cag      256
Gly Val Gly Tyr Asn Phe Ala Gly Trp Trp Ile Gly Trp Val Arg Gln
      25                      30                      35

atg ccc ggg gaa ggc ctg gag ttg atg ggg ctc gtc tat cct ctt gac      304
Met Pro Gly Glu Gly Leu Glu Leu Met Gly Leu Val Tyr Pro Leu Asp
      40                      45                      50                      55

tct aat acc gca tat agt ccg tcc ttc aaa gac cac gtc acc atc tca      352
Ser Asn Thr Ala Tyr Ser Pro Ser Phe Lys Asp His Val Thr Ile Ser
      60                      65                      70

gcc gac agg tcc ctc agc acc gcc tac ctg cag tgg atc agc ctg aag      400
Ala Asp Arg Ser Leu Ser Thr Ala Tyr Leu Gln Trp Ile Ser Leu Lys
      75                      80                      85

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cct cgg aca ccg cca tat att act gtg tg
 Pro Arg Thr Pro Pro Tyr Ile Thr Val
 90 95

429

<210> 41
 <211> 326
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..325

<221> sig_peptide
 <222> 83..139
 <223> score 13.3
 seq LALLLAVLQGVCA/EV

<400> 41
 aaacccaggg ctccctcca cagtgaagtct ccctcactgc ccagctggga tctcagggt 60
 tcattttctg tcytccacca tc atg ggg tca rcc gcc atc ctc gcc ctc ctc 112
 Met Gly Ser Xaa Ala Ile Leu Ala Leu Leu
 -15 -10
 ctg gct gtt ctc caa gga gtc tgt gcc gag gtg cac ctg gtg cag tct 160
 Leu Ala Val Leu Gln Gly Val Cys Ala Glu Val His Leu Val Gln Ser
 -5 1 5
 ggc gca gag ctg aaa aag ccg ggg gag tct ctg acg atc tcc tgt aag 208
 Gly Ala Glu Leu Lys Lys Pro Gly Glu Ser Leu Thr Ile Ser Cys Lys
 10 15 20
 ggc tct gga tac gag ttc ggc act cac tgg atc ggc tgg gtg cgc cag 256
 Gly Ser Gly Tyr Glu Phe Gly Thr His Trp Ile Gly Trp Val Arg Gln
 25 30 35
 atg ccc ggg aaa ggt ctg gag tgg atg ggg atc atc tac cct gat gac 304
 Met Pro Gly Lys Gly Leu Glu Trp Met Gly Ile Ile Tyr Pro Asp Asp
 40 45 50 55
 tct gat acc aga tac aac ccg t 326
 Ser Asp Thr Arg Tyr Asn Pro
 60

<210> 42
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..367

<221> sig_peptide
 <222> 83..139
 <223> score 12.7
 seq LALLLAVLQGVCG/EE

004220"666E7350

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<400> 42
aaacccaggg ctccccctcca cagtgagtct ccctcaactgc ccagctggga tctcagggct      60
tcwttttctg tcctccacca tc atg ggg tca acc gcc atc ctc gcc ctc ctc      112
                        Met Gly Ser Thr Ala Ile Leu Ala Leu Leu
                        -15                               -10

ctg gca gtt ctc caa gga gtc tgt ggc gag gag cag ctg gtg cag tct      160
Leu Ala Val Leu Gln Gly Val Cys Gly Glu Glu Gln Leu Val Gln Ser
                        -5                               1                               5

gga gca gag gtg aaa aag ccc ggg gag tct ctg agg ata tcc tgt acg      208
Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Arg Ile Ser Cys Thr
                        10                               15                               20

ggg tct gga tac tcc ttt acc agt cat tgg atc ggc tgg gtg cgc cag      256
Gly Ser Gly Tyr Ser Phe Thr Ser His Trp Ile Gly Trp Val Arg Gln
                        25                               30                               35

atg ccc ggt act ggc ctg gag tgg acg gcg atc atc tat cct gat gac      304
Met Pro Gly Thr Gly Leu Glu Trp Thr Ala Ile Ile Tyr Pro Asp Asp
40                               45                               50                               55

tct gat acc aag tas agt ccg tcg ttc caa ggc caa gtc act atc tca      352
Ser Asp Thr Lys Xaa Ser Pro Ser Phe Gln Gly Gln Val Thr Ile Ser
                        60                               65                               70

gcc gac aag tcc acc aa      369
Ala Asp Lys Ser Thr
                        75

```

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<210> 43
<211> 372
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 83..370

<221> sig_peptide
<222> 83..139
<223> score 13.3
      seq LALLLAVLQGVCA/EV

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<400> 43
aaacccaggg ctccccctcca cagtgagtct ccctcaactgc ccagctggga tctcagggct      60
tcaktttctg tcytccacca tc atg ggg tca rcc gcc atc ctc gcc ctc ctc      112
                        Met Gly Ser Xaa Ala Ile Leu Ala Leu Leu
                        -15                               -10

ctg gct gtt ctc caa ggc gtc tgt gcc gag gtg cag ctg gtg cag tct      160
Leu Ala Val Leu Gln Gly Val Cys Ala Glu Val Gln Leu Val Gln Ser
                        -5                               1                               5

gga gca gag gtg aaa aag ccc ggg gag tct ctg aag atc tct tgt aag      208
Gly Ala Glu Val Lys Lys Pro Gly Glu Ser Leu Lys Ile Ser Cys Lys
                        10                               15                               20

gcc tct gga tta agc ctt atc gac tgg gtt ggc tgg gtg cgc cag aag      256
Ala Ser Gly Leu Ser Leu Ile Asp Trp Val Gly Trp Val Arg Gln Lys
                        25                               30                               35

```


<221> sig_peptide
 <222> 59..115
 <223> score 9.7
 seq ILFLVAAATSAHS/QV

<400> 45
 atcactcaac raccacwtct gtcctctaga gaaaaccctg tgagcacagc tcctcacc 58
 atg gac tgg acc tgg agg atc ctc ttc ttg gtg gca gca gct aca agt 106
 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Ser
 -15 -10 -5
 gcc cac tcc cag gtg cag ctg gtg cag tct ggg act gaa gtg agg ggg 154
 Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Thr Glu Val Arg Gly
 1 5 10
 cct ggg gcc tca gtg aag gtc tcc tgt aag gct tct gga tac acc ttc 202
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25
 gtc agt tat gat atc aac tgg gta cga cag gcc gct gga caa ggg ctt 250
 Val Ser Tyr Asp Ile Asn Trp Val Arg Gln Ala Ala Gly Gln Gly Leu
 30 35 40 45
 gag tgg atg gga tgg atg aat cct ttc agt ggt gac tca ggc ttt gca 298
 Glu Trp Met Gly Trp Met Asn Pro Phe Ser Gly Asp Ser Gly Phe Ala
 50 55 60
 cag aac ttc cag ggc aga gtc acc ttg acc agg aac tcc tcc ata ggc 346
 Gln Asn Phe Gln Gly Arg Val Thr Leu Thr Arg Asn Ser Ser Ile Gly
 65 70 75
 aca gcc tac atg gaa ctg acc agc ctc aga tct gac gac acg gcc gtc 394
 Thr Ala Tyr Met Glu Leu Thr Ser Leu Arg Ser Asp Asp Thr Ala Val
 80 85 90
 tat tac tgt gcg cga ggc cgg ggc tac act cac tac tac ttc ttc ga 441
 Tyr Tyr Cys Ala Arg Gly Arg Gly Tyr Thr His Tyr Tyr Phe Phe
 95 100 105

<210> 46
 <211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..326

<221> sig_peptide
 <222> 18..74
 <223> score 10.6
 seq TLLLLTXPSWVLS/QX

<400> 46
 gactcctgtg cccacc atg gac aca ctt tgc tmc acr ctc ctg ctg ctg 50
 Met Asp Thr Leu Cys Xaa Thr Leu Leu Leu Leu
 -15 -10
 acc ryc cct tcm tgg gtc ttg tcc cag rtc acc ytg aag gag wct ggt 98

Thr	Xaa	Pro	Ser	Trp	Val	Leu	Ser	Gln	Xaa	Thr	Leu	Lys	Glu	Xaa	Gly	
			-5					1				5				
cct	gys	ctg	gtg	raa	ccc	aca	cag	acc	ctc	acg	ctg	acc	tgc	acc	ttc	146
Pro	Xaa	Leu	Val	Xaa	Pro	Thr	Gln	Thr	Leu	Thr	Leu	Thr	Cys	Thr	Phe	
	10					15					20					
tct	ggg	ttc	tca	ctc	agg	act	agt	gga	gag	ggg	gtg	ggc	tgg	atc	cgt	194
Ser	Gly	Phe	Ser	Leu	Arg	Thr	Ser	Gly	Glu	Gly	Val	Gly	Trp	Ile	Arg	
25					30				35						40	
cag	ccc	cca	ggc	aag	gcc	ctg	gaa	tgg	ctt	gca	ctc	att	tat	tgg	gat	242
Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu	Trp	Leu	Ala	Leu	Ile	Tyr	Trp	Asp	
				45				50						55		
gat	gat	aag	cgc	tat	aga	cca	tct	ctg	aaa	acc	agg	ctc	acc	atc	acc	290
Asp	Asp	Lys	Arg	Tyr	Arg	Pro	Ser	Leu	Lys	Thr	Arg	Leu	Thr	Ile	Thr	
		60						65					70			
aag	gac	acc	tcc	aaa	aac	cag	gtg	gtc	cta	aca	atg	a				327
Lys	Asp	Thr	Ser	Lys	Asn	Gln	Val	Val	Leu	Thr	Met					
		75					80									

<210> 47
 <211> 276
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..275

<221> sig_peptide
 <222> 18..74
 <223> score 10.7
 seq TLLLLTTPSWVLS/QV

<400> 47																
gactcctgtg	ccccacc	atg	gac	aca	ctt	tgc	tac	aca	ctc	ctg	ctg	ctg				50
		Met	Asp	Thr	Leu	Cys	Tyr	Thr	Leu	Leu	Leu	Leu				
					-15						-10					
acc	acc	cct	tcc	tgg	gtc	ttg	tcc	cag	gtc	acc	ttg	aag	gag	tct	ggg	98
Thr	Thr	Pro	Ser	Trp	Val	Leu	Ser	Gln	Val	Thr	Leu	Lys	Glu	Ser	Gly	
		-5						1				5				
cct	gtg	ctg	gtg	aaa	ccc	aca	gag	acc	ctc	acg	ctg	acc	tgc	acc	gtc	146
Pro	Val	Leu	Val	Lys	Pro	Thr	Glu	Thr	Leu	Thr	Leu	Thr	Cys	Thr	Val	
	10					15					20					
tct	ggg	ttc	tca	ctc	aac	aat	gct	gga	atg	ggg	gtg	agc	tgg	gtc	cgt	194
Ser	Gly	Phe	Ser	Leu	Asn	Ala	Gly	Met	Gly	Val	Ser	Trp	Val	Arg		
25					30				35						40	
cag	ccc	cca	ggg	aag	gcc	ctg	gag	tgg	ctt	gca	cac	gag	tat	ccg	cat	242
Gln	Pro	Pro	Gly	Lys	Ala	Leu	Glu	Trp	Leu	Ala	His	Glu	Tyr	Pro	His	
				45				50						55		
gac	caa	aga	tcc	tac	aac	aca	tct	ctg	agc	ggc	c					276
Asp	Gln	Arg	Ser	Tyr	Asn	Thr	Ser	Leu	Ser	Gly						
			60					65								

<210> 48

<211> 361
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..359

<221> sig_peptide
 <222> 63..119
 <223> score 10.8
 seq ILFLVAAATGAHS/QV

<400> 48
 gagcatcacc cagcaaccac atctgtntct tagagaatcc cctgasagct ccgttcctca 60
 cc atg gac tgg acc tgg agg atc ctc ttc ttg gtg gca gca gcc acm 107
 Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr
 -15 -10 -5
 gga gcc cac tcc cag gtg crr ctg stg caa tct ggg gct gag gtg aag 155
 Gly Ala His Ser Gln Val Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys
 1 5 10
 arg cct ggg gcc tcw gtg aag gtc tcc tgy aag rct tct gga tac rcc 203
 Xaa Pro Gly Ala Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Tyr Xaa
 15 20 25
 ttc asc gkc tac tat ata cac tgg sts cgm cag gcc cct gga caa ggg 251
 Phe Xaa Xaa Tyr Tyr Ile His Trp Xaa Arg Gln Ala Pro Gly Gln Gly
 30 35 40
 ctt gag tgg atg gdw cgg ats aat cct aag gat ggt gcc ccc aac tat 299
 Leu Glu Trp Met Gly Arg Xaa Asn Pro Lys Asp Gly Ala Pro Asn Tyr
 45 50 55 60
 gca ccg aac ttt gaa ggc agg gtc acc atg acc agg gac acg tcc atc 347
 Ala Pro Asn Phe Glu Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile
 65 70 75
 acc aca gcg tac at 361
 Thr Thr Ala Tyr
 80

<210> 49
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..419

<221> sig_peptide
 <222> 63..119
 <223> score 10.8
 seq ILFLXAAATGAHS/QV

<400> 49

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gagcatcacc cagcaaccac atctgtcttc kagagaatcc cctgasagct ccgttcctca      60
cc atg gac tgg acc tgg agg atc ctc ttc ttg gyg gca gca gcc aca      107
  Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Xaa Ala Ala Ala Thr
        -15                -10                -5
gga gcc cac tcc cag gtg cgg ctg gtg car tct ggg gct gag gtg aag      155
Gly Ala His Ser Gln Val Arg Leu Val Gln Ser Gly Ala Glu Val Lys
        1                5                10
aar cct ggg gcc tca gtg aag gtc tcc tgc aag rct tck gga tac rcc      203
Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Tyr Xaa
        15                20                25
ytic acc ggc yay twt mtr cac tgg ctg cgm cag gcc cct gga caa ggs      251
Xaa Thr Gly Xaa Xaa Xaa His Trp Leu Arg Gln Ala Pro Gly Gln Gly
        30                35                40
ctt gag tgg atg gga ygg atc aat ccg agg act ggt ggc act aag tcc      299
Leu Glu Trp Met Gly Xaa Ile Asn Pro Arg Thr Gly Gly Thr Lys Ser
        45                50                55                60
gca cag aag twt agg gac ttc ctc acc atg acc agg gat gcg ccc atn      347
Ala Gln Lys Xaa Arg Asp Phe Leu Thr Met Thr Arg Asp Ala Pro Xaa
        65                70                75
aac acg gcc tas atg gaa ttg act gga ctw aga kct gas gaa acg gcc      395
Asn Thr Ala Xaa Met Glu Leu Thr Gly Leu Arg Xaa Xaa Glu Thr Ala
        80                85                90
act tat ttc tgt gcg aga gak caa      419
Thr Tyr Phe Cys Ala Arg Xaa Gln
        95                100

```

<210> 50
 <211> 359
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..358

<221> sig_peptide
 <222> 62..118
 <223> score 9.6
 seq FLFVVAATGVQS/QX

```

<400> 50
agcatcacat aacaaccasa ttctctctct aaagaagccc ctgggagcac agctcatcac      60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt      109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
        -15                -10                -5
gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
        1                5                10
cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc      205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe
        15                20                25
agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg      253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala

```


004220" 666560

```

30          35          40          45
gac gag tcc acg acc aca gtc tac atg cag ctg agc agc cta aca tct      301
Asp Glu Ser Thr Thr Thr Val Tyr Met Gln Leu Ser Ser Leu Thr Ser
          50          55          60
gaa gac acg gcc gtc tat tac tgt gcg aga gag gcg cgg gaa tgg cag      349
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ala Arg Glu Trp Gln
          65          70          75
tgg ctg gtg t
Trp Leu Val
          80

```

<210> 51
 <211> 367
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..367

<221> sig_peptide
 <222> 62..118
 <223> score 9.6
 seq FLFVVAATGVQS/QX

```

<400> 51
agcatcacat aacaaccasa ttctctctct aaagaagccc ctgggagcac agctcatcac      60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt      109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
          -15          -10          -5
gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
          1          5          10
cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc      205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe
          15          20          25
agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg      253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala
          30          35          40          45
gac gag tcc acg acc aca gtc tac atg cag ctg agc agc cta aca tct      301
Asp Glu Ser Thr Thr Thr Val Tyr Met Gln Leu Ser Ser Leu Thr Ser
          50          55          60
gaa gac acg gcc gtc tat tac tgt gcg aga gat tcc gct tcg gtg gtg      349
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Ala Ser Val Val
          65          70          75
atg gcc aat gga ctg ggc
Met Ala Asn Gly Leu Gly
          80

```

<210> 52
 <211> 492
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..490

<221> sig_peptide
 <222> 62..118
 <223> score 9.9
 seq FLFVVAAATGVQS/QV

<400> 52
 agcatcacat aacaaccaca ttcctcctct aaagaagccc ctgggagcac agctcatcac 60
 c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
 -15 -10 -5
 gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 157
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 cct ggg tcc tcg gtg amr gtc kcc tgy aag gct tct gga ggc asc ytc 205
 Pro Gly Ser Ser Val Xaa Val Xaa Cys Lys Ala Ser Gly Gly Xaa Xaa
 15 20 25
 agm agy tat ggt atc agc tgg gtg cga cag gcc cct gga caa ggg ctt 253
 Xaa Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 gag tgg atg gga ggg atc ayc ccn ntc ttw ggn aca kca aac wac gca 301
 Glu Trp Met Gly Gly Ile Xaa Pro Xaa Xaa Gly Thr Xaa Asn Xaa Ala
 50 55 60
 cag aag ttc cag ggc aga gtc acg att acc gcg gac gaa tcc acg aac 349
 Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn
 65 70 75
 aca gtc tat atg gag ctc aac agc ctg ara tct gam gam acg gcc gtc 397
 Thr Val Tyr Met Glu Leu Asn Ser Leu Xaa Ser Xaa Xaa Thr Ala Val
 80 85 90
 tat tas wyt gcg agt cgt gtc gtg gct gga gga ctg gtc ttc tac gct 445
 Tyr Xaa Xaa Ala Ser Arg Val Val Ala Gly Gly Leu Val Phe Tyr Ala
 95 100 105
 atr gac gwc tgg ggc car gga cca cgg tca ccg tct cct cag ctt cc 492
 Xaa Asp Xaa Trp Gly Gln Gly Pro Arg Ser Pro Ser Pro Gln Leu
 110 115 120

<210> 53
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..424
 <221> sig_peptide
 <222> 62..118
 <223> score 9.9
 seq FLFVVAAATGVQS/QV

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<400> 53
agcatcacat aacaaccaca ttcctcctct aaagaagccc ctgggagcac agctcatcac      60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt      109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
        -15                -10                -5

gtc cag tcc cag gts cag ctg gtg cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
        1                5                10

cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc      205
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
        15                20                25

anc asc tat rct wtc agc tgg gtg cga cag gcc cct gga caa ggm ctt      253
Xaa Xaa Tyr Xaa Xaa Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        30                35                40                45

gag tgg atg gga ggg atc atc cct atc ttt ggt ama aca aac tac gca      301
Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Xaa Thr Asn Tyr Ala
        50                55                60

cag aag ttc cag ggs aga gtc acg atg acc gcg gac gaa tcc aca acc      349
Gln Lys Phe Gln Gly Arg Val Thr Met Thr Ala Asp Glu Ser Thr Thr
        65                70                75

aca gtc tac atg gaa ctg agc cgc ctg aca tct gag gac acg gcc gtg      397
Thr Val Tyr Met Glu Leu Ser Arg Leu Thr Ser Glu Asp Thr Ala Val
        80                85                90

tat tac tgt gcg aga gac att aac aga g                                425
Tyr Tyr Cys Ala Arg Asp Ile Asn Arg
        95                100

```

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<210> 54
<211> 411
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> 62..409

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<221> sig_peptide
<222> 62..118
<223> score 9.6
      seq FLFVVAATGVQS/QX

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```

<400> 54
agcatcacat aacaaccasa ttcctcctct aaagaagccc ctgggagcac agctcatcac      60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt      109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
        -15                -10                -5

gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
        1                5                10

cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc      205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe

```

15	20	25	
agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg			253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala			
30	35	40	45
gac gaa tcc acg aac aca gtc tat atg gag ctc aac agc ctg ara tct			301
Asp Glu Ser Thr Asn Thr Val Tyr Met Glu Leu Asn Ser Leu Xaa Ser			
	50	55	60
gam gam acg gcc gtc tat tas wyt gcg agt cgt gtc gtg gct gga gga			349
Xaa Xaa Thr Ala Val Tyr Xaa Xaa Ala Ser Arg Val Val Ala Gly Gly			
	65	70	75
ctg gtc ttc tac gct atr gac gwc tgg ggc car gga cca cgg tca ccg			397
Leu Val Phe Tyr Ala Xaa Asp Xaa Trp Gly Gln Gly Pro Arg Ser Pro			
	80	85	90
tct cct cag ctt cc			411
Ser Pro Gln Leu			
95			

<210> 55
 <211> 407
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..406
 <221> sig_peptide
 <222> 62..118
 <223> score 9.6
 seq FLFVVAATGVQS/QX

<400> 55	
agcatcacat aacaaccasa ttcctcctct aaagaagccc ctgggagcac agctcatcac	60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt	109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly	
	-15 -10 -5
gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag	157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys	
	1 5 10
cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc	205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe	
	15 20 25
agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg	253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala	
	30 35 40 45
gac gra tcc acg asc aca rcc tac atg gag ctg agc agc ctg aga tct	301
Asp Xaa Ser Thr Xaa Thr Xaa Tyr Met Glu Leu Ser Ser Leu Arg Ser	
	50 55 60
gag gac acg gcc stg tat tac tgt gcg aga ggt caa gcc ccc ggt agg	349
Glu Asp Thr Ala Xaa Tyr Tyr Cys Ala Arg Gly Gln Ala Pro Gly Arg	
	65 70 75
gta gta gta cca ctt ttc ctc tgg ggc cag gga acc tgg tca ccg tct	397
Val Val Val Pro Leu Phe Leu Trp Gly Gln Gly Thr Trp Ser Pro Ser	

80
cct cag cct c
Pro Gln Pro
95

85

90

407

<210> 56
<211> 448
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..448

<221> sig_peptide
<222> 62..118
<223> score 9.9
seq FLFVVAATGVQS/QV

<400> 56
agcatcacat aacaaccaca ttcctcctct aaagaagccc ctgggagcac agctcatcac 60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
-15 -10 -5
gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 157
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10
cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc 205
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
15 20 25
agc aac tat gct rtc anc tgg gtg cga cag gcc cct gga caa ggg ctt 253
Ser Asn Tyr Ala Xaa Xaa Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
gag tgg atg gga rgr atc acc ccn atc ytt ggn acr gca aas tac sca 301
Glu Trp Met Gly Xaa Ile Thr Pro Ile Xaa Gly Thr Ala Xaa Tyr Xaa
50 55 60
cag aar ttc cag ggc aga atc acc att acc gcg gac gaa tcc acc agt 349
Gln Lys Phe Gln Gly Arg Ile Thr Ile Thr Ala Asp Glu Ser Thr Ser
65 70 75
aca gcg tac atg gaa ctg act ggt ctg aaa tct gac gac acg gcc gtc 397
Thr Ala Tyr Met Glu Leu Thr Gly Leu Lys Ser Asp Asp Thr Ala Val
80 85 90
tat tac tgt gcg aga gat tcc gct tcg gtg gtg atg gcc aat gga ctg 445
Tyr Tyr Cys Ala Arg Asp Ser Ala Ser Val Val Met Ala Asn Gly Leu
95 100 105
ggc 448
Gly
110

<210> 57
<211> 441
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 62..439
 <221> sig_peptide
 <222> 62..118
 <223> score 9.9
 seq FLFVVAATGVQS/QV

<400> 57
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 c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
 -15 -10 -5
 gtc cag tcc cag gtg car ctg gtg cag tct ggg gct gag gtg aag aag 157
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc 205
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
 15 20 25
 aac asy tat gct atc agc tgg gtg cga cag gcc cct rsa caa ggg ctt 253
 Asn Xaa Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Xaa Gln Gly Leu
 30 35 40 45
 gag tgg atg gga ggg rtc acc cca atc ttt ggg aca sca mac tac gca 301
 Glu Trp Met Gly Gly Xaa Thr Pro Ile Phe Gly Thr Xaa Xaa Tyr Ala
 50 55 60
 cag aas ttc cag ggc aga nts asg att acc gcg gac gaa tcc acg agc 349
 Gln Xaa Phe Gln Gly Arg Xaa Xaa Ile Thr Ala Asp Glu Ser Thr Ser
 65 70 75
 aga gtc tac atg gag ttg agc agc ccg aga tct gag gac acg gcc gtc 397
 Arg Val Tyr Met Glu Leu Ser Ser Pro Arg Ser Glu Asp Thr Ala Val
 80 85 90
 tat tac tgt gtg agc tcc tcc aca gag tgt ggt cgt gat tgc ta 441
 Tyr Tyr Cys Val Ser Ser Ser Thr Glu Cys Gly Arg Asp Cys
 95 100 105

<210> 58
 <211> 344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..343
 <221> sig_peptide
 <222> 62..118
 <223> score 9.6
 seq FLFVVAATGVQS/QX

<400> 58

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c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt      109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
        -15                -10                -5

gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
        1                5                10

cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc      205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe
        15                20                25

agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg      253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala
        30                35                40                45

gac gaa tcc aca acc aca gtc tac atg gaa ctg agc cgc ctg aca tct      301
Asp Glu Ser Thr Thr Thr Val Tyr Met Glu Leu Ser Arg Leu Thr Ser
        50                55                60

gag gac acg gcc gtg tat tac tgt gcg aga gac att aac aga g      344
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ile Asn Arg
        65                70                75

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<210> 59
 <211> 360
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..358

<221> sig_peptide
 <222> 62..118
 <223> score 9.6
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c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt      109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
        -15                -10                -5

gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
        1                5                10

cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc      205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe
        15                20                25

agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg      253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala
        30                35                40                45

gac gaa tcc acg agc aga gtc tac atg gag ttg agc agc ccg aga tct      301
Asp Glu Ser Thr Ser Arg Val Tyr Met Glu Leu Ser Ser Pro Arg Ser
        50                55                60

gag gac acg gcc gtc tat tac tgt gtg agc tcc tcc aca gag tgt ggt      349
Glu Asp Thr Ala Val Tyr Tyr Cys Val Ser Ser Ser Thr Glu Cys Gly

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65 70 75 360
 cgt gat tgc ta
 Arg Asp Cys
 80

<210> 60
 <211> 374
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..373

<221> sig_peptide
 <222> 62..118
 <223> score 8.3
 seq FLFVVAATXVQS/QX

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 c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca grt 109
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Xaa
 -15 -10 -5
 gtc cag tcc cag gkc cag ctg gtg cag tct ggg kct gag gtg aag arg 157
 Val Gln Ser Gln Xaa Gln Leu Val Gln Ser Gly Xaa Glu Val Lys Xaa
 1 5 10
 cct ggg tcc tcg gtg aag gtc tcc tgy aag rct tct ggr ggc ayc ytc 205
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Xaa Ser Gly Gly Xaa Xaa
 15 20 25
 agy asy aat gsc atc ass tgg gtg cga cag gcc cct gga caa ggg ctt 253
 Ser Xaa Asn Xaa Ile Xaa Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 gag tgg atg ggr agg atc atc ccc atg gtt gaa aaa gcg gac acc gca 301
 Glu Trp Met Gly Arg Ile Ile Pro Met Val Glu Lys Ala Asp Thr Ala
 50 55 60
 cag aag ttc cag ggc aga ctc act att agt aca nkn cta tcg acg agc 349
 Gln Lys Phe Gln Gly Arg Leu Thr Ile Ser Thr Xaa Leu Ser Thr Ser
 65 70 75
 asa gsc ttc atg gaa ctg agc agt c 374
 Xaa Xaa Phe Met Glu Leu Ser Ser
 80 85

<210> 61
 <211> 440
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..439

<221> sig_peptide

<222> 62..118
 <223> score 9.4
 seq FLFVVAAATGVQS/QX

<400> 61
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 c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
 -15 -10 -5
 gtc cag tcc cag gks sas ctg gtg cag tct ggg gct gag gtg aag aag 157
 Val Gln Ser Gln Xaa Xaa Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 cct ggs tcc tcg gtg aar rtc tcc tgc aag gct tcy ggr ggc ayc ytc 205
 Pro Gly Ser Ser Val Lys Xaa Ser Cys Lys Ala Ser Gly Gly Xaa Xaa
 15 20 25
 mgc rac sat ggs atc agc tgg gtg cga cag gcc cct gga cag ggc ctg 253
 Xaa Xaa Xaa Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 gag tgg atg gga gac atc atc cct att tat gat ctg gta aac tat gca 301
 Glu Trp Met Gly Asp Ile Ile Pro Ile Tyr Asp Leu Val Asn Tyr Ala
 50 55 60
 cag aaa ttc cag ggc aga gtc acg att acc gcg cac aaa tcc aca acc 349
 Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala His Lys Ser Thr Thr
 65 70 75
 aca gcc tac atg gag gtg att agc ctg acc tct gaa gac acg gcc gtg 397
 Thr Ala Tyr Met Glu Val Ile Ser Leu Thr Ser Glu Asp Thr Ala Val
 80 85 90
 tat tac tgt gcg aga gag gcg cgg gaa tgg cag tgg ctg gtg t 440
 Tyr Tyr Cys Ala Arg Glu Ala Arg Glu Trp Gln Trp Leu Val
 95 100 105

<210> 62
 <211> 448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..448
 <221> sig_peptide
 <222> 62..118
 <223> score 9.4
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 c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
 -15 -10 -5
 gtc cag tcc cag gks sas ctg gtg cag tct ggg gct gag gtg aag aag 157
 Val Gln Ser Gln Xaa Xaa Leu Val Gln Ser Gly Ala Glu Val Lys Lys

	1	5	10	
cct ggs tcc tcg gtg aar rtc tcc tgc aag gct tcy ggr ggc ayc ytc				205
Pro Gly Ser Ser Val Lys Xaa Ser Cys Lys Ala Ser Gly Gly Xaa Xaa				
15	20	25		
mgc rac sat ggs atc agc tgg gtg cga cag gcc cct gga cag ggc ctg				253
Xaa Xaa Xaa Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu				
30	35	40	45	
gag tgg atg gga gac atc atc cct att tat gat ctg gta aac tat gca				301
Glu Trp Met Gly Asp Ile Ile Pro Ile Tyr Asp Leu Val Asn Tyr Ala				
50	55	60		
cag aaa ttc cag ggc aga gtc acg att acc gcg cac aaa tcc aca acc				349
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala His Lys Ser Thr Thr				
65	70	75		
aca gcc tac atg gag gtg att agc ctg acc tct gaa gac acg gcc gtg				397
Thr Ala Tyr Met Glu Val Ile Ser Leu Thr Ser Glu Asp Thr Ala Val				
80	85	90		
tat tac tgt gcg aga gat tcc gct tgc gtg gtg atg gcc aat gga ctg				445
Tyr Tyr Cys Ala Arg Asp Ser Ala Ser Val Val Met Ala Asn Gly Leu				
95	100	105		
ggc				448
Gly				
110				
<210> 63				
<211> 425				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> 62..424				
<221> sig_peptide				
<222> 62..118				
<223> score 9.4				
seq FLFVVAAATGVQS/QX				
<400> 63				
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c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt				109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly				
-15	-10	-5		
gtc cag tcc cag gks sas ctg gtg cag tct ggg gct gag gtg aag aag				157
Val Gln Ser Gln Xaa Xaa Leu Val Gln Ser Gly Ala Glu Val Lys Lys				
1	5	10		
cct ggs tcc tcg gtg aar rtc tcc tgc aag gct tcy ggr ggc ayc ytc				205
Pro Gly Ser Ser Val Lys Xaa Ser Cys Lys Ala Ser Gly Gly Xaa Xaa				
15	20	25		
mgc rac sat ggs atc agc tgg gtg cga cag gcc cct gga cag ggc ctg				253
Xaa Xaa Xaa Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu				
30	35	40	45	
gag tgg atg gga gac atc atc cct att tat gat ctg gta aac tat gca				301
Glu Trp Met Gly Asp Ile Ile Pro Ile Tyr Asp Leu Val Asn Tyr Ala				

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          50          55          60
cag aaa ttc cag ggc aga gtc acg att acc gcg cac aaa tcc aca acc 349
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala His Lys Ser Thr Thr
          65          70          75
aca gcc tac atg gag gtg att agc ctg acc tct gaa gac acg gcc gtg 397
Thr Ala Tyr Met Glu Val Ile Ser Leu Thr Ser Glu Asp Thr Ala Val
          80          85          90
tat tac tgt gcg aga gac att aac aga g 425
Tyr Tyr Cys Ala Arg Asp Ile Asn Arg
          95          100

<210> 64
<211> 488
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..487

<221> sig_peptide
<222> 62..118
<223> score 9.4
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c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
          -15          -10          -5
gtc cag tcc cag gks sas ctg gtg cag tct ggg gct gag gtg aag aag 157
Val Gln Ser Gln Xaa Xaa Leu Val Gln Ser Gly Ala Glu Val Lys Lys
          1          5          10
cct ggs tcc tcg gtg aar rtc tcc tgc aag gct tcy ggr ggc ayc ytc 205
Pro Gly Ser Ser Val Lys Xaa Ser Cys Lys Ala Ser Gly Gly Xaa Xaa
          15          20          25
mgc rac sat ggs atc agc tgg gtg cga cag gcc cct gga cag ggc ctg 253
Xaa Xaa Xaa Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
          30          35          40          45
gag tgg atg gga gac atc atc cct att tat gat ctg gta aac tat gca 301
Glu Trp Met Gly Asp Ile Ile Pro Ile Tyr Asp Leu Val Asn Tyr Ala
          50          55          60
cag aaa ttc cag ggc aga gtc acg att acc gcg cac aaa tcc aca acc 349
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala His Lys Ser Thr Thr
          65          70          75
aca gcc tac atg gag gtg att agc ctg acc tct gaa gac acg gcc gtg 397
Thr Ala Tyr Met Glu Val Ile Ser Leu Thr Ser Glu Asp Thr Ala Val
          80          85          90
tat tac tgt gcg aga ggt caa gcc ccc ggt agg gta gta gta cca ctt 445
Tyr Tyr Cys Ala Arg Gly Gln Ala Pro Gly Arg Val Val Val Pro Leu
          95          100          105
ttc ctc tgg ggc cag gga acc tgg tca ccg tct cct cag cct c 488
Phe Leu Trp Gly Gln Gly Thr Trp Ser Pro Ser Pro Gln Pro

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110

115

120

<210> 65
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..370

<221> sig_peptide
 <222> 62..118
 <223> score 9.9
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 c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt 109
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
 -15 -10 -5
 gtc cag tcc cag gts cag ctg gtk cag tct ggg kct gar gtg aag aag 157
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Xaa Glu Val Lys Lys
 1 5 10
 cct ggg tcc tcg gtg agg gtc tcc tgc aag gct tct ggr ggc ayc ytc 205
 Pro Gly Ser Ser Val Arg Val Ser Cys Lys Ala Ser Gly Gly Xaa Xaa
 15 20 25
 arc ayc wct gcw gtc asc tgg gtg cga cag gcc cct gga caa gga ctt 253
 Xaa Xaa Xaa Ala Val Xaa Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 gag tgg gtg ggg agg ctc atc nnt gtt ctt aat gtg gca cac tat gca 301
 Glu Trp Val Gly Arg Leu Ile Xaa Val Leu Asn Val Ala His Tyr Ala
 50 55 60
 cag aaa tnr cag gac aga gtc acc att acg gcg gac aag tcc acg anc 349
 Gln Lys Xaa Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Xaa
 65 70 75
 aca gcc tac atg gaa ttg cgc 370
 Thr Ala Tyr Met Glu Leu Arg
 80

<210> 66
 <211> 235
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..235

<221> sig_peptide
 <222> 62..118
 <223> score 10.2
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 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Xaa Gly
 -15 -10 -5
 gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 157
 Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 1 5 10
 cct ggg tcc tcg gtg aar rtc tcc tgc gag gct act gga gtc gat gtg 205
 Pro Gly Ser Ser Val Lys Xaa Ser Cys Glu Ala Thr Gly Val Asp Val
 15 20 25
 aaa aaa tat ggt ttt agt tgg gtg aga cag 235
 Lys Lys Tyr Gly Phe Ser Trp Val Arg Gln
 30 35

<210> 67
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..424
 <221> sig_peptide
 <222> 62..118
 <223> score 9.3
 seq FLFVVAATGVQX/QX

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 c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gcw gck aca ggt 109
 Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
 -15 -10 -5
 gtc cag tsy cag gyc cas ctg gtg cag tct rgg gct gag ktg aag aag 157
 Val Gln Xaa Gln Xaa Xaa Leu Val Gln Ser Xaa Ala Glu Xaa Lys Lys
 1 5 10
 cct sgg tcc tca gtg agc gtc tcc tgc aag act tct gga gac acc ttc 205
 Pro Xaa Ser Ser Val Ser Val Ser Cys Lys Thr Ser Gly Asp Thr Phe
 15 20 25
 agg agg ttt act atg agt tgg gtg cga cag gcc cct gga caa gga ctt 253
 Arg Arg Phe Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 gag tgg atg gga agg gtc atc cct atc ctt ggt tct cca acc tac gcc 301
 Glu Trp Met Gly Arg Val Ile Pro Ile Leu Gly Ser Pro Thr Tyr Ala
 50 55 60
 cag aag ttc cag ggc aga gtc acc att acc gcg gac gag tcc acg acc 349
 Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr
 65 70 75
 aca gtc tac atg cag ctg agc agc cta aca tct gaa gac acg gcc gtc 397
 Thr Val Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val

80 85 90 425
tat tac tgt gcg aga gac att aac aga g
Tyr Tyr Cys Ala Arg Asp Ile Asn Arg
95 100

<210> 68
<211> 488
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..487

<221> sig_peptide
<222> 62..118
<223> score 9.3
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Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
-15 -10 -5
gtc cag tsy cag gyc cas ctg gtg cag tct rgg gct gag ktg aag aag 157
Val Gln Xaa Gln Xaa Xaa Leu Val Gln Ser Xaa Ala Glu Xaa Lys Lys
1 5 10
cct sgg tcc tca gtg agc gtc tcc tgc aag act tct gga gac acc ttc 205
Pro Xaa Ser Ser Val Ser Val Ser Cys Lys Thr Ser Gly Asp Thr Phe
15 20 25
agg agg ttt act atg agt tgg gtg cga cag gcc cct gga caa gga ctt 253
Arg Arg Phe Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
gag tgg atg gga agg gtc atc cct atc ctt ggt tct cca acc tac gcc 301
Glu Trp Met Gly Arg Val Ile Pro Ile Leu Gly Ser Pro Thr Tyr Ala
50 55 60
cag aag ttc cag ggc aga gtc acc att acc gcg gac gag tcc acg acc 349
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr
65 70 75
aca gtc tac atg cag ctg agc agc cta aca tct gaa gac acg gcc gtc 397
Thr Val Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
80 85 90
tat tac tgt gcg aga ggt caa gcc ccc ggt agg gta gta gta cca ctt 445
Tyr Tyr Cys Ala Arg Gly Gln Ala Pro Gly Arg Val Val Val Pro Leu
95 100 105
ttc ctc tgg ggc cag gga acc tgg tca ccg tct cct cag cct c 488
Phe Leu Trp Gly Gln Gly Thr Trp Ser Pro Ser Pro Gln Pro
110 115 120

<210> 69
<211> 344
<212> DNA
<213> Homo sapiens

004220 666400

<220>

<221> CDS

<222> 62..343

<221> sig_peptide

<222> 62..118

<223> score 9.6

seq FLFVVAATGVQS/QX

<400> 69

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  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
      -15                -10                -5
gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
      1                5                10
cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc      205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe
      15                20                25
agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg      253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala
      30                35                40                45
cac aaa tcc aca acc aca gcc tac atg gag gtg att agc ctg acc tct      301
His Lys Ser Thr Thr Thr Ala Tyr Met Glu Val Ile Ser Leu Thr Ser
      50                55                60
gaa gac acg gcc gtg tat tac tgt gcg aga gac att aac aga g      344
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ile Asn Arg
      65                70                75

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<210> 70

<211> 359

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 62..358

<221> sig_peptide

<222> 62..118

<223> score 9.6

seq FLFVVAATGVQS/QX

<400> 70

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  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
      -15                -10                -5
gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys

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	1	5	10	
cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc				205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe				
15	20	25		
agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg				253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala				
30	35	40	45	
cac aaa tcc aca acc aca gcc tac atg gag gtg att agc ctg acc tct				301
His Lys Ser Thr Thr Thr Ala Tyr Met Glu Val Ile Ser Leu Thr Ser				
50	55	60		
gaa gac acg gcc gtg tat tac tgt gcg aga gag gcg cgg gaa tgg cag				349
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ala Arg Glu Trp Gln				
65	70	75		
tgg ctg gtg t				359
Trp Leu Val				
80				

<210> 71
 <211> 301
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..301
 <221> sig_peptide
 <222> 62..118
 <223> score 9.9
 seq FLFVVAATGVQS/QV

<400> 71	
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c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt	109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly	
-15	-10
gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag	157
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
1	5
cct ggg tcc tcg gtg aag gtc tcc tgc aag gck tct gga gnc acc ttc	205
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Xaa Thr Phe	
15	20
rgc amc tat sct ntc agc tgg gtg cga cag gcc cct gga caa ggs ctt	253
Xaa Xaa Tyr Xaa Xaa Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30	35
sag tgg atg gga agg atc rwm cct ttg gat gga ata gtc aag tac gca	301
Xaa Trp Met Gly Arg Ile Xaa Pro Leu Asp Gly Ile Val Lys Tyr Ala	
50	55
	60

<210> 72
 <211> 352
 <212> DNA
 <213> Homo sapiens

004220"566E560

<220>

<221> CDS

<222> 62..352

<221> sig_peptide

<222> 62..118

<223> score 9.4

seq FLFVVAATGVQS/QX

<400> 72

agcatcacat arcaaccaga ttcctcctct raagaagccc ctgggagcac agctcatcac 60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gcw aca ggt 109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly

-15 -10 -5
gtc cag tcc cag gkm cag ctg gwr cag tct ggg gcy gag gtg aag aag 157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys

1 5 10
cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct ggr ggc mtc ytc 205
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Xaa Xaa

15 20 25
acg asc atg cta tca rct ggg tgc gac agg ccc ctg gac aag gac ttg 253
Thr Xaa Met Leu Ser Xaa Gly Cys Asp Arg Pro Leu Asp Lys Asp Leu

30 35 40 45
agt ggc tgg gag gct aca tcc cta ttt ttg ata cac caa att acc cac 301
Ser Gly Trp Glu Ala Thr Ser Leu Phe Leu Ile His Gln Ile Thr His

50 55 60
cgg agt tcc agg aca gag tcg cgg ttt cgg tgg aca aat cca cta aca 349
Arg Ser Ser Arg Thr Glu Ser Arg Phe Arg Trp Thr Asn Pro Leu Thr

65 70 75
cag 352
Gln

<210> 73

<211> 440

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 62..439

<221> sig_peptide

<222> 62..118

<223> score 9.3

seq FLFVVAATGVQX/QX

<400> 73

agcatcacat aacaaccaga ttcctcctct aaagaagccc ctgggagcac agctcatcac 60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gcw gck aca ggt 109
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly

-15

-10

-5

004220"666E7560

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gtc cag tsy cag gyc cas ctg gtg cag tct rgg gct gag ktg aag aag      157
Val Gln Xaa Gln Xaa Xaa Leu Val Gln Ser Xaa Ala Glu Xaa Lys Lys
      1              5              10
cct sgg tcc tca gtg agc gtc tcc tgc aag act tct gga gac acc ttc      205
Pro Xaa Ser Ser Val Ser Val Ser Cys Lys Thr Ser Gly Asp Thr Phe
      15              20              25
agg agg ttt act atg agt tgg gtg cga cag gcc cct gga caa gga ctt      253
Arg Arg Phe Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      30              35              40              45
gag tgg atg gga agg gtc atc cct atc ctt ggt tct cca acc tac gcc      301
Glu Trp Met Gly Arg Val Ile Pro Ile Leu Gly Ser Pro Thr Tyr Ala
      50              55              60
cag aag ttc cag ggc aga gtc acc att acc gcg gac gag tcc acg acc      349
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr
      65              70              75
aca gtc tac atg cag ctg agc agc cta aca tct gaa gac acg gcc gtc      397
Thr Val Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
      80              85              90
tat tac tgt gcg aga gag gcg cgg gaa tgg cag tgg ctg gtg t          440
Tyr Tyr Cys Ala Arg Glu Ala Arg Glu Trp Gln Trp Leu Val
      95              100              105

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<210> 74
 <211> 448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..448
 <221> sig_peptide
 <222> 62..118
 <223> score 9.3
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<400> 74
agcatcacat aacaaccaga ttccctcctct aaagaagccc ctgggagcac agctcatcac      60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gcw gck aca ggt      109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
      -15              -10              -5
gtc cag tsy cag gyc cas ctg gtg cag tct rgg gct gag ktg aag aag      157
Val Gln Xaa Gln Xaa Xaa Leu Val Gln Ser Xaa Ala Glu Xaa Lys Lys
      1              5              10
cct sgg tcc tca gtg agc gtc tcc tgc aag act tct gga gac acc ttc      205
Pro Xaa Ser Ser Val Ser Val Ser Cys Lys Thr Ser Gly Asp Thr Phe
      15              20              25
agg agg ttt act atg agt tgg gtg cga cag gcc cct gga caa gga ctt      253
Arg Arg Phe Thr Met Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      30              35              40              45
gag tgg atg gga agg gtc atc cct atc ctt ggt tct cca acc tac gcc      301
Glu Trp Met Gly Arg Val Ile Pro Ile Leu Gly Ser Pro Thr Tyr Ala
      50              55              60

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cag aag ttc cag ggc aga gtc acc att acc gcg gac gag tcc acg acc      349
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Thr
      65                      70                      75

aca gtc tac atg cag ctg agc agc cta aca tct gaa gac acg gcc gtc      397
Thr Val Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
      80                      85                      90

tat tac tgt gcg aga gat tcc gct tcg gtg gtg atg gcc aat gga ctg      445
Tyr Tyr Cys Ala Arg Asp Ser Ala Ser Val Val Met Ala Asn Gly Leu
      95                      100                      105

ggc      448
Gly
110

<210> 75
<211> 367
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..367

<221> sig_peptide
<222> 62..118
<223> score 9.6
      seq FLFVVAATGVQS/QX

<400> 75
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c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt      109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
      -15                      -10                      -5

gtc cag tcc cag rts cag ctr str cag tct ggg gct gag gtg aag aag      157
Val Gln Ser Gln Xaa Gln Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
      1                      5                      10

cct ggg tcc tcg gtg aag gtc tcc tgc gag gct tct gga tac acc ttc      205
Pro Gly Ser Ser Val Lys Val Ser Cys Glu Ala Ser Gly Tyr Thr Phe
      15                      20                      25

agc aac tat gct gtc agc tgg ttc cag ggc aga gtc acg att acc gcg      253
Ser Asn Tyr Ala Val Ser Trp Phe Gln Gly Arg Val Thr Ile Thr Ala
      30                      35                      40                      45

cac aaa tcc aca acc aca gcc tac atg gag gtg att agc ctg acc tct      301
His Lys Ser Thr Thr Thr Ala Tyr Met Glu Val Ile Ser Leu Thr Ser
      50                      55                      60

gaa gac acg gcc gtg tat tac tgt gcg aga gat tcc gct tcg gtg gtg      349
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Ala Ser Val Val
      65                      70                      75

atg gcc aat gga ctg ggc      367
Met Ala Asn Gly Leu Gly
      80

<210> 76
<211> 476

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..474

<221> sig_peptide
<222> 73..138
<223> score 15.3
seq LLLLLTHLPLALG/SP

<400> 76
aggcgctgct cactcctccc cactcctctcc ctctgtccct ctgtccctct gaccctgcac 60
tgtcccagca cc atg gga ccc acc tca ggt ccc agc ctg ctg ctc ctg cta 111
Met Gly Pro Thr Ser Gly Pro Ser Leu Leu Leu Leu Leu
-20 -15 -10
cta acc cac ctc ccc ctg gct ctg ggg agt ccc atg tac tct atc atc 159
Leu Thr His Leu Pro Leu Ala Leu Gly Ser Pro Met Tyr Ser Ile Ile
-5 1 5
acc ccc aac atc ttg cgg ctg gag agc gag gag acc atg gtg ctg gag 207
Thr Pro Asn Ile Leu Arg Leu Glu Ser Glu Glu Thr Met Val Leu Glu
10 15 20
gcc cac gac gcg caa ggg gat gtt cca gtc act gtt act gtc cac gac 255
Ala His Asp Ala Gln Gly Asp Val Pro Val Thr Val Thr Val His Asp
25 30 35
ttc cca ggc aaa aaa cta gtg ctg tcc agt gag aag act gtg ctg acc 303
Phe Pro Gly Lys Lys Leu Val Leu Ser Ser Glu Lys Thr Val Leu Thr
40 45 50 55
cct gcc acc aac cac atg ggc aac gtc acc ttc acg atc cca gcc aac 351
Pro Ala Thr Asn His Met Gly Asn Val Thr Phe Thr Ile Pro Ala Asn
60 65 70
agg gag ttc aag tca gaa aag ggg cnc aac aag ttc gtg acc gtg cag 399
Arg Glu Phe Lys Ser Glu Lys Gly Xaa Asn Lys Phe Val Thr Val Gln
75 80 85
gcc acc ttc ggg acc caa gtg gtg gag aag gtg gtg ctg gtc agc ctg 447
Ala Thr Phe Gly Thr Gln Val Val Glu Lys Val Val Leu Val Ser Leu
90 95 100
cag agc ggg tam ctc ttc atc cag aca ga 476
Gln Ser Gly Xaa Leu Phe Ile Gln Thr
105 110

<210> 77
<211> 476
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..474

<221> sig_peptide
<222> 310..381

<223> score 5.4
seq VYLTIFFLLSSLS/SY

<400> 77
aaaacgtcct gtagacacct ggaccgcgag ggcgcggttc cctgcttctc tagggggcca 60
gacacggcga cggatcttga cgctttttcc tccccacaga caaaaaactt ggactttcgc 120
cgaaagtggg acaaagatga atatgagarr ctcgccgaga agaggctcac ggaagagaga 180
gaaaagaaag atggaaaacc agtgcagcct gtcaagcgag agctttttacg gcatagggac 240
tacaaggtgg acttggaatc caagcttggg aagacaattg tcattaccaa gacaaccct 300
caatctgag atg gga gga tat tac tgc aat gtc tgt ccc att gtc tat ctg 351
Met Gly Gly Tyr Tyr Cys Asn Val Cys Pro Ile Val Tyr Leu
-20 -15

acc atc ttt ctc tta ctg tcc tct ttg tct agc tat ctg gcc tat ctg 399
Thr Ile Phe Leu Leu Leu Ser Ser Leu Ser Ser Tyr Leu Ala Tyr Leu
-10 -5 1 5
tcg atc cat ctt cgt gtc tgt ctt cag ccc cca cct gtt tgt cca tct 447
Ser Ile His Leu Arg Val Cys Leu Gln Pro Pro Pro Val Cys Pro Ser
10 15 20
gtc caa tta cct gtg act ctg tgc atc tt 476
Val Gln Leu Pro Val Thr Leu Cys Ile
25 30

<210> 78
<211> 390
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 151..390

<221> sig_peptide
<222> 151..273
<223> score 4
seq GLPFLPLLSTTLC/PF

<400> 78
tttttttttt ttccgccatc ttttgtcttt ccgtggagct gtcgccatga aggtcgagct 60
gtgcagtttt agcgggtaca agatctaccc cggacacggg aggcgctacg ccaggaccga 120
cgggaagggt ttccagtttc ttaatgcgaa atg cga gtc ggc ttt cct ttc caa 174
Met Arg Val Gly Phe Pro Phe Gln
-40 -35
gag gaa tcc tcg gca gat aaa ctg gac tgt cct cta cag aag gaa gca 222
Glu Glu Ser Ser Ala Asp Lys Leu Asp Cys Pro Leu Gln Lys Glu Ala
-30 -25 -20
cat agg gcc ctg gga ctt ccc ttt ctc cct ctc ctc tcc acc acc ctc 270
His Arg Ala Leu Gly Leu Pro Phe Leu Pro Leu Leu Ser Thr Thr Leu
-15 -10 -5
tgc ccc ttt ggc agc ccc ggt ctt tgg cgg ccc cag ctc agc tgc acg 318
Cys Pro Phe Gly Ser Pro Gly Leu Trp Arg Pro Gln Leu Ser Cys Thr
1 5 10 15
agg gtt ccc tgc atg ctc tgg gca ctg tcg gct aat cag aga gta gca 366

Arg Val Pro Cys Met Leu Trp Ala Leu Ser Ala Asn Gln Arg Val Ala
 20 25 30
 tcc ctt caa tca cag ccc ttc ccc
 Ser Leu Gln Ser Gln Pro Phe Pro
 35

390

<210> 79
 <211> 1206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..1205

<221> sig_peptide
 <222> 30..77
 <223> score 10.1
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<400> 79
 ggcgtgtgga acctgacgga actgccacg atg ctg cca ctt tgg act ctt tca 53
 Met Leu Pro Leu Trp Thr Leu Ser
 -15 -10
 ctg ctg ctg gga gca gta gca gga aaa gaa gtt tgc tac gaa aga ctc 101
 Leu Leu Leu Gly Ala Val Ala Gly Lys Glu Val Cys Tyr Glu Arg Leu
 -5 1 5
 ggc tgc ttc agt gat gac tcc cca tgg tca gga att acg gaa aga ccc 149
 Gly Cys Phe Ser Asp Asp Ser Pro Trp Ser Gly Ile Thr Glu Arg Pro
 10 15 20
 ctc cat ata ttg cct tgg tct cca aaa gat gtc aac acc cgc ttc ctc 197
 Leu His Ile Leu Pro Trp Ser Pro Lys Asp Val Asn Thr Arg Phe Leu
 25 30 35 40
 cta tat act aat gag aac cca aac aac ttt caa gaa gtt gcc gca gat 245
 Leu Tyr Thr Asn Glu Asn Pro Asn Asn Phe Gln Glu Val Ala Ala Asp
 45 50 55
 tca tca agc atc agt ggc tcc aat ttc aaa aca aat aga aaa act cgc 293
 Ser Ser Ser Ile Ser Gly Ser Asn Phe Lys Thr Asn Arg Lys Thr Arg
 60 65 70
 ttt att att cga ttc ata gac aag gga gaa gaa aac tgg ctg gcc aat 341
 Phe Ile Ile Arg Phe Ile Asp Lys Gly Glu Glu Asn Trp Leu Ala Asn
 75 80 85
 gtg tgc aag aat ctg ttc aag gtg gaa agt gtg aac tgt atc tgt gtg 389
 Val Cys Lys Asn Leu Phe Lys Val Glu Ser Val Asn Cys Ile Cys Val
 90 95 100
 gac tgg aaa ggt ggc tcc cga act gga tac aca caa gcc tcg cag aac 437
 Asp Trp Lys Gly Gly Ser Arg Thr Gly Tyr Thr Gln Ala Ser Gln Asn
 105 110 115 120
 atc agg atc gtg gga gca gaa gtg gca tat ttt gtt gaa ttt ctt cag 485
 Ile Arg Ile Val Gly Ala Glu Val Ala Tyr Phe Val Glu Phe Leu Gln
 125 130 135
 tcg gcg ttc ggt tac tca cct tcc aay gtg cat gtc att ggc cac agc 533
 Ser Ala Phe Gly Tyr Ser Pro Ser Asn Val His Val Ile Gly His Ser

	140		145		150	
ctg ggt gcc cac gct gct ggg gag gct gga agg aga acc aat ggg acc						581
Leu Gly Ala His Ala Ala Gly Glu Ala Gly Arg Arg Thr Asn Gly Thr						
	155		160		165	
att gga cgc atc aca ggg ttg gac cca gca gaa cct tgc ttt cag ggc						629
Ile Gly Arg Ile Thr Gly Leu Asp Pro Ala Glu Pro Cys Phe Gln Gly						
	170		175		180	
aca cct gaa tta gtc cga ttg gac ccc agc gat gcc aaa ttt gtg gat						677
Thr Pro Glu Leu Val Arg Leu Asp Pro Ser Asp Ala Lys Phe Val Asp						
	185		190		195	200
gta att cac acg gat ggt gcc ccc ata gtc ccc aat ttg ggg ttt gga						725
Val Ile His Thr Asp Gly Ala Pro Ile Val Pro Asn Leu Gly Phe Gly						
	205		210		215	
atg agc caa gtc gtg ggc cac cta gat ttc ttt cca aat gga gga gtg						773
Met Ser Gln Val Val Gly His Leu Asp Phe Phe Pro Asn Gly Gly Val						
	220		225		230	
gaa atg cct gga tgt aaa aag aac att ctc tct cag att gtg gac ata						821
Glu Met Pro Gly Cys Lys Lys Asn Ile Leu Ser Gln Ile Val Asp Ile						
	235		240		245	
gac gga atc tgg gaa ggg act cga gac ttt gcg gcc tgt aat cac tta						869
Asp Gly Ile Trp Glu Gly Thr Arg Asp Phe Ala Cys Asn His Leu						
	250		255		260	
aga agc tac aaa tat tac act gat agc atc gtc aac cct gat ggc ttt						917
Arg Ser Tyr Lys Tyr Thr Asp Ser Ile Val Asn Pro Asp Gly Phe						
	265		270		275	280
gct gga ttc ccc tgt gcc tct tac aac gtc ttc act gca aac aag tgt						965
Ala Gly Phe Pro Cys Ala Ser Tyr Asn Val Phe Thr Ala Asn Lys Cys						
	285		290		295	
ttc cct tgt cca agt gga ggc tgc mca cag atg ggt cac tat gct gat						1013
Phe Pro Cys Pro Ser Gly Gly Cys Xaa Gln Met Gly His Tyr Ala Asp						
	300		305		310	
aga tat cct ggg aaa aca aat gat gtg ggc cag aaa ttt tat cta gac						1061
Arg Tyr Pro Gly Lys Thr Asn Asp Val Gly Gln Lys Phe Tyr Leu Asp						
	315		320		325	
act ggt gat gcc agt aat ttt gca cgt tgg agg tat aag gta tct gtc						1109
Thr Gly Asp Ala Ser Asn Phe Ala Arg Trp Arg Tyr Lys Val Ser Val						
	330		335		340	
aca ctg tct gga aaa aag gtt aca gga cac ata cta gtt tct ttg ttc						1157
Thr Leu Ser Gly Lys Lys Val Thr Gly His Ile Leu Val Ser Leu Phe						
	345		350		355	360
gga aat aaa gga aac tct aag cag tat gaa att ttc aag ggc aat kga t						1206
Gly Asn Lys Gly Asn Ser Lys Gln Tyr Glu Ile Phe Lys Gly Asn Xaa						
	365		370		375	

<210> 80

<211> 570

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 37..570

<221> sig_peptide

COPIES OF

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<210> 81
<211> 400
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 37..90
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<223> score 11.4
seq WTLGLLLLLATVRG/KE

<400> 81
aacctgctgg gctgtgagtg gaagctctgg tgcagc atg atg ctg ccc cct tgg 54
Met Met Leu Pro Pro Trp
-15
acc ctc ggc ctt ctc ctg ctg gcc aca gtc aga gga aaa gag gtc tgc 102
Thr Leu Gly Leu Leu Leu Leu Ala Thr Val Arg Gly Lys Glu Val Cys
-10 -5 1
tac gga caa ctt ggc tgc ttt tct gat gaa aaa cca tgg gca gga acc 150
Tyr Gly Gln Leu Gly Cys Phe Ser Asp Glu Lys Pro Trp Ala Gly Thr
5 10 15 20
ctt cag cga cct gta aaa tta ctt ccc tgg tcc ccc gag gac att gac 198
Leu Gln Arg Pro Val Lys Leu Leu Pro Trp Ser Pro Glu Asp Ile Asp
25 30 35
acc cgc ttt ctt ctg tac aca aat gaa aat cca aac aac ttc cag gat 246
Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro Asn Asn Phe Gln Asp
40 45 50
gaa cct gag gag gtt cgg ttg gat cca tct gac gcc gtg ttt gtg gat 294
Glu Pro Glu Glu Val Arg Leu Asp Pro Ser Asp Ala Val Phe Val Asp
55 60 65
gtg att cac aca gat tct tct ccc ata gtt cct tcc cta ggt ttc gga 342
Val Ile His Thr Asp Ser Ser Pro Ile Val Pro Ser Leu Gly Phe Gly
70 75 80
atg agc caa aag gtg ggc cat ctg gat ttc ttt cca aat gga gga aag 390
Met Ser Gln Lys Val Gly His Leu Asp Phe Phe Pro Asn Gly Gly Lys
85 90 95 100
gaa atg ccc g 400
Glu Met Pro

<210> 82
<211> 612
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 277..612

<221> sig_peptide
<222> 277..354
<223> score 4.8
seq LIVLLGQFVSIKA/QE

<400> 82
agaccgttgc ttggcagaca ctggatggtt atgagcctgm acaagctgaa aaggggcagg 60
maaagaagtg gaggcagcat tcttcctatt taaagctgca tcgcttgaaa aaagttttcg 120
cagactgtgc tggagctggt gctgaaaaag ggggtttgca gaggctgccc tggggctggt 180
gctgaaagaa gagccacag ctgacttcat ggtgctacaa taacctcaga atctactttt 240
cactctcagg agaaccacaca tgtctaatat ttagac atg atg gca aac tgg gcg 294
Met Met Ala Asn Trp Ala

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                                -25
gaa gca aga cct ctc ctc att ctt att gtt tta tta ggg caa ttt gtc      342
Glu Ala Arg Pro Leu Leu Ile Leu Ile Val Leu Leu Gly Gln Phe Val
-20                                -15                                -10                                -5
tca ata aaa gcc cag gaa gaa gac gag gat gaa gga tat ggt gaa gaa      390
Ser Ile Lys Ala Gln Glu Glu Asp Glu Asp Glu Gly Tyr Gly Glu Glu
                                1                                5                                10
ata gcc tgc act cag aat ggc cag atg tac tta aac agg gac att tgg      438
Ile Ala Cys Thr Gln Asn Gly Gln Met Tyr Leu Asn Arg Asp Ile Trp
                                15                                20                                25
aaa cct gcc cct tgt cag atc tgt gtc tgt gac aat gga gcc att ctc      486
Lys Pro Ala Pro Cys Gln Ile Cys Val Cys Asp Asn Gly Ala Ile Leu
                                30                                35                                40
tgt gay aag ata gaa tgc cag gat gtg ctg gac tgt gcc gac cct gta      534
Cys Asp Lys Ile Glu Cys Gln Asp Val Leu Asp Cys Ala Asp Pro Val
45                                50                                55                                60
acg ccc cct ggg gaa tgc tgt cct gtc tgt tca caa aca cct gga ggt      582
Thr Pro Pro Gly Glu Cys Cys Pro Val Cys Ser Gln Thr Pro Gly Gly
                                65                                70                                75
ggc aat aca aat ttt ggt aga gga aga aag      612
Gly Asn Thr Asn Phe Gly Arg Gly Arg Lys
                                80                                85

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<210> 83
 <211> 612
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 340..612

<221> sig_peptide
 <222> 340..396
 <223> score 7.2
 seq LIWTLFFLGTAVS/LQ

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<400> 83
actatttgtg gccggcgtgg tggaaggaca cagtmgggtt ctcacccccg ccccccgctc      60
ctcgctccca tcccagtncc atcaaaacga acccgggcca gcgcaaggat ctccgagttg      120
cgagtgtgct gaggctggga ctgtcactca ttctccgata agcgcgtgaa cgcagctcgg      180
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ccctaggtct gtcgctcagc cgcgctccac actcgctgca gggggggggg gcacagaatt      300
taccgcggca agaacatccc tcccagccag cagattaca atg ctg caa act aag      354
                                Met Leu Gln Thr Lys
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gat ctc atc tgg act ttg ttt ttc ctg gga act gca gtt tct ctg cag      402
Asp Leu Ile Trp Thr Leu Phe Phe Leu Gly Thr Ala Val Ser Leu Gln
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gtg gat att gtt ccc agc cag ggg gag atc agc gtt gga gag tcc aaa      450
Val Asp Ile Val Pro Ser Gln Gly Glu Ile Ser Val Gly Glu Ser Lys
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ttc ttc tta tgc caa gtg gca gga gat gcc aaa gat aaa gac atc tcc      498

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Phe	Phe	Leu	Cys	Gln	Val	Ala	Gly	Asp	Ala	Lys	Asp	Lys	Asp	Ile	Ser	
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Trp	Phe	Ser	Pro	Asn	Gly	Glu	Lys	Leu	Thr	Pro	Asn	Gln	Gln	Arg	Ile	
35				40				45						50		
tca	gtg	gtg	tgg	aat	gat	gat	tcc	tcc	tcc	acc	ctc	acc	atc	tat	aac	594
Ser	Val	Val	Trp	Asn	Asp	Asp	Ser	Ser	Ser	Thr	Leu	Thr	Ile	Tyr	Asn	
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gcc	aac	atc	gac	gac	gcc											612
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Trp	Glu	Leu	Val	Ala	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Tyr	Leu	Phe	Trp		
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ccc	aag	aga	agg	tgc	cct	ggt	gcc	aag	tac	ccc	aag	agc	ctc	ctg	tcc		155
Pro	Lys	Arg	Arg	Cys	Pro	Gly	Ala	Lys	Tyr	Pro	Lys	Ser	Leu	Leu	Ser		
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ctg	ccc	ctg	gtg	ggc	agc	ctg	cca	ttc	ctc	ccc	aga	cay	ggc	cat	atg		203
Leu	Pro	Leu	Val	Gly	Ser	Leu	Pro	Phe	Leu	Pro	Arg	His	Gly	His	Met		
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cat	aac	aac	ttc	ttc	aag	ctg	cag	aaa	aaa	tat	ggc	ccc	atc	tat	tgc		251
His	Asn	Asn	Phe	Phe	Lys	Leu	Gln	Lys	Lys	Tyr	Gly	Pro	Ile	Tyr	Ser		
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gtt	cgt	atg	ggc	acc	aag	act	aca	gtg	att	gtc	ggc	cac	cac	cag	ctg		299
Val	Arg	Met	Gly	Thr	Lys	Thr	Thr	Val	Ile	Val	Gly	His	His	Gln	Leu		
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gcc	aag	gag	gtg	ctt	att	aag	aag	ggc	aag	gac	ttc	tct	ggg	cgg	cct		347
Ala	Lys	Glu	Val	Leu	Ile	Lys	Lys	Gly	Lys	Asp	Phe	Ser	Gly	Arg	Pro		
			70					75					80				
caa	atg	gca	act	cta	gac	atc	gcg	tcc	aac	aac	cgt	aag	ggg	atc	gcc		395
Gln	Met	Ala	Thr	Leu	Asp	Ile	Ala	Ser	Asn	Asn	Arg	Lys	Gly	Ile	Ala		
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ttc	gct	gac	tct	ggc	gca	nac	tgg	cag	ctg	cat	cga	agg	ctg	gcg	atg		443
Phe	Ala	Asp	Ser	Gly	Ala	Xaa	Trp	Gln	Leu	His	Arg	Arg	Leu	Ala	Met		

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Met Arg Leu Ala Val Leu
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ttc tcg ggg gcc ctg ctg ggg cta ctg gca gcc cag ggg aca ggg aat 161
Phe Ser Gly Ala Leu Leu Gly Leu Leu Ala Ala Gln Gly Thr Gly Asn
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Asp Cys Pro His Lys Lys Ser Ala Thr Leu Leu Pro Ser Phe Thr Val
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aca ccc acg gtt aca gag agc act gga aca acc agc cac agg act acc 257
Thr Pro Thr Val Thr Glu Ser Thr Gly Thr Thr Ser His Arg Thr Thr
25 30 35
aag agc cac aaa acc acc act cac agg aca acc acc aca ggc acc acc 305
Lys Ser His Lys Thr Thr Thr His Arg Thr Thr Thr Thr Gly Thr Thr
40 45 50
agc cac gga ccc acg act gcc act cac aac ccc acc acc acc agc cat 353
Ser His Gly Pro Thr Thr Ala Thr His Asn Pro Thr Thr Thr Ser His
55 60 65 70
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Gly Asn Val Thr Val His Pro Thr Ser Asn Ser Thr Ala Thr
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<221> sig_peptide

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 Arg Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu Ala
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 Leu Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp Glu
 1 5 10 15
 cag gct cag gac tat ctc aag aga ttt tat ctc tat gac tca gaa aca 200
 Gln Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu Thr
 20 25 30
 aaa aat gcc aac agt tta gaa gcc aaa ctc aag gag atg caa aaa ttc 248
 Lys Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys Phe
 35 40 45
 ttt ggc cta cct ata act gga atg tta aac tcc crc gtc ata gaa ata 296
 Phe Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Xaa Val Ile Glu Ile
 50 55 60
 atg cag aag ccc aga tgt gga gtg cca gat gtt gca gaa tac tca cta 344
 Met Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser Leu
 65 70 75 80
 ttt cca aat agc cca aaa tgg act tcc aaa gtg gtc acc tac agg atc 392
 Phe Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg Ile
 85 90 95
 gta tca tat act cga gac tta ccg cat att aca gtg gat cga tta gtg 440
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 100 105 110
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 Ser Lys Ala Leu Asn Met
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 <213> Homo sapiens

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 <222> 89..451

<221> sig_peptide
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Ser Lys Met Met Leu Met Ser Thr Ala Thr Ala Phe Tyr Arg Leu Thr
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Arg Lys Val Phe Ala Asn Pro Glu Asp Cys Val Ala Phe Gly Lys Gly
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gaa aat gcc aag aag tat ctt cga aca gat gac aga gta gaa cgt gta 304
Glu Asn Ala Lys Lys Tyr Leu Arg Thr Asp Asp Arg Val Glu Arg Val
25 30 35
cgc aga gcc cac ctg aat gac ctt gaa aat att att cca ttt ctt gga 352
Arg Arg Ala His Leu Asn Asp Leu Glu Asn Ile Ile Pro Phe Leu Gly
40 45 50
att ggc ctc ctg tat tcc ttg agt ggt ccc gac ccc tct aca gcc atc 400
Ile Gly Leu Leu Tyr Ser Leu Ser Gly Pro Asp Pro Ser Thr Ala Ile
55 60 65
ctg cac ttc aga cta ttt gtc gga gca cgg atc tac cac acc att gca 448
Leu His Phe Arg Leu Phe Val Gly Ala Arg Ile Tyr His Thr Ile Ala
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tat t 452
Tyr

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<221> sig_peptide
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gggagcctgg gtgtgcgtgt ggagtccgga ctggtgggag acgatcgcg atg aac acg 118
Met Asn Thr
-25
gtg ctg tcg cgg gcg aac tca ctg ttc gcc ttc tcg ctg agc gtg atg 166
Val Leu Ser Arg Ala Asn Ser Leu Phe Ala Phe Ser Leu Ser Val Met
-20 -15 -10
gcg gcg ctc acc ttc ggc tgc ttc atc acc acc gcc ttc aaa gac agg 214
Ala Ala Leu Thr Phe Gly Cys Phe Ile Thr Thr Ala Phe Lys Asp Arg
-5 1 5 10
agc gtc ccg gtg cgg ctg cac gtc tcg cgr atc atg cta aaa aat gta 262
Ser Val Pro Val Arg Leu His Val Ser Arg Ile Met Leu Lys Asn Val

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15 20 25 276
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Glu Asp Phe Thr
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<210> 89
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<212> DNA
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<222> 394..633

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acaagagaca atcattacca tatgatctaa tgtgggtgtc agccggattg tgttcattga 180
gggaaacctt attttttaac tgtgctatgg agtagaagca ggaggttttc aacctagtca 240
cagagcagca cctacccctt cctcctttcc acacctgcaa actcttttac ttgggctgaa 300
tatttagtgt aattacatct cagctttgag ggctcctgtg gcaaattccc ggattaaaag 360
gttcacctggt tgtgaaaata catgagataa atc atg aag gcc act atc atc ctc 414
Met Lys Ala Thr Ile Ile Leu
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Leu Leu Leu Ala Gln Val Ser Trp Ala Gly Pro Phe Gln Gln Arg Gly
-5 1 5
tta ttt gac ttt atg cta gaa gat gag gct tct ggg ata ggc cca gaa 510
Leu Phe Asp Phe Met Leu Glu Asp Glu Ala Ser Gly Ile Gly Pro Glu
10 15 20
gtt cct gat gac cgc gac ttc gag ccc tcc cta ggc cca gtg tgc ccc 558
Val Pro Asp Asp Arg Asp Phe Glu Pro Ser Leu Gly Pro Val Cys Pro
25 30 35
ttc cgc tgt caa tgc cat ctt cga gtg gtc cag tgt tct gat ttg ggt 606
Phe Arg Cys Gln Cys His Leu Arg Val Val Gln Cys Ser Asp Leu Gly
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<210> 90
<211> 526
<212> DNA
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<222> 257..526

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 tgggagcaga gaagaggag aaagcagcat cttgcctgga tgagccaggg gacacagaag 180
 agaagccac tatctcattt aatctttaca actctcttgc aaggttccct gggtgtgaaa 240
 atacatgaga taaatc atg aag gcc act atc atc ctc ctt ctg ctt gca caa 292
 Met Lys Ala Thr Ile Ile Leu Leu Leu Leu Ala Gln
 -15 -10 -5
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 Val Ser Trp Ala Gly Pro Phe Gln Gln Arg Gly Leu Phe Asp Phe Met
 1 5 10
 cta gaa gat gag gct tct ggg ata ggc cca gaa gtt cct gat gac cgc 388
 Leu Glu Asp Glu Ala Ser Gly Ile Gly Pro Glu Val Pro Asp Asp Arg
 15 20 25
 gac ttc gag ccc tcc cta ggc cca gtg tgc ccc ttc cgc tgt caa tgc 436
 Asp Phe Glu Pro Ser Leu Gly Pro Val Cys Pro Phe Arg Cys Gln Cys
 30 35 40
 cat ctt cga gtg gtc cag tgt tct gat ttg ggt ctg gac aaa gtg cca 484
 His Leu Arg Val Val Gln Cys Ser Asp Leu Gly Leu Asp Lys Val Pro
 45 50 55 60
 aag gat ctt ccc cct gac aca act ctg cta gac ctg caa aac 526
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<221> sig_peptide
 <222> 69..143
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 Tyr Val Leu Leu Leu Ala Phe Cys Ala Cys Ala Val Gly Leu Ile Ala
 -10 -5 1 5

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Val Gly Val Gly Ala Gln Leu Val Leu Ser Gln Thr Ile Ile Gln Gly	
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gct acc cct ggc tct ctg ttg cca gtg gtc atc atc gca gtg ggt gtc	254
Ala Thr Pro Gly Ser Leu Leu Pro Val Val Ile Ile Ala Val Gly Val	
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Phe Leu Phe Leu Val Ala Phe Val Gly Cys Cys Gly Ala Cys Lys Glu	
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Asn Tyr Cys Leu Met Ile Thr Phe Ala Ile Phe Leu Ser Leu Ile Met	
55 60 65	
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Leu Val Glu Val Ala Ala Ala Ile Ala Gly Tyr Val Phe Arg Asp Lys	
70 75 80 85	
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Val Met Ser Glu Phe Asn Asn Asn Phe Arg Gln Gln Met Glu Asn Tyr	
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Pro Lys Asn Asn His Thr Ala Ser Ile Leu Asp Arg Met Gln Ala Asp	
105 110 115	
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Phe Lys Cys Cys Gly Ala Ala Asn Tyr Thr Asp Trp Glu Lys Ile Pro	
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Ser Met Ser Lys Asn Arg Val Pro Asp Ser Cys Cys Ile Asn Val Thr	
135 140 145	
gtg ggc tgt ggg att aat ttc aac gag aag gcg atc cat aag gag ggc	638
Val Gly Cys Gly Ile Asn Phe Asn Glu Lys Ala Ile His Lys Glu Gly	
150 155 160 165	
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<221> sig_peptide
 <222> 69..143
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Tyr Val Leu Leu Leu Ala Phe Cys Ala Cys Ala Val Gly Leu Ile Ala	
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Ala Thr Pro Gly Ser Leu Leu Pro Val Val Ile Ile Ala Val Gly Val	
25 30 35	
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Phe Leu Phe Leu Val Ala Phe Val Gly Cys Cys Gly Pro Phe Gln Thr	
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<210> 93
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 317..490

<221> sig_peptide
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cactaaaatg ttctatctga agcaagggga agtgtccaaa ttatagttca caaaatacct	180
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aaagggcttt ttcaaaa atg tcc tgt act cac tcc tct tct aac ctg ggt aag	352
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Phe Ser Val His Arg Glu Tyr Arg Val Leu Xaa Leu Cys Asn Ser Arg	
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Val Ser Phe Thr Arg Xaa His Val Lys Arg Pro Pro Xaa Arg Leu Cys	
1 5 10	
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 <211> 539
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 41..538
 <221> sig_peptide
 <222> 41..139
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 Glu Arg Asn Met Lys Val Leu Leu Ala Ala Ala Leu Ile Ala Gly Ser
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 Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe Asp Leu Arg Ile Gly
 5 10 15 20
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 Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu Phe Gly Lys Thr Val
 25 30 35
 cca aaa aca gtg gat aat ttt gtg gcc tta gct aca gga gag aaa gga 295
 Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala Thr Gly Glu Lys Gly
 40 45 50
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 Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val Ile Lys Asp Phe Met
 55 60 65
 atc cag ggc gga gac ttc acc agg gga gat ggc aca gga gga aag agc 391
 Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly Thr Gly Gly Lys Ser
 70 75 80
 atc tac ggt gag cgc ttc ccc gat gag aac ttc aaa ctg aag cac tac 439
 Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe Lys Leu Lys His Tyr
 85 90 95 100
 ggg cct ggc tgg gtg agc atg gcc aac gca ggc aaa aga cac cca ncc 487
 Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly Lys Arg His Pro Xaa
 105 110 115
 ggc tcc cca agt tcy tca tca cga cag tma aag aca gcc tgg cta gat 535
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gaaaacagca acaagctgag ctgctgtgac agaggggaac aag atg gcg gcg ccg 235
Met Ala Ala Pro
-30
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Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu Pro Pro Leu Leu
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ctg ctg acc atg gcc ttg gcc gga ggt tcg ggg acc gct tcg gct gaa 331
Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr Ala Ser Ala Glu
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Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu Glu Glu Leu Tyr
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gca tgt cag aga ggt tgc agg ctg ttt tca att tgt cag ttt gtg gat 475
Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys Gln Phe Val Asp
40 45 50
gat gga att gac tta aat cga act aaa ttg gaa tgt gaa tct gca tgt 523
Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys Glu Ser Ala Cys
55 60 65
aca gaa gca tat tcc caa tct gat gag caa tat gct tgc cat ctt ggt 571
Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly
70 75 80 85
tgc cag aat cag ctg cca ttc gct gaa ctg aga caa gaa caa ctt atg 619
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tc 621

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tgcctagcta gaggatctct gctcctgctc tccctcctcc aggtgacccc agcc atg 177
Met
agg acc ctc gcc atc ctt gct gcc att ctc cct ggg wgg gcc cct gca 225
Arg Thr Leu Ala Ile Leu Ala Ala Ile Leu Pro Gly Xaa Ala Pro Ala
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Gly Pro Arg Leu Ser His Ser Xaa Gln Glu Leu Ile Glu Val Ala Ala
1 5 10 15
gcc ccg gag cag att gca gcg gac atc cca gaa gtg gtt tgt ttc cct 321
Ala Pro Glu Gln Ile Ala Ala Asp Ile Pro Glu Val Val Cys Phe Pro
20 25 30
tgc atg gga cga aag ctt ggc tcc aaa gca tcc agg ctc aag gaa aaa 369
Cys Met Gly Arg Lys Leu Gly Ser Lys Ala Ser Arg Leu Lys Glu Lys
35 40 45
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His Gly Leu Leu Leu Gln Asn Thr Ser Val His Cys Arg Arg Thr Ser
50 55 60
cta tgg aac ctg cat cta cca ggg aag act ctg ggc att ctg ctg ctg 465
Leu Trp Asn Leu His Leu Pro Gly Lys Thr Leu Gly Ile Leu Leu Leu
65 70 75 80
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85 90

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Met Ser Val Pro Thr Met Ala Trp Met Met Leu Leu Leu Gly Leu Leu
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Ala Tyr Gly Ser Gly Xaa Asp Ser Gln Thr Val Val Thr Gln Glu Pro
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Ser	Phe	Ser	Val	Ser	Pro	Gly	Xaa	Thr	Val	Thr	Leu	Thr	Cys	Gly	Leu	
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Xaa	Ser	Gly	Ser	Val	Ser	Thr	Xaa	Xaa	Xaa	Pro	Ser	Trp	Tyr	Gln	Gln	
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Thr	Pro	Gly	Gln	Xaa	Pro	Arg	Thr	Leu	Ile	Tyr	Asn	Thr	Asn	Thr	Arg	
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tct	tct	ggg	gtc	cct	gat	cgc	ttc	tct	ggc	tcc	atc	ctt	ggg	aac	aaa	345
Ser	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ile	Leu	Gly	Asn	Lys	
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Ala	Ala															

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cct	ctc	tgg	ctc	act	ctc	ctc	act	ctt	tgc	ata	ggg	tct	gtg	gtt	tct	104
Pro	Leu	Trp	Leu	Thr	Leu	Leu	Thr	Leu	Cys	Ile	Gly	Ser	Val	Val	Ser	
	-15					-10				-5						
tct	gag	ctg	act	can	gac	cct	gct	gtg	tct	gtg	gcc	ttg	gga	cag	aca	152
Ser	Glu	Leu	Thr	Xaa	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln	Thr	
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gtc	agg	atc	aca	tgc	car	gga	gac	agm	ctc	asa	nac	tat	tmt	gca	agc	200
Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Xaa	Leu	Xaa	Xaa	Tyr	Xaa	Ala	Ser	
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Trp	Xaa	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Xaa	Leu	Val	Xaa	Tyr	Xaa	
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arr	rac	nns	cgg	ccc	tya	ggg	atc	cca	gac	cga	ttc	tct	ggc	tcc	agc	296
Xaa	Xaa	Xaa	Arg	Pro	Xaa	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Ser	
	50					55			60							
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Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu	Asp	
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Glu	Ala	Asp	Tyr	Xaa	Cys	Asn	Ser	Arg	Asp	Ser	Ser	Gly	His	His	Leu	
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Val Phe

399

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tgctgtttct tagggacacg gctgacttcc agat atg acc atg tat ttg tgg ctt 175
Met Thr Met Tyr Leu Trp Leu
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aaa ctc ttg gca ttt ggc ttt gcc ttt ctg gac aca gaa gta ttt gtg 223
Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val
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Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Asp Xaa Tyr Leu Asn Ala
10 15 20
tct gaa aca acc act ctg agc cct tct gga agc gct gtc att tca acc 319
Ser Glu Thr Thr Thr Leu Ser Pro Ser Gly Ser Ala Val Ile Ser Thr
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Pro Arg Gly Thr Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Leu Leu
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Arg Ala Val Leu Ala Val Pro Leu Glu Arg Gly Ala Pro Asn Lys Glu
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Glu Thr Pro Ala Thr Glu Ser Pro Asp Thr Gly Leu Tyr Tyr His Arg
                                15                                20                                25
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Tyr Leu Gln Glu Val Ile Asp Val Leu Glu Thr Asp Gly His Phe Arg
                                30                                35                                40
gag aag ctg cag gct gcc aat gcg gag gac atc aag agc ggg aag ctg 356
Glu Lys Leu Gln Ala Ala Asn Ala Glu Asp Ile Lys Ser Gly Lys Leu
45                                50                                55
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Ser Arg Glu Leu Asp Phe Val Ser His His Val Arg Thr Lys Leu Asp
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gag ctc aag cga cag gag gtg tca cgg ctg cgg atg ctg ctc aag gcc 452
Glu Leu Lys Arg Gln Glu Val Ser Arg Leu Arg Met Leu Leu Lys Ala
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accccgaggt tttcttctct gggaataggg ggcaaagggt gaggagagga gaaagaaatc 180
gctcgaaatc tgctcggtcc ccggcagccg ccgcttcccc tttgacgttt tggtagcccg 240
tgcgcatgcg cctcacatta gaattactgc actgggcaga ctaagttgga tctcctctct 300
tcaagtgaac cctcaattcc atcaaaaact aaaggg atg tgg aga gtg cgg aaa 354
                                Met Trp Arg Val Arg Lys
                                -20
arg ggc tac ttt ggg att tgg tcc ttc ccc tta ata atc gcc gct gtc 402
Xaa Gly Tyr Phe Gly Ile Trp Ser Phe Pro Leu Ile Ile Ala Ala Val

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Thr Val Asp Arg Leu Leu Lys Gly Tyr Asp Ile Arg Leu Arg Pro Asp				
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ttt gga ggt ccc ccc gtg gct gtg ggg atg aac att gac att gcc agc				546
Phe Gly Gly Pro Pro Val Ala Val Gly Met Asn Ile Asp Ile Ala Ser				
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Ile Asp Met Val Ser Glu Val Asn Met Asp Tyr Thr Leu Thr Met Tyr				
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Phe Gln Gln Ala Trp Arg Asp Lys Arg Leu Ser Xaa Asn Val Ile Pro				
65	70	75		
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Leu Asn Leu Thr Leu Asp Asn Arg Val Ala Asp Gln Leu Trp Val Pro				
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gaaggtagag ataaagacac tttttcaaaa atggcaatgg tatcagaatt cctcaagcag				180
gctatgttta gcttgttcta gtctgtggag cattctcctt catagaaaag atgggaaata				240
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cagggccact tctccctgg ttcttcttat ggctttggat gtagcttgaa gac atg				356
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ctc cta gca ttt tca caa gct ctg ctt gtt gtg ttt agt gag cgc aga				404
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Leu Leu Pro Ser Gly Leu Ser Trp Leu Met Gly Ser Cys Ser Cys Leu				
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His Gly Arg Asp Leu Ser Xaa Ala Gly Ile Gly Leu Leu Ala Ala Ala
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Met Met Met Lys Ile Pro Trp Gly Ser
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Ile Pro Val Leu Met Leu Leu Leu Leu Leu Gly Leu Ile Asp Ile Ser
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Gln Ala Gln Leu Ser Cys Thr Gly Pro Pro Ala Ile Pro Gly Ile Pro
1 5 10
ggg atc cct ggg aca cct ggc ccc gat ggc caa cct ggg acc cca ggg 257
Gly Ile Pro Gly Thr Pro Gly Pro Asp Gly Gln Pro Gly Thr Pro Gly
15 20 25 30

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Phe Gly Glu Lys Gly Asp Pro Gly Ile Pro Gly Asn Pro Gly Lys Val	
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Gly Pro Lys Gly Pro Met Gly Leu Lys Val Ala Gln Gly Pro Trp Ser	
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Met Lys Arg Leu Ala Ala Arg Cys Phe Ala Gly Leu Leu Ile	
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Lys Ala Ile Glu Gly Asn Leu Glu Glu Met Glu Glu Val Arg Leu	
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Lys Lys Arg Lys Arg Arg Asn Val Asp Lys Asp Pro Ala Lys Glu	
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Asp Val Glu Lys Ala Lys Lys Arg Arg Gly Arg Pro Pro Ala Glu Lys	
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Leu Ser Pro Asn Pro Pro Lys Leu Thr Lys Gln Met Asn Ala Ile Ile	
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Asp Thr Val Ile Asn Tyr Lys Asp Ser Ser Gly Arg Gln Leu Ser Glu	
75 80 85	
gtc ttc att cag tta cct tca agg aaa gaa tta cca gaa tac tat gaa	506
Val Phe Ile Gln Leu Pro Ser Arg Lys Glu Leu Pro Glu Tyr Tyr Glu	

90 95 100 543
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 Met Lys Thr Leu
 cag tct aca ctt ctc ctg tta ctg ctt gtg cct ctg ata aag cca gca 164
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 Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp Tyr Glu Asp Lys Tyr Leu
 20 25 30
 gat gga aaa aat att aag gaa aaa gaa act gtg ata ata ccc aat gag 308
 Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr Val Ile Ile Pro Asn Glu
 35 40 45
 aaa agt ctt caa tta caa aaa gat gag gca ata aca cca tta cct ccc 356
 Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala Ile Thr Pro Leu Pro Pro
 50 55 60 65
 aag agm gaa aat gat gaa atg ccc acg tgt ctg ctg tgt gtt tgt tta 404
 Lys Xaa Glu Asn Asp Glu Met Pro Thr Cys Leu Leu Cys Val Cys Leu
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 agt ggc tct gta tac tgt gaa gaa gtt gac att gat gct gta cca ccc 452
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 Met Lys Thr Leu Gln Ser Thr Leu Leu Leu Leu Leu Val
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 Tyr Asp Tyr Gly Thr Asp Asn Phe Glu Glu Ser Ile Phe Ser Gln Asp
 15 20 25
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 Tyr Glu Asp Lys Tyr Leu Asp Gly Lys Asn Ile Lys Glu Lys Glu Thr
 30 35 40
 gtg ata ata ccc aat gag aaa agt ctt caa tta caa aaa gat gag gca 423
 Val Ile Ile Pro Asn Glu Lys Ser Leu Gln Leu Gln Lys Asp Glu Ala
 45 50 55
 ata aca cca tta cct ccc aag agm gaa aat gat gaa atg ccc acg tgt 471
 Ile Thr Pro Leu Pro Pro Lys Xaa Glu Asn Asp Glu Met Pro Thr Cys
 60 65 70 75
 ctg ctg tgt gtt tgt tta agt ggc tct gta tac tgt gaa gaa gtt gac 519
 Leu Leu Cys Val Cys Leu Ser Gly Ser Val Tyr Cys Glu Glu Val Asp
 80 85 90
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 Ile Asp Ala Val Pro Pro Leu Pro Arg Asn Gln Pro Ile Phe Thr His
 95 100 105
 gat t 571
 Asp

<210> 109
 <211> 444
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 101..442
 <221> sig_peptide
 <222> 101..172
 <223> score 9.2
 seq LVTLVFLHVLHS/AP

004220-6651399-022400

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<400> 109
aagttactga gaactcataa gacgaagcta aaatccctct tcggatccac agtcaaccgc      60
cctgaacaca tcctgcaaaa agcccagaga aaggagcgcc atg gat tac tac aga      115
                                   Met Asp Tyr Tyr Arg
                                   -20
aaa tat gca gct atc ttt ctg gtc aca ttg tcg gtg ttt ctg cat gtt      163
Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu His Val
                                   -15               -10               -5
ctc cat tcc gct cct gat gtg cag gat tgc cca gaa tgc acg cta cag      211
Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln
                                   1               5               10
gaa aac cca ttc ttc tcc cag ccg ggt gcc cca ata ctt cag tgc atg      259
Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met
                                   15               20               25
ggc tgc tgc ttc tct aga gca tat ccc act cca cta agg tcc aag aag      307
Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys
                                   30               35               40               45
acg atg ttg gtc caa aag aac gtc acc tca gag tcc act tgc tgt gta      355
Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val
                                   50               55               60
gct aaa tca tat aac agg gtc aca gta atg ggg ggt ttc aaa gtg gag      403
Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu
                                   65               70               75
aac cac acg gcg tgc cac tgc agt act tgt tat tat cac aa      444
Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
                                   80               85               90

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<210> 110
<211> 295
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 79..294

<221> sig_peptide
<222> 79..144
<223> score 8.4
      seq SILLFLTEAALG/DA

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<400> 110
agcagaaagc cgcgcacctc ctcccgccag gcgctttctc ggacgccttg cccagcgggc      60
cgcccgaacc cctgcacc atg gac ccc gct cgc ccc ctg ggg ctg tcg att      111
                                   Met Asp Pro Ala Arg Pro Leu Gly Leu Ser Ile
                                   -20               -15
ctg ctg ctt ttc ctg acg gag gct gca ctg ggc gat gct gct cag gag      159
Leu Leu Leu Phe Leu Thr Glu Ala Ala Leu Gly Asp Ala Ala Gln Glu
                                   -10               -5               1               5
cca aca gga aat aac gcg gag atc tgt ctc ctg ccc cta gac yac gga      207
Pro Thr Gly Asn Asn Ala Glu Ile Cys Leu Leu Pro Leu Asp Xaa Gly

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	10		15		20	
ccc tgc cgg gcc cta ctt ctc cgt tac tac tac gac agg tac acg cag						255
Pro Cys Arg Ala Leu Leu Leu Arg Tyr Tyr Tyr Asp Arg Tyr Thr Gln						
	25		30		35	
agc tgc cgc cag ttc ctg tac ggg ggc tgc gag ggc aac g						295
Ser Cys Arg Gln Phe Leu Tyr Gly Gly Cys Glu Gly Asn						
	40		45		50	

<210> 111
 <211> 423
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 173..421

<221> sig_peptide
 <222> 173..295
 <223> score 6.6
 seq LFIFRMLVLGTAA/ES

<400> 111	
gacagatacg attaaaaaga ggggtggaaga ggaacaactg acagggtcaa gagcaaaaag	60
cgtgggcagt tggagaagaa gcagccagag tgtgaagaag cccacggaag gaaagtccag	120
ggaggaggaa aagaagcaga agttttggca tctgttcctt ggctgtgcca ag atg ggc	178
	Met Gly
	-40
gat tgg agc ttc ctg gga aat ttc ctg gag gaa gta cac aag cac tcg	226
Asp Trp Ser Phe Leu Gly Asn Phe Leu Glu Glu Val His Lys His Ser	
	-35 -30 -25
acc gtg gta ggc aag gtc tgg ctc act gtc ctc ttc ata ttc cgt atg	274
Thr Val Val Gly Lys Val Trp Leu Thr Val Leu Phe Ile Phe Arg Met	
	-20 -15 -10
ctc gtg ctg ggc aca gct gct gag tct tcc tgg ggg gat gag cag gct	322
Leu Val Leu Gly Thr Ala Ala Glu Ser Ser Trp Gly Asp Glu Gln Ala	
	-5 1 5
gat ttc cgg tgt gat acg att cag cct ggc tgc cag aat gtc tgc tac	370
Asp Phe Arg Cys Asp Thr Ile Gln Pro Gly Cys Gln Asn Val Cys Tyr	
	10 15 20 25
gac cag gct ttc ccc atc ggg rac att cgc tam tgg gtg ctg cag atc	418
Asp Gln Ala Phe Pro Ile Gly Xaa Ile Arg Xaa Trp Val Leu Gln Ile	
	30 35 40
atc tt	423
Ile	

<210> 112
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 206..499

<221> sig_peptide

<222> 206..343

<223> score 9.2

seq ILLLTAVESAWG/DE

<400> 112

aaaaaagctt ttacgaggta tcagcacttt tctttcatta gggggaaggc gtgaggaaag 60
taccaaacag cagcggagtt ttaaacttta aatagacagg tctgagtgcc tgaacttgcc 120
ttttcatttt acttcatcct ccaaggagtt caatcacttg gcgtgacttc actactttta 180
agcaaaagag tgggtgcccg gcaac atg ggt gac tgg agc gcc tta ggc aaa 232
Met Gly Asp Trp Ser Ala Leu Gly Lys
-45 -40
ctc ctt gac aag gtt caa gcc tac tca act gct gga ggg aag gtg tgg 280
Leu Leu Asp Lys Val Gln Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp
-35 -30 -25
ctg tca gta ctt ttc att ttc cga atc ctg ctg ctg ggg aca gcg gtt 328
Leu Ser Val Leu Phe Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val
-20 -15 -10
gag tca gcc tgg gga gat gag cag tct gcc ttt cgt tgt aac act cag 376
Glu Ser Ala Trp Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln
-5 1 5 10
caa cct ggt tgt gaa aat gtc tgc tat gac aag tct ttc cca atc tct 424
Gln Pro Gly Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser
15 20 25
cat gtg cgc ttc tgg gtc ctg cag atc ata ttt gtg tct gta ccc aca 472
His Val Arg Phe Trp Val Leu Gln Ile Ile Phe Val Ser Val Pro Thr
30 35 40
ctc ttg tac ctg gct cat gtg ttc tat gt 501
Leu Leu Tyr Leu Ala His Val Phe Tyr
45 50

<210> 113

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 73..468

<221> sig_peptide

<222> 73..132

<223> score 11.2

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<400> 113

actcagaagc ttggaccgca tcttagccgc cgactcacac aaggcagggtg ggtgaggaaa 60
tccagagttg cc atg gag aaa att cca gtg tca gca ttc ttg ctc ctt gtg 111
Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val
-20 -15 -10

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gcc ctc tcc tac act ctg gcc aga gat acc aca gtc aaa cct gga gcc      159
Ala Leu Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala
      -5                      1                      5
aaa aag gac aca aag gac tct cga ccc aaa ctg ccc cag acc ctc tcc      207
Lys Lys Asp Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser
10                      15                      20                      25
aga ggt tgg ggt gac caa ctc atc tgg act cag aca tat gaa gaa gct      255
Arg Gly Trp Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala
      30                      35                      40
cta tat aaa tcc aag aca agc aac aaa ccc ttg atg att att cat cac      303
Leu Tyr Lys Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His
      45                      50                      55
ttg gat gag tgc cca cac agt caa gct tta aag aaa gtg ttt gct gaa      351
Leu Asp Glu Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu
      60                      65                      70
aat aaa gaa atc cag aaa ttg gca gag cag ttt gtc ctc ctc aat ctg      399
Asn Lys Glu Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu
      75                      80                      85
ggt tat gaa aca act gac aaa cac ctt tct cct gat ggc cag tat gtc      447
Val Tyr Glu Thr Thr Asp Lys His Leu Ser Pro Asp Gly Gln Tyr Val
90                      95                      100                      105
cca gga tta tgt ttg ttg acc
Pro Gly Leu Cys Leu Leu Thr
      110

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<210> 114
<211> 576
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 195..575

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<221> sig_peptide
<222> 195..287
<223> score 10.1
      seq SLAFLLSLRGAGA/IK

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<400> 114
gtcgaagcgc gcgaactcct cccggttgta gatgtatctc tccaggaagc gctgtgtccc      60
attaaacgcg tasattcctg ccgtccctgg aaaagtgcta gaggccacaca gtttcagtct      120
catctgcttc cactcggcct cagttcctca tcaactgttcc tgtgttcaca gtcataat      180
atagacccca caac atg cgc cct gaa gac aga atg ttc cat atc aga gct      230
      Met Arg Pro Glu Asp Arg Met Phe His Ile Arg Ala
      -30                      -25                      -20
gtg atc ttg aga gcc ctc tcc ttg gct ttc ctg ctg agt ctc cga gga      278
Val Ile Leu Arg Ala Leu Ser Leu Ala Phe Leu Leu Ser Leu Arg Gly
      -15                      -10                      -5
gct ggg gcc atc aag gcg gac cat gtg tca act tat gcc gcg ttt gta      326
Ala Gly Ala Ile Lys Ala Asp His Val Ser Thr Tyr Ala Ala Phe Val
      1                      5                      10
cag acg cat aga cca aca ggg gag ttt atg ttt gaa ttt gat gaa gat      374

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Gln	Thr	His	Arg	Pro	Thr	Gly	Glu	Phe	Met	Phe	Glu	Phe	Asp	Glu	Asp	
15						20					25					
gag	atg	ttc	tat	gtg	gat	ctg	gac	aag	aag	gag	acc	gtc	tgg	cat	ctg	422
Glu	Met	Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Glu	Thr	Val	Trp	His	Leu	
30					35					40					45	
gag	gag	ttt	ggc	caa	gcc	ttt	tcc	ttt	gag	gct	cag	ggc	ggg	ctg	gct	470
Glu	Glu	Phe	Gly	Gln	Ala	Phe	Ser	Phe	Glu	Ala	Gln	Gly	Gly	Leu	Ala	
			50						55					60		
aac	att	gct	ata	ttg	aac	aac	aac	ttg	aat	acc	ttg	atc	cag	cgt	tcc	518
Asn	Ile	Ala	Ile	Leu	Asn	Asn	Asn	Leu	Asn	Thr	Leu	Ile	Gln	Arg	Ser	
			65					70					75			
aac	cac	act	cag	gcc	acc	aac	gat	ccc	cct	gag	gtg	acc	gtg	ttt	ccc	566
Asn	His	Thr	Gln	Ala	Thr	Asn	Asp	Pro	Pro	Glu	Val	Thr	Val	Phe	Pro	
			80				85					90				
aag	gag	cct	g													576
Lys	Glu	Pro														
95																

<210> 115
 <211> 476
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 95..475

<221> sig_peptide
 <222> 95..187
 <223> score 10.1
 seq SLAFLLSLRGAGA/IK

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tgtgctcaca	gtcatcaatt	atagacccca	caac atg	cgc cct	gaa gac	aga atg										115
			Met Arg	Pro Glu	Asp Arg	Met										
			-30			-25										
ttc cat	atc aga	gct gtg	atc ttg	aga gcc	ctc tcc	ttg gct	ttc ctg									163
Phe His	Ile Arg	Ala Val	Ile Leu	Arg Ala	Leu Ser	Leu Ala	Phe Leu									
		-20		-15		-10										
ctg agt	ctc cga	gga gct	ggg gcc	atc aag	gcg gac	cat gtg	tca act									211
Leu Ser	Leu Arg	Gly Ala	Gly Ala	Ile Lys	Ala Asp	His Val	Ser Thr									
		-5		1		5										
tat gcc	gcg ttt	gta cag	acg cat	aga cca	aca ggg	gag ttt	atg ttt									259
Tyr Ala	Ala Phe	Val Gln	Thr His	Arg Pro	Thr Gly	Glu Phe	Met Phe									
		10		15		20										
gaa ttt	gat gaa	gat gag	atg ttc	tat gtg	gat ctg	gac aag	aag gag									307
Glu Phe	Asp Glu	Asp Glu	Met Phe	Tyr Val	Asp Leu	Asp Lys	Lys Glu									
		25		30		35										
acc gtc	tgg cat	ctg gag	gag ttt	ggc caa	gcc ttt	tcc ttt	gag gct									355
Thr Val	Trp His	Leu Glu	Glu Phe	Gly Gln	Ala Phe	Ser Phe	Glu Ala									
		45		50		55										
cag ggc	ggg ctg	gct aac	att gct	ata ttg	aac aac	aac ttg	aat acc									403

004220" 666E7560

Gln Gly Gly Leu Ala Asn Ile Ala Ile Leu Asn Asn Asn Leu Asn Thr
60 65 70
ttg atc cag cgt tcc aac cac act cag gcc acc aac gat ccc cct gag 451
Leu Ile Gln Arg Ser Asn His Thr Gln Ala Thr Asn Asp Pro Pro Glu
75 80 85
gtg acc gtg ttt ccc aag gag cct g 476
Val Thr Val Phe Pro Lys Glu Pro
90 95

<210> 116
<211> 458
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 139..456

<221> sig_peptide
<222> 139..192
<223> score 10.5
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<400> 116
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gcccatagtt tattataaag gtgactgcac cctgcagcca ccagcactgc ctggctccac 120
gtgcctcctg gtctcagt atg gcg ctg tcc tgg gtt ctt aca gtc ctg agc 171
Met Ala Leu Ser Trp Val Leu Thr Val Leu Ser
-15 -10
ctc cta cct ctg ctg gaa gcc cag atc cca ttg tgt gcc aac cta gta 219
Leu Leu Pro Leu Leu Glu Ala Gln Ile Pro Leu Cys Ala Asn Leu Val
-5 1 5
ccg gtg ccc atc acc aac gcc acc ctg gac crg atc act ggc aag tgg 267
Pro Val Pro Ile Thr Asn Ala Thr Leu Asp Xaa Ile Thr Gly Lys Trp
10 15 20 25
ttt tat atc gca tcg gcc ttt cga aac gag gag tac aat aag tcg gtt 315
Phe Tyr Ile Ala Ser Ala Phe Arg Asn Glu Glu Tyr Asn Lys Ser Val
30 35 40
cag gag atc caa gca acc ttc ttt tac ttc acc ccc aac aag mca sag 363
Gln Glu Ile Gln Ala Thr Phe Phe Tyr Phe Thr Pro Asn Lys Xaa Xaa
45 50 55
gac acg atc ttt ctc aga gag tac cag acy cga cag gac cag tgc atc 411
Asp Thr Ile Phe Leu Arg Glu Tyr Gln Thr Arg Gln Asp Gln Cys Ile
60 65 70
tat aac acc acc tac ccg gsa tcc tcg tta acc cta aca aaa aaa ac 458
Tyr Asn Thr Thr Tyr Pro Xaa Ser Ser Leu Thr Leu Thr Lys Lys
75 80 85

<210> 117
<211> 435
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 201..434

<221> sig_peptide
 <222> 201..332
 <223> score 6.3
 seq WLIFAFFVDTGFC/RV

<400> 117
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 ccggttctag gcgcttcggg agccgcggct tatggtgcag acatggccaa gtccaagaac 120
 cacaccacac acatactttt tatgttattt ttggggagag wcttgctctg ctgcccaggc 180
 tgggggtgcag tggcatratc atg gct cac tgc agc ctt gac cac ccc cag ggt 233
 Met Ala His Cys Ser Leu Asp His Pro Gln Gly
 -40 -35
 tgc agt gat cgt gcc acc tgc gcc tgc tgg gta gct ggg act gca gac 281
 Ser Ser Asp Arg Ala Thr Ser Ala Cys Trp Val Ala Gly Thr Ala Asp
 -30 -25 -20
 agg cac cct gcc tgg cta att ttt gca ttt ttt gtg gac acg ggg ttt 329
 Arg His Pro Ala Trp Leu Ile Phe Ala Phe Phe Val Asp Thr Gly Phe
 -15 -10 -5
 tgc cgt gtt gcc cag gct ggt ctc aat ctc ctc ggc tca agt caa cag 377
 Cys Arg Val Ala Gln Ala Gly Leu Asn Leu Leu Gly Ser Ser Gln Gln
 1 5 10 15
 cct gcc tct gcc tcc cga tgt gtt sng att aca gga ata aac tac tat 425
 Pro Ala Ser Ala Ser Arg Cys Val Xaa Ile Thr Gly Ile Asn Tyr Tyr
 20 25 30
 gcc caa ctc a 435
 Ala Gln Leu

<210> 118
 <211> 514
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 41..514

<221> sig_peptide
 <222> 41..163
 <223> score 4.3
 seq VALFCGCGHEALS/GT

<400> 118
 gctctctctt ggggactgca gagaagcagg acctcgggcc atg ggg tgt ttt gaa 55
 Met Gly Cys Phe Glu
 -40
 tgc tgt atc aaa tgc ctg ggg ggc att ccc tat gcc tct ctg att gcc 103
 Cys Cys Ile Lys Cys Leu Gly Gly Ile Pro Tyr Ala Ser Leu Ile Ala
 -35 -30 -25

acc atc ctg ctc tat gcg ggt gtt gcc ctg ttc tgt ggc tgc ggt cat	151
Thr Ile Leu Leu Tyr Ala Gly Val Ala Leu Phe Cys Gly Cys Gly His	
-20 -15 -10 -5	
gaa gcg ctt tct gga act gtc aac att ctg caa acc tac ttt gag atg	199
Glu Ala Leu Ser Gly Thr Val Asn Ile Leu Gln Thr Tyr Phe Glu Met	
1 5 10	
gca aga act gct gga gac aca ctg gat gtt ttt acc atg att gac atc	247
Ala Arg Thr Ala Gly Asp Thr Leu Asp Val Phe Thr Met Ile Asp Ile	
15 20 25	
ttt aag tat gtg atc tac ggc atc gca gct gcg ttc ttt gtg tat ggc	295
Phe Lys Tyr Val Ile Tyr Gly Ile Ala Ala Ala Phe Phe Val Tyr Gly	
30 35 40	
att ttg ctg atg gtg gaa ggt ttc ttc aca act ggg gcc atc aaa gat	343
Ile Leu Leu Met Val Glu Gly Phe Phe Thr Thr Gly Ala Ile Lys Asp	
45 50 55 60	
ctc tat ggg gat ttc aaa atc acc act tgt ggc aga tgt gtg agc gct	391
Leu Tyr Gly Asp Phe Lys Ile Thr Thr Cys Gly Arg Cys Val Ser Ala	
65 70 75	
tgg ttc att atg ctg aca tat ctt ttc atg ttg gcc tgg ctg gga gtc	439
Trp Phe Ile Met Leu Thr Tyr Leu Phe Met Leu Ala Trp Leu Gly Val	
80 85 90	
acg gct ttc acc tca ctg cca gtt tac atg tac ttc aat ctg tgg acc	487
Thr Ala Phe Thr Ser Leu Pro Val Tyr Met Tyr Phe Asn Leu Trp Thr	
95 100 105	
atc tgc cgg aac acc aca tta gtg gag	514
Ile Cys Arg Asn Thr Thr Leu Val Glu	
110 115	

<210> 119
 <211> 326
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..325

<221> sig_peptide
 <222> 74..133
 <223> score 4.4
 seq LRYVASAVFGVIG/SQ

<400> 119	
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cagacatcac aac atg ggg ctc acc aag cag tac cta cgc tat gtt gct	109
Met Gly Leu Thr Lys Gln Tyr Leu Arg Tyr Val Ala	
-20 -15 -10	
agt gcg gtc ttt ggc gtt atc ggc agc caa aaa ggt aat att gtc ttt	157
Ser Ala Val Phe Gly Val Ile Gly Ser Gln Lys Gly Asn Ile Val Phe	
-5 1 5	
gtg aca ctt cgt ggt gag aaa gga cgt tat gtg gca gta cca gct tgt	205
Val Thr Leu Arg Gly Glu Lys Gly Arg Tyr Val Ala Val Pro Ala Cys	
10 15 20	

seq WMSALFLGVGVRA/EE

<400> 121
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 ctggaggtgg gatccacaca gctcagaaca gctggatctt gctcagtctc tgccagggga 120
 agattccttg gaggaggccc tgcagcgac atg gag gga gct gct ttg ctg aga 173
 Met Glu Gly Ala Ala Leu Leu Arg
 -25 -20
 gtc tct gtc ctc tgc atc tgg atg agt gca ctt ttc ctt ggt gtg gga 221
 Val Ser Val Leu Cys Ile Trp Met Ser Ala Leu Phe Leu Gly Val Gly
 -15 -10 -5
 gtg agg gca gag gaa gct gga gcg agg gtg caa caa aac gtt cca agt 269
 Val Arg Ala Glu Glu Ala Gly Ala Arg Val Gln Gln Asn Val Pro Ser
 1 5 10
 ggg aca gat act gga gat cct caa agt aag ccc ctc ggt gac tgg gct 317
 Gly Thr Asp Thr Gly Asp Pro Gln Ser Lys Pro Leu Gly Asp Trp Ala
 15 20 25
 gct ggc acc atg gac cca gag agc agt atc ttt att gag gat gcc att 365
 Ala Gly Thr Met Asp Pro Glu Ser Ser Ile Phe Ile Glu Asp Ala Ile
 30 35 40 45
 aag tat ttc aag gaa aaa gtg agc aca cag aat ctg cta ctc ctg ctg 413
 Lys Tyr Phe Lys Glu Lys Val Ser Thr Gln Asn Leu Leu Leu Leu
 50 55 60
 act gat aat gag gcc tgg aac gga ttc gtg gct gct gct gaa ctg ccc 461
 Thr Asp Asn Glu Ala Trp Asn Gly Phe Val Ala Ala Ala Glu Leu Pro
 65 70 75
 agg 464
 Arg

<210> 122
 <211> 329
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 144..329

<221> sig_peptide
 <222> 144..203
 <223> score 9.3
 seq LFLCYLLLFTCSG/VE

<400> 122
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 catctatcag caggctccgg gctgaagatt gcttctcttc tctcctccaa ggtctagtga 120
 cggagcccgc gcgcggcgcc acc atg cgg cag aag gcg gta tcg ctt ttc ttg 173
 Met Arg Gln Lys Ala Val Ser Leu Phe Leu
 -20 -15
 tgc tac ctg ctg ctc ttc act tgc agt ggg gtg gag gca ggt aag aaa 221
 Cys Tyr Leu Leu Leu Phe Thr Cys Ser Gly Val Glu Ala Gly Lys Lys
 -10 -5 1 5


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aag tgc tcg gag agc tcg gac agc ggc tcc ggg ttc tgg aag gcc ctg      269
Lys Cys Ser Glu Ser Ser Asp Ser Gly Ser Gly Phe Trp Lys Ala Leu
      10                      15                      20
acc ttc atg gcc gtc gga gga gna ctc gca gtc gcc ggg ctg ccc gcg      317
Thr Phe Met Ala Val Gly Gly Xaa Leu Ala Val Ala Gly Leu Pro Ala
      25                      30                      35
ctg ggc ttc acc      329
Leu Gly Phe Thr
      40

<210> 123
<211> 467
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 57..467

<221> sig_peptide
<222> 57..110
<223> score 7.1
      seq IFVLLLSAIVSIS/AX

<400> 123
agttgtcttt ggtagttttt ttgcactaac ttcaggaacc agctcatgat ctcagg atg      59
                                Met
tat gga aaa ata atc ttt gta tta cta ttg tca gca att gtg agc ata      107
Tyr Gly Lys Ile Ile Phe Val Leu Leu Leu Ser Ala Ile Val Ser Ile
      -15                      -10                      -5
tca gca tya agt acc act ggt gtg gca atg cac act tca acc tct tct      155
Ser Ala Xaa Ser Thr Thr Gly Val Ala Met His Thr Ser Thr Ser Ser
      1                      5                      10                      15
tca gtc aca aag agt tac atc tca tca cag aca aat gat acg cac aaa      203
Ser Val Thr Lys Ser Tyr Ile Ser Ser Gln Thr Asn Asp Thr His Lys
      20                      25                      30
cgg gac aca tat gca gcc act cct aga gct cat gaa gtt tca gaa att      251
Arg Asp Thr Tyr Ala Ala Thr Pro Arg Ala His Glu Val Ser Glu Ile
      35                      40                      45
tct gtt aga act gtt tac cct cca gaa gag gaa acc gga gaa agg gta      299
Ser Val Arg Thr Val Tyr Pro Pro Glu Glu Glu Thr Gly Glu Arg Val
      50                      55                      60
caa ctt gcc cat cat ttc tct gaa cca gag ata aca ctc att att ttt      347
Gln Leu Ala His His Phe Ser Glu Pro Glu Ile Thr Leu Ile Ile Phe
      65                      70                      75
ggg gtg atg gct ggt gtt att gga acg atc ctc tta att tct tac ggt      395
Gly Val Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly
      80                      85                      90                      95
att cgc cga ctg ata aag aga caa gtg atc aat gag aat ctg ttc acc      443
Ile Arg Arg Leu Ile Lys Arg Gln Val Ile Asn Glu Asn Leu Phe Thr
      100                      105                      110
aaa cca aat gtg gaa aga aca caa      467
Lys Pro Asn Val Glu Arg Thr Gln

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115

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sgacagggcc ctgtctctc agcttcaggc accaccactg acctgggaca gtgaatcgac 180
a atg ccg tct tct gtc tgc tgg ggc atc ctc ctg ctg gca ggc ctg tgc 229
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
-20 -15 -10
tgc ctg gtc cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc 277
Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
-5 1 5
cag aag aca gat aca tcc cac cat gat cag gat cac cca acc ttc aac 325
Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
10 15 20
aag atc acc ccc aac ctg gct gag ttc gcc ttc agc cta tac agc aca 373
Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Ser Thr
25 30 35 40
cac agc aca cag atg agc aca cag cac aca cac aaa cgc aca gca cac 421
His Ser Thr Gln Met Ser Thr Gln His Thr His Lys Arg Thr Ala His
45 50 55
ata cg 426
Ile

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 taatattcac cagcagcctc ccccggtgcc cctctggatc cactgcttaa atacggacga 120
 sgacagggcc ctgtctctc agcttcaggc accaccactg acctgggaca gtgaatcgac 180
 a atg ccg tct tct gtc tgc tgg ggc atc ctc ctg ctg gca ggc ctg tgc 229
 Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys

-20 -15 -10
 tgc ctg gtc cct gtc tcc ctg gct gag gat ccc cag gga gat gct gcc 277
 Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala

-5 1 5
 cag aag aca gat aca tcc cac cat gat cag gat cac cca acc ttc aac 325
 Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
 10 15 20

aag atc acc ccc aac ctg gct gag ttc gcc ttc agc cta tac cgc cag 373
 Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
 25 30 35 40

ctg gca cac cag tcc aac agc acc aat atc ttc ttc tcc cca gtg agc 421
 Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
 45 50 55

atc gct aca gcc ttt gca atg ctc tcc ctg ggg acc aag gct gac act 469
 Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
 60 65 70

cac gat gaa atc ctg gag ggc ctg aat ttc aac ctc acg gag att ccg 517
 His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
 75 80 85

gag gct cag atc cat gaa ggc ttc cag gaa ctc ctn cgt acc ctc aac 565
 Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
 90 95 100

cag cca gac agc cag ctc cag ctg acc acc ggc aat ggc ctg ttc ctc 613
 Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
 105 110 115 120

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 caggtttctcg tatccctcgg ccaagggat cctctgcaaa cctctgcaaa cccagcgcaa 120
 ctacgggtccc ccggtcagac ccagg atg ggg cca gaa cgg aca ggg gcc gcg 172
 Met Gly Pro Glu Arg Thr Gly Ala Ala
 -20 -15
 ccg ctg ccg ctg ctg ctg gtg tta gcg ctc agt caa ggc att tta aat 220

Pro	Leu	Pro	Leu	Leu	Leu	Val	Leu	Ala	Leu	Ser	Gln	Gly	Ile	Leu	Asn	
			-10					-5					1			
tgt	tgt	ttg	gcc	tac	aat	gtt	ggt	ctc	cca	gaa	gca	aaa	ata	ttt	tcc	268
Cys	Cys	Leu	Ala	Tyr	Asn	Val	Gly	Leu	Pro	Glu	Ala	Lys	Ile	Phe	Ser	
5						10				15						
ggt	cct	tca	agt	gaa	cag	ttt	ggc	tat	gca	gtg	cag	cag	ttt	ata	aat	316
Gly	Pro	Ser	Ser	Glu	Gln	Phe	Gly	Tyr	Ala	Val	Gln	Gln	Phe	Ile	Asn	
20				25				30						35		
cca	aaa	ggc	aac	tgg	tta	ctg	gtt	ggt	tca	ccc	tgg	agt	ggc	ttt	cct	364
Pro	Lys	Gly	Asn	Trp	Leu	Leu	Val	Gly	Ser	Pro	Trp	Ser	Gly	Phe	Pro	
			40					45					50			
gag	aac	cga	atg	gga	gat	gtg	tat	aaa	tgt	cct	gtt	gac	cta	tcc	act	412
Glu	Asn	Arg	Met	Gly	Asp	Val	Tyr	Lys	Cys	Pro	Val	Asp	Leu	Ser	Thr	
			55					60				65				
gcc	aca	tgt	gaa	aaa	cta	aat	ttg	caa	act	tca	aca	agc	att	cca	aat	460
Ala	Thr	Cys	Glu	Lys	Leu	Asn	Leu	Gln	Thr	Ser	Thr	Ser	Ile	Pro	Asn	
		70					75					80				
ggt	act	gag	atg	ara	acc	aa										480
Val	Thr	Glu	Met	Xaa	Thr											
			85													

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 <213> Homo sapiens

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<221> sig_peptide
 <222> 23..64
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			Met	Ala	Met	Arg	Leu	Ile	Leu	Phe	Phe	Gly				
						-10						-5				
gcc	ctt	ttt	ggg	cat	atc	tac	tgt	cta	gaa	aca	ttt	gtg	gga	gac	caa	100
Ala	Leu	Phe	Gly	His	Ile	Tyr	Cys	Leu	Glu	Thr	Phe	Val	Gly	Asp	Gln	
			1				5				10					
ggt	ctt	gag	att	gta	cca	agc	aat	gaa	gaa	caa	att	aaa	aat	ctg	cta	148
Val	Leu	Glu	Ile	Val	Pro	Ser	Asn	Glu	Glu	Gln	Ile	Lys	Asn	Leu	Leu	
		15				20				25						
caa	ttg	gag	gct	caa	gaa	cat	ctc	cag	ctt	gat	ttt	tgg	aaa	tca	ccc	196
Gln	Leu	Glu	Ala	Gln	Glu	His	Leu	Gln	Leu	Asp	Phe	Trp	Lys	Ser	Pro	
		30				35				40						
acc	acc	cca	ggg	gag	aca	gcc	cac	gtc	cga	ggt	ccc	ttc	gtc	aac	gtc	244
Thr	Thr	Pro	Gly	Glu	Thr	Ala	His	Val	Arg	Val	Pro	Phe	Val	Asn	Val	
		45			50			55			60					
cag	gca	gtc	aaa	gtg	ttc	ttg	gag	tcc	cag	gga	att	gcc	tat	tcc	atc	292
Gln	Ala	Val	Lys	Val	Phe	Leu	Glu	Ser	Gln	Gly	Ile	Ala	Tyr	Ser	Ile	

	65		70		75	
atg att gaa gac gtg cag gtc ctg ttg gac aaa gag aat gaa gaa atg						340
Met Ile Glu Asp Val Gln Val Leu Leu Asp Lys Glu Asn Glu Glu Met						
	80		85		90	
ctt ttt aat agg aga aga gaa cgg agt ggt aac ttc aat ttt ggg gcc						388
Leu Phe Asn Arg Arg Arg Glu Arg Ser Gly Asn Phe Asn Phe Gly Ala						
	95		100		105	
tac cat acc ctg gaa gag att tcc caa gaa atg gat aac ctc gtg gct						436
Tyr His Thr Leu Glu Glu Ile Ser Gln Glu Met Asp Asn Leu Val Ala						
	110		115		120	
gag cac cct ggt cta gtg agc aaa gtg aat att ggc tct tct ttt gag						484
Glu His Pro Gly Leu Val Ser Lys Val Asn Ile Gly Ser Ser Phe Glu						
	125		130		135	140
aac cgg cct atg aac gtg ctc aag ttc agc acc gna gga gac aag cca						532
Asn Arg Pro Met Asn Val Leu Lys Phe Ser Thr Xaa Gly Asp Lys Pro						
	145		150		155	
gct atc tgg ctg gat gct ggg atc cat gct cga gag tgg gtt a						575
Ala Ile Trp Leu Asp Ala Gly Ile His Ala Arg Glu Trp Val						
	160		165		170	
<210> 128						
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<222> 137..460						
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<223> score 5.8						
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aaaaaggaag tctgctgacg ttagttagtt aaatttaaca tctttttatg tgtaacactt						120
gactttggaa gcaaaa atg aac ttt gcg gag aga gag ggc tct aag aga tac						172
Met Asn Phe Ala Glu Arg Glu Gly Ser Lys Arg Tyr						
	-40		-35			
tgc att caa acg aaa cat gtg gcc att ctc tgt gcg gtg gtg gtg ggt						220
Cys Ile Gln Thr Lys His Val Ala Ile Leu Cys Ala Val Val Val Gly						
	-30		-25		-20	-15
gta gga tta ata gtg gga ctt gcc gtg ggc ttg acc aga tcg tgt gac						268
Val Gly Leu Ile Val Gly Leu Ala Val Gly Leu Thr Arg Ser Cys Asp						
	-10		-5		1	
tcc agc ggg gac ggc ggg ccg ggc act gcg cca snt cct tcc cac ctg						316
Ser Ser Gly Asp Gly Gly Pro Gly Thr Ala Pro Xaa Pro Ser His Leu						
	5		10		15	
cct tct tcc acg gcc agc ccc tca ggt cct cct gcc cag gac cag gac						364
Pro Ser Ser Thr Ala Ser Pro Ser Gly Pro Pro Ala Gln Asp Gln Asp						
	20		25		30	
atc tgc ccg gcc agt gag gat gag agc gga cag tgg aaa aac ttt cga						412

Ile	Cys	Pro	Ala	Ser	Glu	Asp	Glu	Ser	Gly	Gln	Trp	Lys	Asn	Phe	Arg	
35					40				45					50		
ctg	ccg	gac	ttc	gtc	aac	cca	gtc	cac	tac	gac	ctg	cac	gtg	aag	ccc	460
Leu	Pro	Asp	Phe	Val	Asn	Pro	Val	His	Tyr	Asp	Leu	His	Val	Lys	Pro	
				55					60					65		462

tg

<210> 129
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 151..438

<221> sig_peptide
 <222> 151..234
 <223> score 12.5
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ccgtgtcctc	ttgcctggga	gaggggaagc	agatctgagg	acatctctgt	gccaggccag											120	
aaaccgcca	cctgcagttc	cttctccggg	atg gac	gtg ggg	ccc agc	tcc ctg										174	
			Met	Asp	Val	Gly	Pro	Ser	Ser	Leu							
							-25										
ccc cac	ctt ggg	ctg aag	ctg ctg	ctg ctc	ctg ctg	ctg ctg	ctg ctc	ctg ctc	ctg ctc	ctg ctc	ctg ctc	ctg ctc	ctg ctc	ctg ctc	ctg ctc	ctg ctc	222
Pro His	Leu Gly	Leu Lys	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	Leu Leu	
-20		-15					-10									-5	
agg ggc	caa gcc	aac aca	ggc tgc	tac ggg	atc cca	ggg atg	ccc ggc										270
Arg Gly	Gln Ala	Asn Thr	Gly Cys	Tyr Gly	Ile Pro	Gly Met	Pro Gly										
		1		5		10											
ctg ccc	ggg gca	cca ggg	aag gat	ggg tac	gac gga	ctg ccg	ggg ccc										318
Leu Pro	Gly Ala	Pro Gly	Lys Asp	Gly Tyr	Asp Gly	Leu Pro	Gly Pro										
	15		20		25												
aag ggg	gag cca	gga atc	cca gcc	att ccc	ggg atc	cga gga	ccc aaa										366
Lys Gly	Glu Pro	Gly Ile	Pro Ala	Ile Pro	Gly Ile	Arg Gly	Pro Lys										
	30		35		40												
ggg cag	aag gga	gaa ccc	ggc tta	ccc ggc	cat cct	ggg aaa	aat ggc										414
Gly Gln	Lys Gly	Glu Pro	Gly Leu	Pro Gly	His Pro	Gly Lys	Asn Gly										
45		50		55		60											
ccc atg	gga ccc	cct ggg	atg cca														438
Pro Met	Gly Pro	Pro Gly	Met Pro														
			65														

<210> 130
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 <212> DNA
 <213> Homo sapiens

<220>
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<222> 45..437

<221> sig_peptide

<222> 45..98

<223> score 8.2

seq LLLLLLSFLAPWA/TI

<400> 130

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Met Gly Arg Arg
-15
gcc ctc ctg ctc ctg ctt ctg tct ttt ctg gcg ccc tgg gcc acc ata 104
Ala Leu Leu Leu Leu Leu Leu Ser Phe Leu Ala Pro Trp Ala Thr Ile
-10 -5 1
gcc ctc cgg ccg gmc tta agg gcc ctc ggc agc cta cac ttg cca acc 152
Ala Leu Arg Pro Xaa Leu Arg Ala Leu Gly Ser Leu His Leu Pro Thr
5 10 15
aac ccc aca tcc ctc ccg gct gta gcc aag aac tat tcg gtt ctc tac 200
Asn Pro Thr Ser Leu Pro Ala Val Ala Lys Asn Tyr Ser Val Leu Tyr
20 25 30
ttc caa cag aag gtt gat cat ttt gga ttt aat act gtg aaa act ttt 248
Phe Gln Gln Lys Val Asp His Phe Gly Phe Asn Thr Val Lys Thr Phe
35 40 45 50
aat cag cgg tac cta gta gct gat aaa tac tgg aag aaa aat ggt gga 296
Asn Gln Arg Tyr Leu Val Ala Asp Lys Tyr Trp Lys Lys Asn Gly Gly
55 60 65
tca ata ctt ttc tac act ggt aat gaa ggg gac att atc tgg nnt tgt 344
Ser Ile Leu Phe Tyr Thr Gly Asn Glu Gly Asp Ile Ile Trp Xaa Cys
70 75 80
aat aac acg ggg ttc atg tgg gat gtg gct gag gaa ctg aaa gct atg 392
Asn Asn Thr Gly Phe Met Trp Asp Val Ala Glu Glu Leu Lys Ala Met
85 90 95
ttg gtg ttt gct gaa cat cga ata cta tgg aag agt ctc tcc cct tt 439
Leu Val Phe Ala Glu His Arg Ile Leu Trp Lys Ser Leu Ser Pro
100 105 110

<210> 131

<211> 190

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> 7..189

<221> sig_peptide

<222> 7..66

<223> score 4.8

seq PLTVSLVLEGSEA/RH

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Met Ser Gly Ile Lys Pro Leu Pro Leu Thr Val Ser Leu Val
 -20 -15 -10
 ctc gaa ggc tcg gaa gcc cgt cac cat gtc gtg cga gtc gtc tat ggt 96
 Leu Glu Gly Ser Glu Ala Arg His His Val Val Arg Val Val Tyr Gly
 -5 1 5 10
 tct cgg gta ctg gga tat tcg tgg ggt gag tgc cgt ctc aac ggt aga 144
 Ser Arg Val Leu Gly Tyr Ser Trp Gly Glu Cys Arg Leu Asn Gly Arg
 15 20 25
 gcc gct cgg tca aag aga ctg acg cgg aga ggg cac tca cct aga a 190
 Ala Ala Arg Ser Lys Arg Leu Thr Arg Arg Gly His Ser Pro Arg
 30 35 40

<210> 132
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 222..407

<221> sig_peptide
 <222> 222..284
 <223> score 8.4
 seq CAVLALVLAPAGA/FR

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 caggcattgc ctgcgtgctt tcttttctcc aagacgggct gaggattgta cagctctagg 120
 cggagttggg gctcttcgga tcgcttagat tctcctcttt gctgcatttc cccccacgtc 180
 ctctgttctcc cgcgtctgcc tgcggaccgc gagaaggag a atg gag agg ggg ctg 236
 Met Glu Arg Gly Leu
 -20
 ccg ctc ctc tgc gcc gtg ctc gcc ctc gtc ctc gcc ccg gcc ggy gct 284
 Pro Leu Leu Cys Ala Val Leu Ala Leu Val Leu Ala Pro Ala Gly Ala
 -15 -10 -5
 ttt cgc aac gat aaa tgt ggc gat act ata aaa att gaa agc ccc ggg 332
 Phe Arg Asn Asp Lys Cys Gly Asp Thr Ile Lys Ile Glu Ser Pro Gly
 1 5 10 15
 tac ctt aca tct cct ggt tat cct cat tct tat cac cca agt gaa aaa 380
 Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr His Pro Ser Glu Lys
 20 25 30
 tgc gaa tgg ctg att cag gct ccg gac c 408
 Cys Glu Trp Leu Ile Gln Ala Pro Asp
 35 40

<210> 133
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<222> 54..377

<221> sig_peptide

<222> 54..131

<223> score 7.4

seq GVVVLLLLQGGS/YK

<400> 133

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gga gca acc acc atg gac cag aag tct ctc tgg gca ggt gta gtg gtc 104
Gly Ala Thr Thr Met Asp Gln Lys Ser Leu Trp Ala Gly Val Val Val
-25 -20 -15 -10
ttg ctg ctt ctc cag gga gga tct gcc tac aaa ctg gtt tgc tac ttt 152
Leu Leu Leu Leu Gln Gly Gly Ser Ala Tyr Lys Leu Val Cys Tyr Phe
-5 1 5
acc aac tgg tcc cag gac cgg cag gaa cca gga aaa ttc acc cct gag 200
Thr Asn Trp Ser Gln Asp Arg Gln Glu Pro Gly Lys Phe Thr Pro Glu
10 15 20
aat att gac ccc ttc cta tgc tct cat ctc atc tat tca ttc gcc agc 248
Asn Ile Asp Pro Phe Leu Cys Ser His Leu Ile Tyr Ser Phe Ala Ser
25 30 35
atc gaa aac aac aag gtt atc atc aag gac aag agt gaa gtg atg ctc 296
Ile Glu Asn Asn Lys Val Ile Ile Lys Asp Lys Ser Glu Val Met Leu
40 45 50 55
tac cag acc atc aac agt ctc aaa acc aag aat ccc aaa ctg aaa att 344
Tyr Gln Thr Ile Asn Ser Leu Lys Thr Lys Asn Pro Lys Leu Lys Ile
60 65 70
ctc ttg tcc att gga ggg tac tgt ttg gtt cca aa 379
Leu Leu Ser Ile Gly Gly Tyr Cys Leu Val Pro
75 80

<210> 134

<211> 463

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 220..462

<221> sig_peptide

<222> 220..288

<223> score 4.2

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<400> 134

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ggaaaactag ctgcacatat ctttttttac tgcagattta ctttaaggct catattctcc 120
aagtctattc tgcttttaaaa agaagacaag aaaagaagtg gtttatcaaa atcacgttat 180
aatcagattt tgaccaagca ttttgtaaga ttgccaagt atg ccc acg gac atg 234
Met Pro Thr Asp Met

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                                -20
gaa cac aca gga cat tac cta cat ctt gcc ttt ctg atg aca aca gtt      282
Glu His Thr Gly His Tyr Leu His Leu Ala Phe Leu Met Thr Thr Val
                                -15                -10                -5
ttt tct ttg tct cct gga aca aaa gca aac tat acc cgt ctg tgg gct      330
Phe Ser Leu Ser Pro Gly Thr Lys Ala Asn Tyr Thr Arg Leu Trp Ala
                                1                5                10
aac agt act tct tcc tgg gat tca gtt att caa aac aag aca ggc aga      378
Asn Ser Thr Ser Ser Trp Asp Ser Val Ile Gln Asn Lys Thr Gly Arg
15                20                25                30
aac caa aat gaa aac att aac aca aac cct ata act cct gaa gta gat      426
Asn Gln Asn Glu Asn Ile Asn Thr Asn Pro Ile Thr Pro Glu Val Asp
                                35                40                45
tat aaa ggt aat tct aca aac atg cct gaa aca tct c      463
Tyr Lys Gly Asn Ser Thr Asn Met Pro Glu Thr Ser
                                50                55

<210> 135
<211> 555
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<221> sig_peptide
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aaagaagtta acagctgaga taacgaggaa atattctgaa atg gat ccc aaa tat      115
                                Met Asp Pro Lys Tyr
                                -45
ttc atc tta att ttg ttt tgt gga cac ctg aac aat aca ttt ttt tca      163
Phe Ile Leu Ile Leu Phe Cys Gly His Leu Asn Asn Thr Phe Phe Ser
-40                -35                -30
aag aca gag aca att aca aca gag aag cag tca cag cct acc tta ttc      211
Lys Thr Glu Thr Ile Thr Thr Glu Lys Gln Ser Gln Pro Thr Leu Phe
-25                -20                -15                -10
aca tca tca atg tca cag gta ttg gct aat tct caa aac aca aca ggg      259
Thr Ser Ser Met Ser Gln Val Leu Ala Asn Ser Gln Asn Thr Thr Gly
                                -5                1                5
aat cct ttg ggt caa cca aca caa ttc agc gac act ttt tct gga caa      307
Asn Pro Leu Gly Gln Pro Thr Gln Phe Ser Asp Thr Phe Ser Gly Gln
10                15                20
tca ata tca cct gcc aaa gtc act gct gga caa cca aca cca gct gkc      355
Ser Ile Ser Pro Ala Lys Val Thr Ala Gly Gln Pro Thr Pro Ala Xaa
25                30                35
tat acc tct tct gaa aaa cca gaa gca cat act tct gct gga caa cca      403
Tyr Thr Ser Ser Glu Lys Pro Glu Ala His Thr Ser Ala Gly Gln Pro

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40		45		50		55	
ctt gcc tac aac acc aaa caa cca aac acc aat agc caa mac ctc ctc							451
Leu Ala Tyr Asn Thr Lys Gln Pro Asn Thr Asn Ser Gln Xaa Leu Leu							
	60		65		70		
cca gca agc cgt gtt cac ctc tgc cag aca act acc atc tgc ccg tac							499
Pro Ala Ser Arg Val His Leu Cys Gln Thr Thr Thr Ile Cys Pro Tyr							
	75		80		85		
ttc tac cac aca acc acc aaa gtc att tgt cta tac ttt tac tca aca							547
Phe Tyr His Thr Thr Thr Lys Val Ile Cys Leu Tyr Phe Tyr Ser Thr							
	90		95		100		
atc atc at							555
Ile Ile							
105							

<210> 136
 <211> 293
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..291

 <221> sig_peptide
 <222> 55..123
 <223> score 5.5
 seq ALALXTVMSXCGG/EX

<400> 136	
acaatttinst ctayagctca gaacagcaac tgctgagdgct gccttgaggaa raag atg	57
	Met
atc cta aac aaa gct ctg atg mtg ggr gcc ctc gcc ctg amm acm gtg	105
Ile Leu Asn Lys Ala Leu Met Xaa Gly Ala Leu Ala Leu Xaa Thr Val	
-20 -15 -10	
atg agc yct tgt gga ggt gaa sac att rts gmt gac cac gtw gch tct	153
Met Ser Xaa Cys Gly Gly Glu Xaa Ile Xaa Xaa Asp His Val Ala Ser	
-5 1 5 10	
tac rgt gta aac ttg tac cak yct tac ggt ccc tct ggc cag ttc acc	201
Tyr Xaa Val Asn Leu Tyr Xaa Xaa Tyr Gly Pro Ser Gly Gln Phe Thr	
15 20 25	
cat gaa ttt gat gga gay gag gag ttc tat gtg gac ctg gag agg aak	249
His Glu Phe Asp Gly Asp Glu Glu Phe Tyr Val Asp Leu Glu Arg Xaa	
30 35 40	
gag ast gtc tgg aag ttg cct ctg ttc cay aga mtt aga ttt ga	293
Glu Xaa Val Trp Lys Leu Pro Leu Phe His Arg Xaa Arg Phe	
45 50 55	

<210> 137
 <211> 352
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 62..352

<221> sig_peptide
<222> 62..130
<223> score 6.9
seq ALALTTVMSPCGG/ED

<400> 137
aggctctcac aattgctcta carctcagaa cagcaactgc traggctgcc ttgggaagag 60
g atg atc cta aac aaa gct ctg atg ctg ggg gcc cty gcc ctg acc acc 109
Met Ile Leu Asn Lys Ala Leu Met Leu Gly Ala Leu Ala Leu Thr Thr
-20 -15 -10
gtg atg agc ccy tgt gga ggt gaa gac att gtg gct gac cay gty gcc 157
Val Met Ser Pro Cys Gly Gly Glu Asp Ile Val Ala Asp His Val Ala
-5 1 5
tct tay ggt gta aac ttg tac cag tct tay ggt ccc tct ggs cag tac 205
Ser Tyr Gly Val Asn Leu Tyr Gln Ser Tyr Gly Pro Ser Gly Gln Tyr
10 15 20 25
asc cat gaa ttt gat gga gay gag sag ttc tay gtg gac ctg grg agg 253
Xaa His Glu Phe Asp Gly Asp Glu Xaa Phe Tyr Val Asp Leu Xaa Arg
30 35 40
aag gag act gtc tgg ygn ttg cct gtt cyc aga ttt aga aga ttt gac 301
Lys Glu Thr Val Trp Xaa Leu Pro Val Xaa Arg Phe Arg Arg Phe Asp
45 50 55
ccg caa ttt gca ctg aca aac atc gct gtg cta aaa cat aac ttg aac 349
Pro Gln Phe Ala Leu Thr Asn Ile Ala Val Leu Lys His Asn Leu Asn
60 65 70
atc 352
Ile

<210> 138
<211> 454
<212> DNA
<213> Homo sapiens

<220>
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<222> 31..453

<221> sig_peptide
<222> 31..78
<223> score 13.3
seq LLLLLAFLLLPTGA/EA

<400> 138
agcaactgac tgggcagcct ttcaggaaag atg cag cca ctc ctg ctt ctg ctg 54
Met Gln Pro Leu Leu Leu Leu Leu
-15 -10
gcc ttt ctc cta ccc act ggg gct gag gca ggg gag atc atc gga ggc 102
Ala Phe Leu Leu Pro Thr Gly Ala Glu Ala Gly Glu Ile Ile Gly Gly
-5 1 5

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cgg gag agc agg ccc cac tcc cgc ccc tac atg gcg tat ctt cag atc      150
Arg Glu Ser Arg Pro His Ser Arg Pro Tyr Met Ala Tyr Leu Gln Ile
  10                      15                      20
cag agt cca gca ggt cag agc aga tgt gga ggg ttc ctg gtg cga gaa      198
Gln Ser Pro Ala Gly Gln Ser Arg Cys Gly Gly Phe Leu Val Arg Glu
  25                      30                      35                      40
gac ttt gtg ctg aca gca gct cat tgc tgg gga agc aat ata aat gtc      246
Asp Phe Val Leu Thr Ala Ala His Cys Trp Gly Ser Asn Ile Asn Val
          45                      50                      55
acc ctg ggc gcc cac aat atc cag aga cgg gaa aac acc cag caa cac      294
Thr Leu Gly Ala His Asn Ile Gln Arg Arg Glu Asn Thr Gln Gln His
          60                      65                      70
atc act gcg cgc aga gcc atc cgc cac cct caa tat aat cag cgg acc      342
Ile Thr Ala Arg Arg Ala Ile Arg His Pro Gln Tyr Asn Gln Arg Thr
          75                      80                      85
atc cag aat gac atc atg tta ttg cag ctg agc aga aga gtc aga cgg      390
Ile Gln Asn Asp Ile Met Leu Leu Gln Leu Ser Arg Arg Val Arg Arg
          90                      95                      100
aat sgw rac gtg aac cca gtg gct ctg cta gag cca gga ggg act gag      438
Asn Xaa Xaa Val Asn Pro Val Ala Leu Leu Glu Pro Gly Gly Thr Glu
  105                      110                      115                      120
acc cgg gac gct gtg c
Thr Arg Asp Ala Val
          125

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<210> 139
 <211> 577
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 167..577

<221> sig_peptide
 <222> 167..217
 <223> score 6.9
 seq LFLTMLTLALVKS/QD

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ctcctcctcy tcttgccgcc gmrsncgctg cmrgaacttg ccagatcaga cccacggggc      60
tgccctcccc tgcgcactcc cctcgctgcc cgggcccggga gcgcassngg ccgcacaggt      120
atctttgctg tgctgtgcaa ggaactctgc tagctcaaga ttcaca atg ttg aaa      175
                                   Met Leu Lys
                                   -15
gcc ctt ttc cta act atg ctg act ctg gcg ctg gtc aag tca cag gac      223
Ala Leu Phe Leu Thr Met Leu Thr Leu Ala Leu Val Lys Ser Gln Asp
          -10                      -5                      1
acc gaa gaa acc atc acg tac acg caa tgc act gac gga tat gag tgg      271
Thr Glu Glu Thr Ile Thr Tyr Thr Gln Cys Thr Asp Gly Tyr Glu Trp
          5                      10                      15
gat cct gtg aga cag caa tgc aaa gat att gat gaa tgt gac att gtc      319
Asp Pro Val Arg Gln Gln Cys Lys Asp Ile Asp Glu Cys Asp Ile Val

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20	25	30	
cca gac gct tgt waa ggt gga atg aag tgt gtc aac cac tat gga gga			367
Pro Asp Ala Cys Xaa Gly Gly Met Lys Cys Val Asn His Tyr Gly Gly			
35	40	45	50
tas ctc tgc ctt ccg aaa aca gcc cag att att gtc aat aat gaa cag			415
Xaa Leu Cys Leu Pro Lys Thr Ala Gln Ile Ile Val Asn Asn Glu Gln			
55	60	65	
cct cag cag gaa aca caa cca gca gaa gga acc tca ggg gca acc acc			463
Pro Gln Gln Glu Thr Gln Pro Ala Glu Gly Thr Ser Gly Ala Thr Thr			
70	75	80	
ggg gtt gta gct gcc nnc agc atg gca acc agt gna gtg ttg mnn ggg			511
Gly Val Val Ala Ala Xaa Ser Met Ala Thr Ser Xaa Val Leu Xaa Gly			
85	90	95	
ggg gtt gta gct gcc nnc agc atg gca acc agt gna gtg ttg mnn ggg			559
Gly Gly Phe Val Ala Ser Ala Ala Ala Val Ala Gly Pro Glu Met Gln			
100	105	110	
act ggc cgg aat aac ttt			577
Thr Gly Arg Asn Asn Phe			
115	120		
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<211> 424			
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<222> 12..422			
<221> sig_peptide			
<222> 12..110			
<223> score 8.5			
seq LSFCVLLAGLCRG/NS			
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agagaggcaa g atg gct acg gca ggg ggt ggc tct ggg gct gac ccg gga			
Met Ala Thr Ala Gly Gly Gly Ser Gly Ala Asp Pro Gly			
-30 -25			
agt cgg ggt ctc ctt cgc ctt ctg tct ttc tgc gtc cta cta gca ggt			
Ser Arg Gly Leu Leu Arg Leu Leu Ser Phe Cys Val Leu Leu Ala Gly			
-20 -15 -10 -5			
ttg tgc agg gga aac tca gtg gag agg aag ata tat atc ccc tta aat			
Leu Cys Arg Gly Asn Ser Val Glu Arg Lys Ile Tyr Ile Pro Leu Asn			
1 5 10			
aaa aca gct ccc tgt gtt cgc ctg ctc aac gcc act cat cag att ggc			
Lys Thr Ala Pro Cys Val Arg Leu Leu Asn Ala Thr His Gln Ile Gly			
15 20 25			
tgc cag tct tca att agt gga gac aca ggg gtt atc cac gta gta gag			
Cys Gln Ser Ser Ile Ser Gly Asp Thr Gly Val Ile His Val Val Glu			
30 35 40			
aaa gag gag gac cta cag tgg gta ttg act gat ggc ccc aac ccc cct			
Lys Glu Glu Asp Leu Gln Trp Val Leu Thr Asp Gly Pro Asn Pro Pro			
45 50 55 60			

tac atg gtt ctg ctg gag agc aag cat ttt acc agg gat tta atg gag	338
Tyr Met Val Leu Leu Glu Ser Lys His Phe Thr Arg Asp Leu Met Glu	
65 70 75	
aag ctg aaa ggg aga acc agc cga att gct ggt ctt gca gtg tcc ttg	386
Lys Leu Lys Gly Arg Thr Ser Arg Ile Ala Gly Leu Ala Val Ser Leu	
80 85 90	
acc aag ccc agt cct gcc tca ggc ttc tct cct agt gt	424
Thr Lys Pro Ser Pro Ala Ser Gly Phe Ser Pro Ser	
95 100	

<210> 141
 <211> 490
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 118..489

<221> sig_peptide
 <222> 118..168
 <223> score 13
 seq IFLLCLAGRALA/AP

<400> 141	
gagtggtttc ctgttgccctg tctctaaacc cctccacatt cccgcggtcc ttcagactgc	60
ccggagagcg cgctctgcct gccgcctgcc tgcctgccac tgaggggtcc cagcacc	117
atg agg gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg	165
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu	
-15 -10 -5	
gca gcc cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa	213
Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu	
1 5 10 15	
gaa act gtg gca gag gtg act gag gta tct gtg gga gct aat cct gtc	261
Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val	
20 25 30	
cag gtg gaa gta gga gaa ttt gat gat ggt gca gag gaa acc gaa gag	309
Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu	
35 40 45	
gag gtg gtg gcg gaa aat ccc tgc cag aac cac cac tgc aaa cac ggc	357
Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly	
50 55 60	
aag gtg tgc gag ctg gat gag aac aac acc ccc atg tgc gtg tgc cag	405
Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln	
65 70 75	
gac ccc acc agc tgc cca gcc ccc att ggc gag ttt gag aag gtg tgc	453
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys	
80 85 90 95	
agc aat gac aac aag acc ttc gac tct tcc tgc cac t	490
Ser Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His	
100 105	

<210> 142

<211> 304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 118..303

<221> sig_peptide
 <222> 118..168
 <223> score 13
 seq IFLLCLAGRALA/AP

<400> 142
 gagtgggtttc ctgttgccctg tctctaaacc cctccacatt cccgcggtcc ttcagactgc 60
 ccggagagcg cgctctgcct gccgcctgcc tgccctgccac tgagggttcc cagcacc 117
 atg agg gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg 165
 Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 -15 -10 -5
 gca gcc cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa 213
 Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
 1 5 10 15
 gaa act gtg gca gag gtg act gag gta tct gtg gga gct aat cct gtc 261
 Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
 20 25 30
 cag gtg gaa gta gga gaa ttc ata ctt aat aaa caa ttt agg a 304
 Gln Val Glu Val Gly Glu Phe Ile Leu Asn Lys Gln Phe Arg
 35 40 45

<210> 143
 <211> 335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 118..333

<221> sig_peptide
 <222> 118..168
 <223> score 13
 seq IFLLCLAGRALA/AP

<400> 143
 gagtgggtttc ctgttgccctg tctctaaacc cctccacatt cccgcggtcc ttcagactgc 60
 ccggagagcg cgctctgcct gccgcctgcc tgccctgccac tgagggttcc cagcacc 117
 atg agg gcc tgg atc ttc ttt ctc ctt tgc ctg gcc ggg agg gcc ttg 165
 Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 -15 -10 -5
 gca gcc cct cag caa gaa gcc ctg cct gat gag aca gag gtg gtg gaa 213
 Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
 1 5 10 15

gaa act gtg gca gag gtg act gag gta tct gtg gga gct aat cct gtc	261
Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val	
20 25 30	
caa aat gaa att cat tgt ctc ctc caa acc tct acc acc aaa aca agt	309
Gln Asn Glu Ile His Cys Leu Leu Gln Thr Ser Thr Thr Lys Thr Ser	
35 40 45	
gtg ttg ctt ctg ggt tcc cat ctg tc	335
Val Leu Leu Leu Gly Ser His Leu	
50 55	

<210> 144
 <211> 305
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 41..304

<221> sig_peptide
 <222> 41..178
 <223> score 6.5
 seq LLIFVLLPKVVNT/SD

<400> 144	
caaaacatca gaggttgtca gactgcccta tcctctccaa atg aaa tct tca ggt	55
Met Lys Ser Ser Gly	
-45	
cca cct tct tac ttt att aaa agg gaa tcg tgg ggc tgg aca gac ttt	103
Pro Pro Ser Tyr Phe Ile Lys Arg Glu Ser Trp Gly Trp Thr Asp Phe	
-40 -35 -30	
cta atg aac ccg atg gtt atg atg atg gtt ctt cct tta ttg ata ttt	151
Leu Met Asn Pro Met Val Met Met Met Val Leu Pro Leu Leu Ile Phe	
-25 -20 -15 -10	
gtg ctt ctg cct aaa gtg gtc aac aca agt gat cct gac atg aga cgg	199
Val Leu Leu Pro Lys Val Val Asn Thr Ser Asp Pro Asp Met Arg Arg	
-5 1 5	
gaa atg gag cag tca atg aat atg ctg aat tcc aac cat gag ttg cct	247
Glu Met Glu Gln Ser Met Asn Met Leu Asn Ser Asn His Glu Leu Pro	
10 15 20	
gat gtt tct gag ttc atg aca aga ctc ttc tct tca aaa tca tct ggc	295
Asp Val Ser Glu Phe Met Thr Arg Leu Phe Ser Ser Lys Ser Ser Gly	
25 30 35	
aaa tct agc a	305
Lys Ser Ser	
40	

<210> 145
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 <212> DNA
 <213> Homo sapiens

<220>

004220"666ET560

00513999 "022400

<221> CDS
<222> 146..415

<221> sig_peptide
<222> 146..289
<223> score 4.1
seq VFMLIVSVLALIP/ET

<400> 145
aagagagcgg gaagccgagc tgggcgagaa gtaggggagg gcggtgctcc gccgcggtgg 60
cggttgctat cgcttcgcag aacctactca ggcagccagc tgagaagagt tgagggaaag 120
tgctgctgct gggctcgcag acgcg atg gat aac gtg cag ccg aaa ata aaa 172
Met Asp Asn Val Gln Pro Lys Ile Lys
-45 -40
cat cgc ccc ttc tgc ttc agt gtg aaa ggc cac gtg aag atg ctg cgg 220
His Arg Pro Phe Cys Phe Ser Val Lys Gly His Val Lys Met Leu Arg
-35 -30 -25
ctg gat att atc aac tca ctg gta aca aca gta ttc atg ctc atc gta 268
Leu Asp Ile Ile Asn Ser Leu Val Thr Val Phe Met Leu Ile Val
-20 -15 -10
tct gtg ttg gca ctg ata cca gaa acc aca aca ttg aca gtt ggt gga 316
Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr Val Gly Gly
-5 1 5
ggg gtg ttt gca ctt gtg aca gca gta tgc tgt ctt gcc gac ggg gcc 364
Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala Asp Gly Ala
10 15 20 25
ctt att tac cgg aag ctt ctg ttc aat ccc agc ggt cct tac cag aaa 412
Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro Tyr Gln Lys
30 35 40
aag 415
Lys

<210> 146
<211> 461
<212> DNA
<213> Homo sapiens

<220>
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<222> 29..460

<221> sig_peptide
<222> 29..109
<223> score 8.6
seq ATVLLLSFGSVAA/SH

<400> 146
aggtagcggga agtctgaagc cggtaaac atg gcc gtc acc gac agc ctc agc 52
Met Ala Val Thr Asp Ser Leu Ser
-25 -20
cgg gct gcg act gtc ttg gca act gtg ttg ctc ttg tcc ttc ggc agc 100
Arg Ala Ala Thr Val Leu Ala Thr Val Leu Leu Leu Ser Phe Gly Ser

	-15		-10		-5	
gtg gcc gct agt cat atc gag gat caa gca gaa caa ttc ttt aga agt						148
Val Ala Ala Ser His Ile Glu Asp Gln Ala Glu Gln Phe Phe Arg Ser						
	1		5		10	
ggc cat aca aac aac tgg gct gtt ctg gtg tgt aca tcc cga ttc tgg						196
Gly His Thr Asn Asn Trp Ala Val Leu Val Cys Thr Ser Arg Phe Trp						
	15		20		25	
ttt aat tat cga cat gtt gca aat acc ctt tct gtt tat aga agt gtc						244
Phe Asn Tyr Arg His Val Ala Asn Thr Leu Ser Val Tyr Arg Ser Val						
	30		35		40	45
aag agg cta ggt att cct gac agt cac att gtc cta atg ctt gca gat						292
Lys Arg Leu Gly Ile Pro Asp Ser His Ile Val Leu Met Leu Ala Asp						
	50		55		60	
gat atg gcc tgt aat cct aga aat ccc aaa cca gct aca gtg ttt agt						340
Asp Met Ala Cys Asn Pro Arg Asn Pro Lys Pro Ala Thr Val Phe Ser						
	65		70		75	
cac aag aat atg gaa cta aat gtg tat gga gat gat gtg gaa gtg gat						388
His Lys Asn Met Glu Leu Asn Val Tyr Gly Asp Asp Val Glu Val Asp						
	80		85		90	
tat aga agt tat gag gta act gtg gag aat ttt tta cgg gta nta act						436
Tyr Arg Ser Tyr Glu Val Thr Val Glu Asn Phe Leu Arg Val Xaa Thr						
	95		100		105	
ggg agg atc cca cct agt act cct c						461
Gly Arg Ile Pro Pro Ser Thr Pro						
	110		115			

<210> 147
 <211> 649
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 269..649

<221> sig_peptide
 <222> 269..337
 <223> score 4.1
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<400> 147	
gagagaaaga gaaacgggag caagagagaa ggaggcccag acagtgaggg caggagggag	60
agaagagacg cagaaggaga gcgagcgaga gagaaagggg tctggattgg aggggagagc	120
aagggagggga ggaaggcggg gagagagggc ggggcctcgg gagggtgaaa ggagggagga	180
gaagggcggg gcacggaggc ccgagcgagg gacaagactc cgactccagc tctgactttt	240
ttcgcggctc tcggcttcca ctgcagcc atg tca ctc ctc ttg ctg gtg gtc	292
	Met Ser Leu Leu Leu Leu Val Val
	-20
tca gcc ctt cac atc ctc att ctt ata ctg ctt ttc gtg gcc act ttg	340
Ser Ala Leu His Ile Leu Ile Leu Ile Leu Leu Phe Val Ala Thr Leu	
	-15 -10 -5 1
gac aag tcc wgg tgg act ctc cct ggg aaa gag tcc ctg aat ctc tgg	388
Asp Lys Ser Xaa Trp Thr Leu Pro Gly Lys Glu Ser Leu Asn Leu Trp	

	5		10		15		
tac gac tgc acg tgg aac aac gac acc aaa aca tgg gcc tgc agt aat						436	
Tyr Asp Cys Thr Trp Asn Asn Asp Thr Lys Thr Trp Ala Cys Ser Asn							
	20		25		30		
gtc agc gag aat ggc tgg ctg aag gcg gtg cag gtc ctc atg gtg ctc						484	
Val Ser Glu Asn Gly Trp Leu Lys Ala Val Gln Val Leu Met Val Leu							
	35		40		45		
tcc ctc att ctc tgc tgt ctc tcc ttc atc ctg ttc atg ttc cag ctc						532	
Ser Leu Ile Leu Cys Cys Leu Ser Phe Ile Leu Phe Met Phe Gln Leu							
	50		55		60		
tac acc atg cga cga gga ggt ctc ttc tat gcc acc ggc ctc tgc cag						580	
Tyr Thr Met Arg Arg Gly Gly Leu Phe Tyr Ala Thr Gly Leu Cys Gln							
	70		75		80		
ctt tgc acc agc gtg gcg gtg ttt act nnn gcc ttg atc tat gcc att						628	
Leu Cys Thr Ser Val Ala Val Phe Thr Xaa Ala Leu Ile Tyr Ala Ile							
	85		90		95		
cac gcc gag gag atc ctg gag						649	
His Ala Glu Glu Ile Leu Glu							
	100						

<210> 148
 <211> 547
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 269..547

<221> sig_peptide
 <222> 269..406
 <223> score 9.8
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<400> 148	
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agaagagacg cagaaggaga gcgagcgaga gagaaaggg tctggattgg aggggagagc	120
aaggagggga ggaaggcggg gagagaggcg ggggcctcgg gagggtgaaa ggagggagga	180
gaaggcgggg gcacggaggc ccgagcgagg gacaagactc cgactccagc tctgactttt	240
ttcgcggtct tcggcttcca ctgcagcc atg tca ctc ctc ttg ctg gtg gtc	292
	Met Ser Leu Leu Leu Leu Val Val
	-45 -40
tca gcc ctt cac atc ctc att ctt ata ctg ctt ttc gtg ggc mac ttt	340
Ser Ala Leu His Ile Leu Ile Leu Ile Leu Leu Phe Val Gly Xaa Phe	
	-35 -30 -25
gga caa ggc tgg ctg aag gcg gtg cag gtc ctc atg gtg ctc tcc ctc	388
Gly Gln Gly Trp Leu Lys Ala Val Gln Val Leu Met Val Leu Ser Leu	
	-20 -15 -10
att ctc tgc tgt ctc tcc ttc atc ctg ttc atg ttc cag ctc tac rsc	436
Ile Leu Cys Cys Leu Ser Phe Ile Leu Phe Met Phe Gln Leu Tyr Xaa	
	-5 1 5 10
atg cga cga gga ggt ctc ttc tat gcc asc ggc ctc tgc cag ctt tgc	484
Met Arg Arg Gly Gly Leu Phe Tyr Ala Xaa Gly Leu Cys Gln Leu Cys	

	15	20	25	
acc agc gtg gcg gtg ttw act nnn gcc ttg atc tat gcc att cac gcc				532
Thr Ser Val Ala Val Xaa Thr Xaa Ala Leu Ile Tyr Ala Ile His Ala				
	30	35	40	
gag gag atc ctg gag				547
Glu Glu Ile Leu Glu				
	45			
<210> 149				
<211> 415				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> 4..414				
<221> sig_peptide				
<222> 4..120				
<223> score 5.5				
seq LLLRAAFQSL LDA/QA				
<400> 149				
aca atg gag ctc tgc gag tct gtg cag aaa ggc ttc cag atg ctg gcg				48
Met Glu Leu Ser Glu Ser Val Gln Lys Gly Phe Gln Met Leu Ala				
	-35	-30	-25	
gat ccc cgc tcc ttc gac tcc aac gcc ttc acg ctt ctc ctc cgg gcg				96
Asp Pro Arg Ser Phe Asp Ser Asn Ala Phe Thr Leu Leu Leu Arg Ala				
	-20	-15	-10	
gca ttc cag agt ctg ctg gac gcc cag gcg gac gag gcc gtg tta gat				144
Ala Phe Gln Ser Leu Leu Asp Ala Gln Ala Asp Glu Ala Val Leu Asp				
	-5	1	5	
cat cca gac ttg aaa cat atc gac cca gtg gtt tta aaa cat tgt cat				192
His Pro Asp Leu Lys His Ile Asp Pro Val Val Leu Lys His Cys His				
	10	15	20	
gca gca gct gca act tac ata cta gag gca gga aag cac cga gct gac				240
Ala Ala Ala Ala Thr Tyr Ile Leu Glu Ala Gly Lys His Arg Ala Asp				
	25	30	35	40
aag tca act cta agc act tat cta gaa gac tgt aaa ttt gac aga gag				288
Lys Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu				
	45	50	55	
cga ata gaa ctg ttt tgc acg gaa tat cag aat aat aag aat tcc cta				336
Arg Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu				
	60	65	70	
gaa atc cta ctg gga agt ata ggc aga tct ctc cct cat ata acg gat				384
Glu Ile Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp				
	75	80	85	
gtt tct tgg cgc ttg gaa tat cag ata aag a				415
Val Ser Trp Arg Leu Glu Tyr Gln Ile Lys				
	90	95		
<210> 150				
<211> 285				

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..283

<221> sig_peptide
<222> 74..151
<223> score 9.3
seq MXPLLWLLPXXWA/VP

<400> 150
actctcgggg agggagttgg ggaagctggg ttggctgggt tggtagctcc tacctactgt 60
gtggcaagaa ggt atg ggt cat gaa cag aac caa gga gct gcg ctg cta 109
Met Gly His Glu Gln Asn Gln Gly Ala Ala Leu Leu
-25 -20 -15
cag atg thw cca ctt ctg tgg ctg cta ccc cam wcc tgg gcc gtc cct 157
Gln Met Xaa Pro Leu Leu Trp Leu Leu Pro Xaa Xaa Trp Ala Val Pro
-10 -5 1
gaa rgg ttt cct atc gct gaa gtg ttc acg ctg aag ccc ctg gag ttt 205
Glu Xaa Phe Pro Ile Ala Glu Val Phe Thr Leu Lys Pro Leu Glu Phe
5 10 15
ggc aag ccc aac act ttg gtc tgt wtt rwc agt aat ctc ttc cca ccc 253
Gly Lys Pro Asn Thr Leu Val Cys Xaa Xaa Ser Asn Leu Phe Pro Pro
20 25 30
atg ctg aca gtg aam wgg cag cat cat tcc gt 285
Met Leu Thr Val Xaa Xaa Gln His His Ser
35 40

<210> 151
<211> 659
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 174..659

<221> sig_peptide
<222> 174..221
<223> score 5.6
seq KWLLCMLLVLGTA/IV

<400> 151
agggttcgt gcggtgaggc tcgctcgcgc ggcagsrgat ggccgaggcc tcttggttct 60
gcggcacgtg acggtcgggc cgctccgcc tctctcttta ctgcggcgcg gggcaagggtg 120
tgcgggcggg aaggggcacg ggcacccccg cggtccycgg gaggctagag atc atg 176
Met
gaa ggg aag tgg ttg ctg tgt atg tta ctg gtg ctt gga act gct att 224
Glu Gly Lys Trp Leu Leu Cys Met Leu Leu Val Leu Gly Thr Ala Ile
-15 -10 -5 1

gtt gag gct cat gat gga cat gat gat gat gtg att gat att gag gat	272
Val Glu Ala His Asp Gly His Asp Asp Asp Val Ile Asp Ile Glu Asp	
5 10 15	
gac ctt gac gat gtc att gaa gag gta gaa gac tca aaa cca gat acc	320
Asp Leu Asp Asp Val Ile Glu Glu Val Glu Asp Ser Lys Pro Asp Thr	
20 25 30	
act gct cct cct tca tct ccc aag gtt act tac aaa gct cca gtt cca	368
Thr Ala Pro Pro Ser Ser Pro Lys Val Thr Tyr Lys Ala Pro Val Pro	
35 40 45	
aca ggg gaa gta tat ttt gct gat tct ttt gac aga gga act ctg tca	416
Thr Gly Glu Val Tyr Phe Ala Asp Ser Phe Asp Arg Gly Thr Leu Ser	
50 55 60 65	
ggg tgg att tta tcc aaa gcc aag aaa gac gat acc gat gat gaa att	464
Gly Trp Ile Leu Ser Lys Ala Lys Lys Asp Asp Thr Asp Asp Glu Ile	
70 75 80	
gcc aaa tat gat gga aag tgg gag gta gag gaa atg aag gag tca aag	512
Ala Lys Tyr Asp Gly Lys Trp Glu Val Glu Glu Met Lys Glu Ser Lys	
85 90 95	
ctt cca ggt gat aaa gga ctt gtg ttg atg tct cgg gcc aag cat cat	560
Leu Pro Gly Asp Lys Gly Leu Val Leu Met Ser Arg Ala Lys His His	
100 105 110	
gcc atc tct gct aaa ctg aac aag ccc ttc ctg ttt gac acc aag cct	608
Ala Ile Ser Ala Lys Leu Asn Lys Pro Phe Leu Phe Asp Thr Lys Pro	
115 120 125	
ctc att gtt cag tat gag gtt aat ttc caa aat gga ata gaa tgt ggt	656
Leu Ile Val Gln Tyr Glu Val Asn Phe Gln Asn Gly Ile Glu Cys Gly	
130 135 140 145	
ggt	659
Gly	

<210> 152
 <211> 629
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 144..629

<221> sig_peptide
 <222> 144..191
 <223> score 5.6
 seq KWLLCMLLVLGTA/IV

<400> 152	
agggcttcgt gcggtgaggc tcgctcgcgc ggcagsrgat ggccgaggcc tcttggttct	60
gcggcacgtg acggtcgggc cgctccgcc tcyctcttta ctgcggcgcg ggcaccccg	120
cggctcctcgg gaggetagag atc atg gaa ggg aag tgg ttg ctg tgt atg tta	173
Met Glu Gly Lys Trp Leu Leu Cys Met Leu	
-15 -10	
ctg gtg ctt gga act gct att gtt gag gct cat gat gga cat gat gat	221
Leu Val Leu Gly Thr Ala Ile Val Glu Ala His Asp Gly His Asp Asp	
-5 1 5 10	

gat gtg att gat att gag gat gac ctt gac gat gtc att gaa gag gta	269
Asp Val Ile Asp Ile Glu Asp Asp Leu Asp Asp Val Ile Glu Glu Val	
15 20 25	
gaa gac tca aaa cca gat acc act gct cct cct tca tct ccc aag gtt	317
Glu Asp Ser Lys Pro Asp Thr Thr Ala Pro Pro Ser Ser Pro Lys Val	
30 35 40	
act tac aaa gct cca gtt cca aca ggg gaa gta tat ttt gct gat tct	365
Thr Tyr Lys Ala Pro Val Pro Thr Gly Glu Val Tyr Phe Ala Asp Ser	
45 50 55	
ttt gac aga gga act ctg tca ggg tgg att tta tcc aaa gcc aag aaa	413
Phe Asp Arg Gly Thr Leu Ser Gly Trp Ile Leu Ser Lys Ala Lys Lys	
60 65 70	
gac gat acc gat gat gaa att gcc aaa tat gat gga aag tgg gag gta	461
Asp Asp Thr Asp Asp Glu Ile Ala Lys Tyr Asp Gly Lys Trp Glu Val	
75 80 85 90	
gag gaa atg aag gag tca aag ctt cca ggt gat aaa gga ctt gtg ttg	509
Glu Glu Met Lys Glu Ser Lys Leu Pro Gly Asp Lys Gly Leu Val Leu	
95 100 105	
atg tct cgg gcc aag cat cat gcc atc tct gct aaa ctg aac aag ccc	557
Met Ser Arg Ala Lys His His Ala Ile Ser Ala Lys Leu Asn Lys Pro	
110 115 120	
ttc ctg ttt gac acc aag cct ctc att gtt cag tat gag gtt aat ttc	605
Phe Leu Phe Asp Thr Lys Pro Leu Ile Val Gln Tyr Glu Val Asn Phe	
125 130 135	
caa aat gga ata gaa tgt ggt ggt	629
Gln Asn Gly Ile Glu Cys Gly Gly	
140 145	
<210> 153	
<211> 290	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 39..290	
<221> sig_peptide	
<222> 39..86	
<223> score 11.9	
seq VLLSVVLLALSSA/QS	
<400> 153	
aacgcagagt tgggagcaac tccagagcct ccttcaag atg ctg ctg gtc ctg ctc	56
Met Leu Leu Val Leu Leu	
-15	
tca gtg gtc ctt ctg gct ctg agc tca gct cag agc aca gat aat gat	104
Ser Val Val Leu Leu Ala Leu Ser Ser Ala Gln Ser Thr Asp Asn Asp	
-10 -5 1 5	
gtg aac tat gaa gac ttt act ttc acc ata cca gat gta gag gac tca	152
Val Asn Tyr Glu Asp Phe Thr Phe Thr Ile Pro Asp Val Glu Asp Ser	
10 15 20	
agt cag aga cca gat cag gga ccc cag aga cct cct cct gaa gga ctc	200

Ser	Gln	Arg	Pro	Asp	Gln	Gly	Pro	Gln	Arg	Pro	Pro	Pro	Glu	Gly	Leu	
	25						30					35				
cta	cct	aga	ccc	cct	ggt	gat	agt	ggt	aac	caa	gat	gat	ggt	cct	cag	248
Leu	Pro	Arg	Pro	Pro	Gly	Asp	Ser	Gly	Asn	Gln	Asp	Asp	Gly	Pro	Gln	
	40					45					50					
cag	aga	cca	cca	aaa	cca	gga	ggc	cat	cac	cgc	cat	cct	ccc			290
Gln	Arg	Pro	Pro	Lys	Pro	Gly	Gly	His	His	Arg	His	Pro	Pro			
55					60					65						

<210> 154
 <211> 460
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..459

<221> sig_peptide
 <222> 10..99
 <223> score 12.2
 seq LLLLLLLCVFLVKS/QG

<400> 154																	
ctagtctac	atg	aaa	agg	atg	ggt	tct	tgg	agc	ttc	cac	aaa	ctt	aaa	acc		51	
	Met	Lys	Arg	Met	Val	Ser	Trp	Ser	Phe	His	Lys	Leu	Lys	Thr			
	-30					-25					-20						
atg	aaa	cat	cta	tta	ttg	cta	cta	ttg	tgt	ggt	ttt	cta	ggt	aag	tcc	99	
Met	Lys	His	Leu	Leu	Leu	Leu	Leu	Cys	Val	Phe	Leu	Val	Lys	Ser			
	-15					-10				-5							
caa	ggt	gtc	aac	gac	aat	gag	gag	ggt	ttc	ttc	agt	gcc	cgt	ggt	cat	147	
Gln	Gly	Val	Asn	Asp	Asn	Glu	Glu	Gly	Phe	Phe	Ser	Ala	Arg	Gly	His		
1			5					10					15				
cga	ccc	ctt	gac	aag	aag	aga	gaa	gag	gct	ccc	agc	ctg	agg	cct	gcc	195	
Arg	Pro	Leu	Asp	Lys	Lys	Arg	Glu	Glu	Ala	Pro	Ser	Leu	Arg	Pro	Ala		
			20					25				30					
cca	ccg	ccc	atc	agt	gga	ggt	ggc	tat	cgg	gct	cgt	cca	gcc	aaa	gca	243	
Pro	Pro	Pro	Ile	Ser	Gly	Gly	Gly	Tyr	Arg	Ala	Arg	Pro	Ala	Lys	Ala		
			35				40				45						
gct	gcc	act	caa	aag	aaa	gta	gaa	aga	aaa	gcc	cct	gat	gct	gga	ggc	291	
Ala	Ala	Thr	Gln	Lys	Lys	Val	Glu	Arg	Lys	Ala	Pro	Asp	Ala	Gly	Gly		
	50					55				60							
tgt	ctt	cac	gct	gac	cca	gac	ctg	ggg	gtg	ttg	tgt	cct	aca	gga	tgt	339	
Cys	Leu	His	Ala	Asp	Pro	Asp	Leu	Gly	Val	Leu	Cys	Pro	Thr	Gly	Cys		
	65				70				75			80					
cag	ttg	caa	gag	gct	ttg	cta	caa	cag	gaa	agg	cca	atc	aga	aat	agt	387	
Gln	Leu	Gln	Glu	Ala	Leu	Leu	Gln	Gln	Glu	Arg	Pro	Ile	Arg	Asn	Ser		
				85				90					95				
ggt	gat	gag	tta	aat	aac	aat	gtg	gaa	gct	ggt	tcc	cag	acc	tcc	tct	435	
Val	Asp	Glu	Leu	Asn	Asn	Asn	Val	Glu	Ala	Val	Ser	Gln	Thr	Ser	Ser		
			100				105					110					
tct	tcc	ttt	cag	tac	atg	tat	ttg	c								460	
Ser	Ser	Phe	Gln	Tyr	Met	Tyr	Leu										

115

120

<210> 155
 <211> 363
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..363

<221> sig_peptide
 <222> 10..99
 <223> score 12.2
 seq LLLLLLCVFLVKS/QG

<400> 155
 ctagtctac atg aaa agg atg gtt tct tgg agc ttc cac aaa ctt aaa acc 51
 Met Lys Arg Met Val Ser Trp Ser Phe His Lys Leu Lys Thr
 -30 -25 -20
 atg aaa cat cta tta ttg cta cta ttg tgt gtt ttt cta gtt aag tcc 99
 Met Lys His Leu Leu Leu Leu Cys Val Phe Leu Val Lys Ser
 -15 -10 -5
 caa ggt gtc aac gac aat gag gag ggt ttc ttc agt gcc cgt ggt cat 147
 Gln Gly Val Asn Asp Asn Glu Glu Gly Phe Phe Ser Ala Arg Gly His
 1 5 10 15
 cga ccc ctt gac aag aag aga gtg ccc tcc cga gta gcc ggg acc aca 195
 Arg Pro Leu Asp Lys Lys Arg Val Pro Ser Arg Val Ala Gly Thr Thr
 20 25 30
 ggc acc cgc cac cac gcc caa cta att ttt gta ttt tta gta gag aca 243
 Gly Thr Arg His His Ala Gln Leu Ile Phe Val Phe Leu Val Glu Thr
 35 40 45
 ggg ttt cac ctt att ggc cag gtt ggt cta gaa ctt cag acc tca agt 291
 Gly Phe His Leu Ile Gly Gln Val Gly Leu Glu Leu Gln Thr Ser Ser
 50 55 60
 cat ctg ccc acc tca gcc tcc caa agt gta ggg att tca ggt ggg agc 339
 His Leu Pro Thr Ser Ala Ser Gln Ser Val Gly Ile Ser Gly Gly Ser
 65 70 75 80
 cac tgc acc agc acc ccc aac gcc 363
 His Cys Thr Ser Thr Pro Asn Ala
 85

<210> 156
 <211> 333
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 97..333

<221> sig_peptide
 <222> 97..216

<223> score 4.3
seq LVPVFLLPKALAS/AQ

<400> 156
actctctcag cttcagaggg aaaaaatggt tgtagatttc tggacttggg agcagacatt 60
tcaagaacta atccaagagg caaaaccccg ggccac atg gac gct gaa gtt gga 114
Met Asp Ala Glu Val Gly
-40 -35
tgg caa cct tca gct aga ctg cct ggc tca agg gtg gaa gca ata cca 162
Trp Gln Pro Ser Ala Arg Leu Pro Gly Ser Arg Val Glu Ala Ile Pro
-30 -25 -20
aca gag agc att tgg ctg gtt ccg gtg ttc ctc ctg cca gcg aag ttg 210
Thr Glu Ser Ile Trp Leu Val Pro Val Phe Leu Leu Pro Ala Lys Leu
-15 -10 -5
gct tcc gcc caa gtg cag att ctg tgc cac acg tac tgg gag cac tgg 258
Ala Ser Ala Gln Val Gln Ile Leu Cys His Thr Tyr Trp Glu His Trp
1 5 10
aca tcc cag ggt cag gtg cgt atg agg ctc ttt ggc caa agg tgc cag 306
Thr Ser Gln Gly Gln Val Arg Met Arg Leu Phe Gly Gln Arg Cys Gln
15 20 25 30
aag tgc tcc tgg tcc caa tat gag atg 333
Lys Cys Ser Trp Ser Gln Tyr Glu Met
35

<210> 157
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 189..485

<221> sig_peptide
<222> 189..230
<223> score 4
seq ALLTAFSSSVAVT/DK

<400> 157
agccatttct actttgcccc cccacagatg tagttttctc tgcgcgtgtg cgttttccct 60
cctccccgcc ctcagggtcc acggccacca tggcgtatta ggggcagcag tgcctgcggc 120
agcattggcc tttgcagcgg cggcagcagc accaggctct gcagcggcaa cccccagcgg 180
cttaagcc atg gcg ctt ctc acg gca ttc agc agc agc gtt gct gta acc 230
Met Ala Leu Leu Thr Ala Phe Ser Ser Ser Val Ala Val Thr
-10 -5
gac aaa gac acc ttc gaa tta agc aca ttc ctc gat tcc agc aaa gca 278
Asp Lys Asp Thr Phe Glu Leu Ser Thr Phe Leu Asp Ser Ser Lys Ala
1 5 10 15
ccg caa cat gac cga aat gag ctt cct gag cag cga ggt gtt ggt ggg 326
Pro Gln His Asp Arg Asn Glu Leu Pro Glu Gln Arg Gly Val Gly Gly
20 25 30
gga ctt gat gtc ccc ttc gac cmg tgc ggt ttg ggg gct gaa gaa agc 374

Gly	Leu	Asp	Val	Pro	Phe	Asp	Xaa	Ser	Gly	Leu	Gly	Ala	Glu	Glu	Ser		
		35					40					45					
cta	ggt	ctc	tta	gat	gat	tac	ctg	grg	gtg	gcc	aag	cac	ttc	aaa	cct		422
Leu	Gly	Leu	Leu	Asp	Asp	Tyr	Leu	Xaa	Val	Ala	Lys	His	Phe	Lys	Pro		
		50				55					60						
cat	ggg	ttc	tcc	agc	gac	aag	gct	aag	gcg	ggc	tcc	tcc	gaa	tgg	ctg		470
His	Gly	Phe	Ser	Ser	Asp	Lys	Ala	Lys	Ala	Gly	Ser	Ser	Glu	Trp	Leu		
65					70					75					80		
gct	gtg	gat	ggg	ttg	gt												487
Ala	Val	Asp	Gly	Leu													
					85												

<210> 158
 <211> 216
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 26..214

 <221> sig_peptide
 <222> 26..91
 <223> score 3.7
 seq VGASASATPVVRA/AR

<400> 158																	
agtccttaaa	acccggagga	gcggg	atg	gcg	cgc	ttt	gac	tct	gga	gtg	gga						52
			Met	Ala	Arg	Phe	Asp	Ser	Gly	Val	Gly						
			-20								-15						
gtg	gga	gcg	agc	gct	tct	gcg	act	cca	ggt	gtg	aga	gcc	gca	agg	gca		100
Val	Gly	Ala	Ser	Ala	Ser	Ala	Thr	Pro	Val	Val	Arg	Ala	Ala	Arg	Ala		
			-10				-5					1					
tgg	gaa	ttg	acg	cca	ctc	acc	gac	ccc	cag	tct	caa	tct	caa	cgc	tgt		148
Trp	Glu	Leu	Thr	Pro	Leu	Thr	Asp	Pro	Gln	Ser	Gln	Ser	Gln	Arg	Cys		
5					10					15							
gag	gaa	acc	tcg	act	ttg	cca	ggt	ccc	caa	ggg	cag	cgg	ggc	tcg	gcg		196
Glu	Glu	Thr	Ser	Thr	Leu	Pro	Gly	Pro	Gln	Gly	Gln	Arg	Gly	Ser	Ala		
20					25					30					35		
agc	gag	gca	ccc	ttc	ycc	gc											216
Ser	Glu	Ala	Pro	Phe	Xaa												
					40												

<210> 159
 <211> 413
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..412

 <221> sig_peptide

<222> 92..160
 <223> score 13.6
 seq LVLLLLLVLLPTDA/SV

<400> 159
 cagttgcttt gggaagtgtt tgggaccaga tggattgtag ggagtaggggt acaatacagt 60
 ctgktctcct ccagctcctt ctttctgcaa c atg ggg aag aac aaa ctc ctt 112
 Met Gly Lys Asn Lys Leu Leu
 -20
 cat cca agt ctg gtt ctt ctc ctc ttg gtc ctc ctg ccc aca gac gcc 160
 His Pro Ser Leu Val Leu Leu Leu Val Leu Leu Pro Thr Asp Ala
 -15 -10 -5
 tca gtc tct gga aaa ccg cag tat atg gtt ctg gtc ccc tcc ctg ctc 208
 Ser Val Ser Gly Lys Pro Gln Tyr Met Val Leu Val Pro Ser Leu Leu
 1 5 10 15
 cac act gag acc act gag aag ggc tgt gtc ctt ctg agc tac ctg aat 256
 His Thr Glu Thr Thr Glu Lys Gly Cys Val Leu Leu Ser Tyr Leu Asn
 20 25 30
 gag aca gtg act gta agt gct tcc ttg gag tct gtc agg gga aac agg 304
 Glu Thr Val Thr Val Ser Ala Ser Leu Glu Ser Val Arg Gly Asn Arg
 35 40 45
 agc ctc ttc act gac ctg gag gcg gag aat gac gta ctc cac tgt gtc 352
 Ser Leu Phe Thr Asp Leu Glu Ala Glu Asn Asp Val Leu His Cys Val
 50 55 60
 gcc ttc gct gtc cca aag tct tca tcc aat gag gag gta atg ttc ctc 400
 Ala Phe Ala Val Pro Lys Ser Ser Ser Asn Glu Glu Val Met Phe Leu
 65 70 75 80
 act gtc caa gtg a 413
 Thr Val Gln Val

<210> 160
 <211> 403
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 120..401

<221> sig_peptide
 <222> 120..200
 <223> score 9.8
 seq LIPLIFLISGAEA/AS

<400> 160
 atataagcag aggagctgtc cgtgtgtctga aacggcccga gaagctcgcc cggagaacgg 60
 ggaggaatat gctgtggagc tcctctgccataatacaaaa aagaggaaat ctttcaaac 119
 atg gct gaa gca aag acc cac tgg ctt gga gca gcc ctg tct ctt atc 167
 Met Ala Glu Ala Lys Thr His Trp Leu Gly Ala Ala Leu Ser Leu Ile
 -25 -20 -15
 cct tta att ttc ctc atc tct ggg gct gaa gca gct tca ttt cag aga 215
 Pro Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg

-10	-5	1	5	
aac cag ctg ctt cag aaa gaa cca gac ctc agg ttg gaa aat gtc caa				263
Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val Gln				
10	15	20		
aag ttt ccc agt cct gaa atg atc agg gct ttg gag tac ata gaa aac				311
Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu Asn				
25	30	35		
ctc cga caa caa gct cat aag gaa gaa agc agc cca gat tat aat ccc				359
Leu Arg Gln Gln Ala His Lys Glu Glu Ser Ser Pro Asp Tyr Asn Pro				
40	45	50		
tac caa ggt gtc tct gtc ccc ctt cag caa aaa gaa aat ggc ga				403
Tyr Gln Gly Val Ser Val Pro Leu Gln Gln Lys Glu Asn Gly				
55	60	65		

<210> 161
 <211> 459
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..457
 <221> sig_peptide
 <222> 17..106
 <223> score 8.8
 seq ALLLLALGVERALA/LP

<400> 161	
accaagggaa cgga aa atg gcg cct cac ggc ccg ggt agt ctt acg acc ctg	52
Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu	
-30	-25
gtg ccc tgg gct gcc gcc ctg ctc ctc gct ctg ggc gtg gaa agg gct	100
Val Pro Trp Ala Ala Ala Leu Leu Leu Ala Leu Gly Val Glu Arg Ala	
-15	-10
ctg gcg cta ccc gag ata tgc acc caa tgt cca ggg agc gtg caa aat	148
Leu Ala Leu Pro Glu Ile Cys Thr Gln Cys Pro Gly Ser Val Gln Asn	
1	5
ttg tca aaa gtg gcc ttt tat tgt aaa acg aca cga gag cta atg ctg	196
Leu Ser Lys Val Ala Phe Tyr Cys Lys Thr Arg Glu Leu Met Leu	
15	20
cat gcc cgt tgc tgc ctg aat cag aag ggc acc atc ttg ggg ctg gat	244
His Ala Arg Cys Cys Leu Asn Gln Lys Gly Thr Ile Leu Gly Leu Asp	
35	40
ctc cag aac tgt tct ctg gag gac cct ggt cca aac ttt cat cag gca	292
Leu Gln Asn Cys Ser Leu Glu Asp Pro Gly Pro Asn Phe His Gln Ala	
50	55
cat acc act gtc atc ata gac ctg caa gca aac ccc ctc aaa ggt gac	340
His Thr Thr Val Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp	
65	70
ttg gcc aac acc ttc cgt ggc ttt act cag ctc cag act ctg ata ctg	388
Leu Ala Asn Thr Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu	
80	85
	90

cca caa cat gtc aac tgt cct gga gga att aat gcc tgg aat act atc 436
 Pro Gln His Val Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile
 95 100 105 110
 acc tct tat ata gac aac caa at 459
 Thr Ser Tyr Ile Asp Asn Gln
 115

<210> 162
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 98..391

<221> sig_peptide
 <222> 98..160
 <223> score 7.9
 seq GLVLATLLSQVSP/FK

<400> 162
 tttccggtac ctgtgagtca gctaggggag ggcagctctc acccaggctg atagttcggg 60
 gacctggcctt tatctactgg atgagttccg ctgggag atg gaa cat agc acg ttt 115
 Met Glu His Ser Thr Phe
 -20
 ctc tct ggc ctg gta ctg gct acc ctt ctc tcg caa gtg agc ccc ttc 163
 Leu Ser Gly Leu Val Leu Ala Thr Leu Leu Ser Gln Val Ser Pro Phe
 -15 -10 -5 1
 aag ata cct ata gag gaa ctt gag gac aga gtg ttt gtg aat tgc aat 211
 Lys Ile Pro Ile Glu Glu Leu Glu Asp Arg Val Phe Val Asn Cys Asn
 5 10 15
 acc agc atc aca trg gta gag gga acg gtg gga aca ctg ctc tca gac 259
 Thr Ser Ile Thr Xaa Val Glu Gly Thr Val Gly Thr Leu Leu Ser Asp
 20 25 30
 att aca aga ctg gac ctg gga aaa cgc atc ctg gac cca cga gga ata 307
 Ile Thr Arg Leu Asp Leu Gly Lys Arg Ile Leu Asp Pro Arg Gly Ile
 35 40 45
 tat agg tgt aat ggg aca gat ata tac aag gac aaa gaa tct acc gtg 355
 Tyr Arg Cys Asn Gly Thr Asp Ile Tyr Lys Asp Lys Glu Ser Thr Val
 50 55 60 65
 caa gtt cat tat cga atg tgc cag agc tgt gtg gag ct 393
 Gln Val His Tyr Arg Met Cys Gln Ser Cys Val Glu
 70 75

<210> 163
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 99..302

<221> sig_peptide
 <222> 99..215
 <223> score 3.7
 seq VFFSPMSMSCALA/MV

<400> 163
 asnccgnngc ctccccgcga gtatttgagg tccggggcgg ctccggcgcc tctgcccgcc 60
 gttctgctcg ctgctcccc gctctggagt ctgccatc atg gat gtt ctc gca gaa 116
 Met Asp Val Leu Ala Glu
 -35
 gca aat ggc acc ttt gcc tta aac ctt ttg aaa acg ctg ggt aaa gac 164
 Ala Asn Gly Thr Phe Ala Leu Asn Leu Leu Lys Thr Leu Gly Lys Asp
 -30 -25 -20
 aac tcg aag aat gtg ttt ttc tca ccc atg agc atg tcc tgt gcc ctg 212
 Asn Ser Lys Asn Val Phe Phe Ser Pro Met Ser Met Ser Cys Ala Leu
 -15 -10 -5
 gcc atg gtc tac atg ggg gca aag gga aac acc gct gca cag atg gcc 260
 Ala Met Val Tyr Met Gly Ala Lys Gly Asn Thr Ala Ala Gln Met Ala
 1 5 10 15
 cag ata ctt tct ttc aat aaa agt ggc ggt ggt gga gac acc c 303
 Gln Ile Leu Ser Phe Asn Lys Ser Gly Gly Gly Gly Asp Thr
 20 25

<210> 164
 <211> 199
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..197

<221> sig_peptide
 <222> 36..104
 <223> score 4
 seq AAAAVAAAAAVTA/GE

<400> 164
 tcagctgcgt tggctgtaga agagaacgga cggcgc atg gcg acg gtc gca gca 53
 Met Ala Thr Val Ala Ala
 -20
 aat cca gct gct gct gcg gcg gct gtg gcg gcg gca gcg gcg gtg act 101
 Asn Pro Ala Ala Ala Ala Val Ala Ala Ala Ala Val Thr
 -15 -10 -5
 gca gga gaa tgg cat gaa ccg cag ggg gcg gga ctg cag gaa gcc aag 149
 Ala Gly Glu Trp His Glu Pro Gln Gly Ala Gly Leu Gln Glu Ala Lys
 1 5 10 15
 atc gca cca ctg cac tcc agc cta ggt gac agc gag act ccg tct caa 197
 Ile Ala Pro Leu His Ser Ser Leu Gly Asp Ser Glu Thr Pro Ser Gln
 20 25 30
 aa 199

<210> 165
 <211> 425
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 196..423

<221> sig_peptide
 <222> 196..282
 <223> score 7.1
 seq LLFLLSAVYLGPG/CQ

<400> 165
 agcagtttct ctccactcac agcctgaagc atacccggca gggctgtccc caggcccaac 60
 aagcaaaggg ccagtagcg agggccactg gagcccatct ccggggggct gggcaggaag 120
 taggggtgggg tttggggtag ggatctggta ccctgggact gctgcaactc aaactaacca 180
 acccactggg agaag atg cct ggg ggt cca gga gtc ctc caa gct ctg cct 231
 Met Pro Gly Gly Pro Gly Val Leu Gln Ala Leu Pro
 -25 -20
 gcc acc atc ttc ctc ctc ttc ctg ctg tct gct gtc tac ctg ggc cct 279
 Ala Thr Ile Phe Leu Leu Phe Leu Leu Ser Ala Val Tyr Leu Gly Pro
 -15 -10 -5
 ggg tgc cag gcc ctg tgg atg cac aag gtc cca gca tca ttg atg gtg 327
 Gly Cys Gln Ala Leu Trp Met His Lys Val Pro Ala Ser Leu Met Val
 1 5 10 15
 agc ctg ggg gaa gac gcc cac ttc caa tgc ccg cac aat agc agc aac 375
 Ser Leu Gly Glu Asp Ala His Phe Gln Cys Pro His Asn Ser Ser Asn
 20 25 30
 aac gcc aac gtc acc tgg tgg cgc gtc ctc cat ggc aac tac acg tgg 423
 Asn Ala Asn Val Thr Trp Trp Arg Val Leu His Gly Asn Tyr Thr Trp
 35 40 45
 cc 425

<210> 166
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 280..507

<221> sig_peptide
 <222> 280..402
 <223> score 3.6
 seq AGAGLPALDLAKA/QR

<400> 166
 gtccccgtta gacaatgcc cggagccgcc agaccgtcgc gcccctgccc catcgtagta 60

tatgagctcg cctacacaag gacccccgct aaaagccaga gctcccagtc cccgaggctt 120
 gaagacgggg actcccttct ccaccaactc tgtcctcggg ggggtggggcc ccagccgaga 180
 tcacagcgcg acaggagtgg ggggtggccgc tggagacagg tgaagaaaca agaaaactaa 240
 gaaatccgag cggttggagg gggagtctgt gtggatggg atg ggg acg ccg ggg 294
 Met Gly Thr Pro Gly

-40
 gag ggg ctg ggs cgc tgc tcc cat gcc ctg atc cgg gga gtc cca gag 342
 Glu Gly Leu Gly Arg Cys Ser His Ala Leu Ile Arg Gly Val Pro Glu
 -35 -30 -25

agc ctg gcg tgc ggg gaa ggt gcg ggg gct ggc ctt ccc gct ctg gat 390
 Ser Leu Ala Ser Gly Glu Gly Ala Gly Ala Gly Leu Pro Ala Leu Asp
 -20 -15 -10 -5

ctg gcc aaa gct caa agg gag cac ggg gtg ctg gga ggt aaa ctg agg 438
 Leu Ala Lys Ala Gln Arg Glu His Gly Val Leu Gly Gly Lys Leu Arg
 1 5 10

caa cga ctg ggg cta cag ctg cta gaa ctg cca cct gag gag tca ttg 486
 Gln Arg Leu Gly Leu Gln Leu Leu Glu Leu Pro Pro Glu Glu Ser Leu
 15 20 25

ccg ctg gga ccg ctg ctt ggc 507
 Pro Leu Gly Pro Leu Leu Gly
 30 35

<210> 167
 <211> 446
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 96..446

<221> sig_peptide
 <222> 96..182
 <223> score 8.5
 seq LLGLLMAACFTFC/LS

<400> 167
 gcgtttgcgc aggggggagct ggtcgccgcc gcggccgcct ggaattgtgg gagttgtgtc 60
 tgccactcgg ctgccggags cgaaggtccg tgact atg gct ccc cag agc ctg 113
 Met Ala Pro Gln Ser Leu
 -25

cct tca tct agg atg gct cct ctg ggc atg ctg ctt ggg ctg ctg atg 161
 Pro Ser Ser Arg Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met
 -20 -15 -10

gcc gcc tgc ttc acc ttc tgc ctc agt cat cag aac ctg aag gag ttt 209
 Ala Ala Cys Phe Thr Phe Cys Leu Ser His Gln Asn Leu Lys Glu Phe
 -5 1 5

gcc ctg acc aac cca gag aag agc agc acc aaa gaa acg gag aga aaa 257
 Ala Leu Thr Asn Pro Glu Lys Ser Ser Thr Lys Glu Thr Glu Arg Lys
 10 15 20 25

gaa acc aaa gcc gag gag gag ctg gat gcc gaa gtc ctg gag gtg ttc 305
 Glu Thr Lys Ala Glu Glu Glu Leu Asp Ala Glu Val Leu Glu Val Phe
 30 35 40

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cac ccg acg cat gag tgg cag gcc ctt cag cca ggg cag gct gtc cct      353
His Pro Thr His Glu Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro
      45                      50                      55

gca gga tcc cac gta cgg ctg aat ctt cag act ggg gaa aga gag gca      401
Ala Gly Ser His Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala
      60                      65                      70

aaa ctc caa tat gag gac aag ttc cga aat aat ttg aaa ggc aaa      446
Lys Leu Gln Tyr Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys
      75                      80                      85

<210> 168
<211> 439
<212> DNA
<213> Homo sapiens

<220>
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<222> 17..439

<221> sig_peptide
<222> 17..94
<223> score 8.3
      seq CLLLLCGSITLALG/NA

<400> 168
accagcatca ttcccc atg cga ggt ggc aaa tgc aac atg ctc tcc agt ttg      52
      Met Arg Gly Gly Lys Cys Asn Met Leu Ser Ser Leu
      -25                      -20                      -15

ggg tgt cta ctt ctc tgt gga agt att aca cta gcc ctg gga aat gca      100
Gly Cys Leu Leu Leu Cys Gly Ser Ile Thr Leu Ala Leu Gly Asn Ala
      -10                      -5                      1

cag aaa ttg cca aaa ggt aaa agg cca aac ctc aaa gtc cac atc aat      148
Gln Lys Leu Pro Lys Gly Lys Arg Pro Asn Leu Lys Val His Ile Asn
      5                      10                      15

acc aca agt gac tcc atc ctc ttg aag ttc ttg cgt cca agt cca aat      196
Thr Thr Ser Asp Ser Ile Leu Leu Lys Phe Leu Arg Pro Ser Pro Asn
      20                      25                      30

gta aag ctt gaa ggt ctt ctc ctg gga tat ggc agc aat gta tca cca      244
Val Lys Leu Glu Gly Leu Leu Leu Gly Tyr Gly Ser Asn Val Ser Pro
      35                      40                      45                      50

aac cag tac ttc cct ctt ccc gct gaa ggg aaa ttc aca gaa gct ata      292
Asn Gln Tyr Phe Pro Leu Pro Ala Glu Gly Lys Phe Thr Glu Ala Ile
      55                      60                      65

gtt gat gca gag ccg aaa tat ctg ata gtt gtg cga cct gct cca cct      340
Val Asp Ala Glu Pro Lys Tyr Leu Ile Val Val Arg Pro Ala Pro Pro
      70                      75                      80

cca agt caa aag aag tca tgt tca ggt aaa act cgt tct cgc aaa cct      388
Pro Ser Gln Lys Lys Ser Cys Ser Gly Lys Thr Arg Ser Arg Lys Pro
      85                      90                      95

ctg cag ctg gtg gtt ggc act ctg aca ccg agc tcr gtc ttc ctg tcc      436
Leu Gln Leu Val Val Gly Thr Leu Thr Pro Ser Ser Val Phe Leu Ser
      100                      105                      110

tgg      439

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Trp
115

<210> 169
<211> 319
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 65..319

<221> sig_peptide
<222> 65..133
<223> score 4
seq LLLXLHWKHGAGS/PL

<400> 169
atgaacctct gaaaactgcc ggcactctgag gtttcctcca aggccctctg aagtgcagcc 60
cata atg aag gtc ttg gcg gca gga gtt gtg ccc ctg ctg ttg gkt ctg 109
Met Lys Val Leu Ala Ala Gly Val Val Pro Leu Leu Leu Xaa Leu
-20 -15 -10
cac tgg aaa cat ggg gcg ggg agc ccc ctc ccc atc acc cct gtc aac 157
His Trp Lys His Gly Ala Gly Ser Pro Leu Pro Ile Thr Pro Val Asn
-5 1 5
gcc acc tgt gcc ata cgc cac cca tgt cac aac aac ctc atg aac cag 205
Ala Thr Cys Ala Ile Arg His Pro Cys His Asn Asn Leu Met Asn Gln
10 15 20
atc agg agc caa ctg gca cag ctc aat ggc agt gcc aat gcc ctc ttt 253
Ile Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu Phe
25 30 35 40
att ctc tat tac aca gcc cag ggg gag ccg ttc ccc aac aac ctg gac 301
Ile Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn Asn Leu Asp
45 50 55
aag cta tgt ggc ccc aac 319
Lys Leu Cys Gly Pro Asn
60

<210> 170
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 119..433

<221> sig_peptide
<222> 119..175
<223> score 11.7
seq IALLLTVLQVSRG/QK

<400> 170
 gaaaaaaaaa acctgcgggc tccgagctgg gtgcagcaac cggaggcggc ggcgcgtctg 60
 gaggaggctg cagcagcgga agaccccagt ccagatccag gactgagatc ccagaacc 118
 atg aac ctg gcc atc agc atc gct ctc ctg cta aca gtc ttg cag gtc 166
 Met Asn Leu Ala Ile Ser Ile Ala Leu Leu Leu Thr Val Leu Gln Val
 -15 -10 -5
 tcc cga ggg cag aag gtg acc agc cta acg gcc tgc cta gtg gac cag 214
 Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys Leu Val Asp Gln
 1 5 10
 agc ctt cgt ctg gac tgc cgc cat gag aat acc agc agt tca ccc atc 262
 Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser Ser Ser Pro Ile
 15 20 25
 cag tac gag ttc agc ctg acc cgt gag aca aag aag cac gtg ctc ttt 310
 Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys His Val Leu Phe
 30 35 40 45
 ggc act gtg ggg gtg cct gag cac aca tac cgc tcc cga acc aac ttc 358
 Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser Arg Thr Asn Phe
 50 55 60
 acc agc aaa tac aac atg aag gtc ctc tac tta tcc gct tca cta gca 406
 Thr Ser Lys Tyr Asn Met Lys Val Leu Tyr Leu Ser Ala Ser Leu Ala
 65 70 75
 agg acg agg gca cta cac gtg tgc act c 434
 Arg Thr Arg Ala Leu His Val Cys Thr
 80 85

<210> 171
 <211> 428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 200..427
 <221> sig_peptide
 <222> 200..310
 <223> score 3.6
 seq PLSLDCGHSFCQA/CI

<400> 171
 actcagctcc tgtggggaaa ctcatttgtg gagaccagcc ctctggcttg gtgagtgaat 60
 ctgggtttaca cggctcctg ccctgccttc actctttctcc cctgattcaa gactcctctg 120
 ctttgactg aagcactgca ggagtttgtg accaagaact tcaagagtca agacagaagg 180
 aagccaaggg agcagtgca atg gat ttc tca gta aag gta gac ata gag aag 232
 Met Asp Phe Ser Val Lys Val Asp Ile Glu Lys
 -35 -30
 gag gtg acc tgc ccc atc tgc ctg gag ctc ctg aca gaa cct ctg agc 280
 Glu Val Thr Cys Pro Ile Cys Leu Glu Leu Leu Thr Glu Pro Leu Ser
 -25 -20 -15
 cta gat tgt ggc cac agc ttc tgc caa gcc tgc atc act gcr aag atc 328
 Leu Asp Cys Gly His Ser Phe Cys Gln Ala Cys Ile Thr Ala Lys Ile
 -10 -5 1 5
 aag gag tca gts atc atc tca aga ggg gaa agc agc tgt cct gtg tgt 376

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Lys Glu Ser Val Ile Ile Ser Arg Gly Glu Ser Ser Cys Pro Val Cys
      10      15      20
cag asc aga tts cag cct ggg aac ctc cga cct aat cgg cat ctg gcc      424
Gln Xaa Arg Xaa Gln Pro Gly Asn Leu Arg Pro Asn Arg His Leu Ala
      25      30      35
aac a      428
Asn

<210> 172
<211> 637
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 49..636

<221> sig_peptide
<222> 49..105
<223> score 11.8
      seq ALLVCAVLGLCLA/VP

<400> 172
acagaagcga gtccgactgt gctcgtctgct cagcgccgca cccggagg atg agg ctc      57
                                     Met Arg Leu
gcc gtg gga gcc ctg ctg gtc tgc gcc gtc ctg ggg ctg tgt ctg gct      105
Ala Val Gly Ala Leu Leu Val Cys Ala Val Leu Gly Leu Cys Leu Ala
      -15      -10      -5
gtc cct gat aaa act gtg aga tgg tgt gca gtg tgc gag cat gag gcc      153
Val Pro Asp Lys Thr Val Arg Trp Cys Ala Val Ser Glu His Glu Ala
      1      5      10      15
act aag tgc cag agt ttc cgc gac cat atg aaa agc gtc att cca tcc      201
Thr Lys Cys Gln Ser Phe Arg Asp His Met Lys Ser Val Ile Pro Ser
      20      25      30
gat ggt ccc agt gtt gct tgt gtg aag aaa gcc tcc tac ctt gat tgc      249
Asp Gly Pro Ser Val Ala Cys Val Lys Lys Ala Ser Tyr Leu Asp Cys
      35      40      45
atc agg gcc att gcg gca aac gaa gcg gat gct gtg aca ctg gat gca      297
Ile Arg Ala Ile Ala Ala Asn Glu Ala Asp Ala Val Thr Leu Asp Ala
      50      55      60
ggg ttg gtg tat gat gct tac ctg gct ccc aat aac ctg aag cct gtg      345
Gly Leu Val Tyr Asp Ala Tyr Leu Ala Pro Asn Asn Leu Lys Pro Val
      65      70      75      80
gtg gca gag ttc tat ggg tca aaa gag gat cca cag act ttc tat tat      393
Val Ala Glu Phe Tyr Gly Ser Lys Glu Asp Pro Gln Thr Phe Tyr Tyr
      85      90      95
gct gtt gct gtg gtg aag aag gat agt ggc ttc cag atg aac cag ctt      441
Ala Val Ala Val Val Lys Lys Asp Ser Gly Phe Gln Met Asn Gln Leu
      100      105      110
cga ggc aag aag tcc tgc cac acg ggt cta ggc agg tcc gct ggg tgg      489
Arg Gly Lys Lys Ser Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp
      115      120      125
aac atc ccc ata ggc tta ctt tac tgt gac tta cct gag cca cgt aaa      537

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Asn	Ile	Pro	Ile	Gly	Leu	Leu	Tyr	Cys	Asp	Leu	Pro	Glu	Pro	Arg	Lys	
130						135					140					
cct	ctt	gag	aaa	gca	gtg	gcc	aat	ttc	ttc	tcg	ggc	agc	tgt	gcc	cct	585
Pro	Leu	Glu	Lys	Ala	Val	Ala	Asn	Phe	Phe	Ser	Gly	Ser	Cys	Ala	Pro	
145					150					155					160	
tgt	gcg	gat	ggg	acg	gac	ttc	ccc	cag	ctg	tgt	caa	ctg	tgt	cca	ggg	633
Cys	Ala	Asp	Gly	Thr	Asp	Phe	Pro	Gln	Leu	Cys	Gln	Leu	Cys	Pro	Gly	
				165				170						175		
tgt	g															637
Cys																

<210> 173
 <211> 497
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 234..497

<221> sig_peptide
 <222> 234..290
 <223> score 7.4
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cctgcctgcc	ttcctgactt	ctgttccaga	gcaaagggtca	ttcagccgct	tgaatcagcc											120
ttttccccc	acccggtccc	caactttgtt	taccggataa	ggaagggtcag	cattcaaagt											180
caagaagcgc	catttatctt	cccgtgcgct	ctacaaatag	ttccgtgaga	aag atg											236
					Met											
gcc ggg aac	tcg atc	ctg ctg	gct gct	gtc tct	att ctc	tcg gcc	tgt									284
Ala Gly Asn	Ser Ile	Leu Leu	Ala Ala	Val Ser	Ile Leu	Ser Ala	Cys									
	-15		-10		-5											
cag caa agt	tat ttt	gct ttg	caa gtt	gga aag	gca aga	tta aaa	tac									332
Gln Gln Ser	Tyr Phe	Ala Leu	Gln Val	Gly Lys	Ala Arg	Leu Lys	Tyr									
	1		5		10											
aaa gtt acg	ccc cca	gca gtc	act ggg	tca cca	gag ttt	gag aga	gta									380
Lys Val Thr	Pro Pro	Ala Val	Thr Gly	Ser Pro	Glu Phe	Glu Arg	Val									
	15		20		25		30									
ttt cgg gca	caa caa	aac tgt	gtg gag	ttt tat	cct ata	ttc ata	att									428
Phe Arg Ala	Gln Gln	Asn Cys	Val Glu	Phe Tyr	Pro Ile	Phe Ile	Ile									
	35		40		45											
aca ttg tgg	atg gct	ggg tgg	tat ttc	aac caa	gtt ttt	gct act	ngt									476
Thr Leu Trp	Met Ala	Gly Trp	Tyr Phe	Asn Gln	Val Phe	Ala Thr	Xaa									
	50		55		60											
cnn ggt ctg	gtg tac	ata tat														497
Xaa Gly Leu	Val Tyr	Ile Tyr														
	65															

<210> 174
 <211> 451
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 140..451

<221> sig_peptide

<222> 140..223

<223> score 3.9

seq FQSFSSASSPVNC/QW

<400> 174

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cttcctgctg ttgaaaactt acccggccct tacagaggaa atcttcctcc tctcttctgc 120
cctgaatgtt ttcccaaac atg aag gtg ata agc tta ttc att ttg gtg gga 172

Met Lys Val Ile Ser Leu Phe Ile Leu Val Gly
-25 -20

ttt ata gga gag ttc caa agt ttt tca agt gcc tcc tct cca gtc aac 220
Phe Ile Gly Glu Phe Gln Ser Phe Ser Ser Ala Ser Ser Pro Val Asn
-15 -10 -5

tgc cag tgg gac ttc tat gcc cct tgg tca gaa tgc aat ggc tgt acc 268
Cys Gln Trp Asp Phe Tyr Ala Pro Trp Ser Glu Cys Asn Gly Cys Thr
1 5 10 15

aag act cag act cgc agg cgg tca gtt gct gtg tat ggg cag tat gga 316
Lys Thr Gln Thr Arg Arg Arg Ser Val Ala Val Tyr Gly Gln Tyr Gly
20 25 30

ggc cag cct tgt gtt gga aat gct ttt gaa aca cag tcc tgt gaa cct 364
Gly Gln Pro Cys Val Gly Asn Ala Phe Glu Thr Gln Ser Cys Glu Pro
35 40 45

aca aga gga tgt cca aca gag gag gga tgt gga gag cgt ttc agg tgc 412
Thr Arg Gly Cys Pro Thr Glu Glu Gly Cys Gly Glu Arg Phe Arg Cys
50 55 60

ttt tca ggt cag tgc atc agc aaa tca tgg ttt gca tgg 451
Phe Ser Gly Gln Cys Ile Ser Lys Ser Trp Phe Ala Trp
65 70 75

<210> 175

<211> 422

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 92..421

<221> sig_peptide

<222> 92..148

<223> score 13.5

seq LLLLLSACLAVSA/GP

<400> 175

agttcacagc tgccctgttg cagggaggcg gtggcccttc tgttgctaga ccgagcctgt 60


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gggatataacc aaggcagagg agcccatagc c atg agg agc ctc ggg gcc ctg      112
                                Met Arg Ser Leu Gly Ala Leu
                                -15

ctc ttg ctg ctg agc gcc tgc ctg gcg gtg agc gct ggc cct gtg cca      160
Leu Leu Leu Leu Ser Ala Cys Leu Ala Val Ser Ala Gly Pro Val Pro
-10                                -5                                1

acg ccg ccc gac aac atc caa gtg cag gaa aac ttc aat atc tct cgg      208
Thr Pro Pro Asp Asn Ile Gln Val Gln Glu Asn Phe Asn Ile Ser Arg
5                                10                                15                                20

atc tat ggg aag tgg tac aac ctg gcc atc ggt tcc acc tgc ccc tgg      256
Ile Tyr Gly Lys Trp Tyr Asn Leu Ala Ile Gly Ser Thr Cys Pro Trp
25                                30                                35

ctg aag aag atc atg gac agg atg aca gtg agc acg ctg gtg ctg gga      304
Leu Lys Lys Ile Met Asp Arg Met Thr Val Ser Thr Leu Val Leu Gly
40                                45                                50

gag ggc gct aca gag gcg gag atc agc atg acc agc act cgt tgg cgg      352
Glu Gly Ala Thr Glu Ala Glu Ile Ser Met Thr Ser Thr Arg Trp Arg
55                                60                                65

aaa ggt gtc tgt gag aga cgt ctg gag ctt atg agw aaa cag mta ctg      400
Lys Gly Val Cys Glu Arg Arg Leu Glu Leu Met Xaa Lys Gln Xaa Leu
70                                75                                80

atg gga agt ttc tct atc aca a      422
Met Gly Ser Phe Ser Ile Thr
85                                90

<210> 176
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 222..473

<221> sig_peptide
<222> 222..284
<223> score 12.9
      seq LLLLLLLTLLGLG/LV

<400> 176
acctcaccac gccccatct ccgtccgtgt acacacactc acacaaggac gccaacccca      60
cctagatgca aagcaggatt caaaagaaca tctttgcgtt ttctaccggc tccccatcat      120
cgtactaggg aggaagaagc gggtagaaaa caaaacttct ttccattgtc ctgcccgttt      180
ctgcggactt gttctgaggc cgaggcacct ctaagatact g atg gct ctg cag agg      236
                                Met Ala Leu Gln Arg
                                -20

acc cat tca ttg ctt ctg ctt ttg ctg ctg acc ctg ctg ggg ctg ggg      284
Thr His Ser Leu Leu Leu Leu Leu Leu Leu Thr Leu Leu Gly Leu Gly
-15                                -10                                -5

ctg gtc cag ccc tcc tat ggc cag gat ggc atg tac cag cga ttc ctg      332
Leu Val Gln Pro Ser Tyr Gly Gln Asp Gly Met Tyr Gln Arg Phe Leu
1                                5                                10                                15

cgg caa cac gtg cac cct gag gag aca ggt ggc agt gat cgc tac tgc      380

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<220>
 <221> CDS
 <222> 116..313

<221> sig_peptide
 <222> 116..187
 <223> score 11.7
 seq FVLGLGLTPPTLA/QD

<400> 178
 gttcacacaa ctggaaccca tctccaggaa caaacagctg gaacccatct cccgttgaag 60
 ggaaactgcc agatttttgt aagattcttc ctctgggag cctgtgttg aagag atg 118
 Met
 gtg atg ggc ctg ggc ktt ttg ttg gtc ttc gtg ctg ggt ctg ggt 166
 Val Met Gly Leu Gly Xaa Leu Leu Leu Val Phe Val Leu Gly Leu Gly
 -20 -15 -10
 ctg acc cca ccg acc ctg gct cag gat aac tcc agg tac aca cac ttc 214
 Leu Thr Pro Pro Thr Leu Ala Gln Asp Asn Ser Arg Tyr Thr His Phe
 -5 1 5
 ctg acc cag cac tat gat gcc aaa cca cag ggc cgg gat gac aga tac 262
 Leu Thr Gln His Tyr Asp Ala Lys Pro Gln Gly Arg Asp Asp Arg Tyr
 10 15 20 25
 tgt gaa agc atc atg agg aga cgg ggc ctg acc tca ccc tgc aaa gac 310
 Cys Glu Ser Ile Met Arg Arg Arg Gly Leu Thr Ser Pro Cys Lys Asp
 30 35 40
 atc a 314
 Ile

<210> 179
 <211> 477
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..475

<221> sig_peptide
 <222> 74..172
 <223> score 11.2
 seq ILCLLAWAGLAAG/DR

<400> 179
 agctataaat agggcatcgt gacccggcca ggggaagaag ctgccgttgt tctgggtact 60
 acagcagaag ggt atg cgg aag cga gca ccc cag tct gag atg gct cct 109
 Met Arg Lys Arg Ala Pro Gln Ser Glu Met Ala Pro
 -30 -25
 gcc ggt gtg agc ctg agg gcc acc atc ctc tgc ctc ctg gcc tgg gct 157
 Ala Gly Val Ser Leu Arg Ala Thr Ile Leu Cys Leu Leu Ala Trp Ala
 -20 -15 -10
 ggc ctg gct gca ggt gac cgg gtg tac ata cac ccc ttc cac ctc gtc 205
 Gly Leu Ala Ala Gly Asp Arg Val Tyr Ile His Pro Phe His Leu Val

-5	1	5	10	
atc cac aat gag agt acc tgt gag cag ctg gca aag gcc aat gcc ggg				253
Ile His Asn Glu Ser Thr Cys Glu Gln Leu Ala Lys Ala Asn Ala Gly				
15	20	25		
aag ccc aaa gac ccc acc ttc ata cct gct cca att cag gcc aag aca				301
Lys Pro Lys Asp Pro Thr Phe Ile Pro Ala Pro Ile Gln Ala Lys Thr				
30	35	40		
tcc cct gtg gat gaa aag gcc cta cag gac cag ctg gtg cta gtc gct				349
Ser Pro Val Asp Glu Lys Ala Leu Gln Asp Gln Leu Val Leu Val Ala				
45	50	55		
gca aaa ctt gac acc gaa gac aag ttg agg gcc gca atg gtc ggg atg				397
Ala Lys Leu Asp Thr Glu Asp Lys Leu Arg Ala Ala Met Val Gly Met				
60	65	70	75	
ctg gcc aac tct tgg gct tcc gta tat atg gca tgc aca gtg agc tat				445
Leu Ala Asn Ser Trp Ala Ser Val Tyr Met Ala Cys Thr Val Ser Tyr				
80	85	90		
ggg gcg tgg tcc atg ggg cca mcg tcc tct cc				477
Gly Ala Trp Ser Met Gly Pro Xaa Ser Ser				
95	100			

<210> 180
 <211> 553
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 105..551

<221> sig_peptide
 <222> 105..239
 <223> score 3.7
 seq EDLLMYLLQLVQA/LK

<400> 180	
ttasgaatca agaaaaagcc ttgacaaaat tcttgaaatg tgtwaattgg gatctacctc	60
aagaggccaa acaggccttg gaacttctgg gaaaatggaa gccg atg gat gta gag	116
Met Asp Val Glu	
-45	
gac tcc ttg gag ctg tta tcc tct cat tac acc aac cca act gtg agg	164
Asp Ser Leu Glu Leu Leu Ser Ser His Tyr Thr Asn Pro Thr Val Arg	
-40	-35
cgt tat gct gtt gcc cgg ttg cga cag gcc gat gat gag gat ttg ttg	212
Arg Tyr Ala Val Ala Arg Leu Arg Gln Ala Asp Asp Glu Asp Leu Leu	
-25	-20
atg tac cta tta caa ttg gtc cag gct ctc aaa tat gaa aat ttt gat	260
Met Tyr Leu Leu Gln Leu Val Gln Ala Leu Lys Tyr Glu Asn Phe Asp	
-5	1
gat ata aag aat gga ttg gaa cct acc aag aag gat agt cag agt tca	308
Asp Ile Lys Asn Gly Leu Glu Pro Thr Lys Lys Asp Ser Gln Ser Ser	
10	15
gtg tca gaa aat gtg tca aat tct gga ata aat tct gca gaa ata gat	356
Val Ser Glu Asn Val Ser Asn Ser Gly Ile Asn Ser Ala Glu Ile Asp	

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      25              30              35
agc tcc caa att ata acc agc ccc ctt cct tca gtc tct tca cct cct      404
Ser Ser Gln Ile Ile Thr Ser Pro Leu Pro Ser Val Ser Ser Pro Pro
40              45              50              55
cct gca tca aaa aca aaa gaa gtt cca gat ggc gaa aat ctg gaa caa      452
Pro Ala Ser Lys Thr Lys Glu Val Pro Asp Gly Glu Asn Leu Glu Gln
      60              65              70
gat ctc tgt acc ttc ttg ata tcg aga gcc tgc aaa aac tca aca ctg      500
Asp Leu Cys Thr Phe Leu Ile Ser Arg Ala Cys Lys Asn Ser Thr Leu
      75              80              85
gct aat tat tta tac tgg tat gtg ata gtg gaa tgt gaa gat caa gat      548
Ala Asn Tyr Leu Tyr Trp Tyr Val Ile Val Glu Cys Glu Asp Gln Asp
      90              95              100
act ca
Thr
<210> 181
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..400

<221> sig_peptide
<222> 38..88
<223> score 6.5
      seq WTITLFLLGAAKG/KE

<400> 181
gatccggtgg gagggaacat ctggaacatt agacagg atg ctg atc ttc tgg aca      55
                                Met Leu Ile Phe Trp Thr
                                -15
atc aca ctt ttc ctg ctg gga gca gcc aaa gga aaa gaa gtt tgc tat      103
Ile Thr Leu Phe Leu Leu Gly Ala Ala Lys Gly Lys Glu Val Cys Tyr
      -10              -5              1              5
gag gac ctc ggg tgc ttt tct gac act gag ccc tgg ggc ggg aca gca      151
Glu Asp Leu Gly Cys Phe Ser Asp Thr Glu Pro Trp Gly Gly Thr Ala
      10              15              20
atc agg ccc ctg aaa att ctc ccc tgg agc cct gag aag atc ggc acc      199
Ile Arg Pro Leu Lys Ile Leu Pro Trp Ser Pro Glu Lys Ile Gly Thr
      25              30              35
cgc ttc ctg ctg tac acc aat gaa aac cca aac aac ttt caa att ctc      247
Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro Asn Asn Phe Gln Ile Leu
      40              45              50
ctc ctc tct gat cca tca aca att gag gca tca aat ttt caa atg gac      295
Leu Leu Ser Asp Pro Ser Thr Ile Glu Ala Ser Asn Phe Gln Met Asp
      55              60              65
aga aag acc cgg ttc atc atc cat ggc ttc ata gac aaa gga gat gag      343
Arg Lys Thr Arg Phe Ile Ile His Gly Phe Ile Asp Lys Gly Asp Glu
      70              75              80              85
agc tgg gtg aca gac atg tgc aag aaa ctg ttc gag gtg gag gag gtg      391

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Ser Trp Val Thr Asp Met Cys Lys Lys Leu Phe Glu Val Glu Glu Val
 90 95 100

aac tgc atc
 Asn Cys Ile

400

<210> 182
 <211> 364
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..362

<221> sig_peptide
 <222> 63..128
 <223> score 5.8
 seq LGIILLVLIGXQG/TP

<400> 182
 aaaaagaatt tctcaggctc aaaatccaat acaggagtga cttggaactc cattctatca 60
 ct atg aag aaa agt ggt gtt ctt ttc ctc ttg ggc atc atc ttg ctg 107
 Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu
 -20 -15 -10
 gtt ctg att gga rtg caa gga acc cca gta gtg aga aag ggt cgc tgt 155
 Val Leu Ile Gly Xaa Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys
 -5 1 5
 tcc tgc atc agc acc aac caa ggg act atc cac cta caa tcc ttg aaa 203
 Ser Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys
 10 15 20 25
 gac ctt aaa caa ttt gcc cca agc cct tcc tgc gag aaa att gaa atc 251
 Asp Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile
 30 35 40
 att gct aca ctg aag aat gga gtn caa aca tgt cta aac cca gat tca 299
 Ile Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser
 45 50 55
 gca gat gtg aag gaa ctg att waa aag tgg gar aac agg tca gcc aaa 347
 Ala Asp Val Lys Glu Leu Ile Xaa Lys Trp Glu Asn Arg Ser Ala Lys
 60 65 70
 aga aaa agc aaa aga at 364
 Arg Lys Ser Lys Arg
 75

<210> 183
 <211> 483
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..481

<221> sig_peptide

<222> 92..130
 <223> score 4.2
 seq MLSVRVAAAVVRA/LP

<400> 183
 cttcttgacc ttytttgagg ctgagccatt ttgtcccagt cagtccggag gctgaggctg 60
 cagaagtacc gcctgaggag taactgcaaa g atg ctg tcc gtg cgc gtt gct 112
 Met Leu Ser Val Arg Val Ala
 -10
 gcg gcc gtg gtc cgc gcc ctt cct cgg cgg gcc gga ctg gtc tcc aga 160
 Ala Ala Val Val Arg Ala Leu Pro Arg Arg Ala Gly Leu Val Ser Arg
 -5 1 5 10
 aat gct ttg ggt tca tct ttc att gct gca agg aac ttc cat gcc tct 208
 Asn Ala Leu Gly Ser Ser Phe Ile Ala Ala Arg Asn Phe His Ala Ser
 15 20 25
 aac act cat ctt caa aag act ggg act gct gag atg tcc tct att ctt 256
 Asn Thr His Leu Gln Lys Thr Gly Thr Ala Glu Met Ser Ser Ile Leu
 30 35 40
 gaa gag cgt att ctt gga gct gat acc tct gtt gat ctt gaa gaa act 304
 Glu Glu Arg Ile Leu Gly Ala Asp Thr Ser Val Asp Leu Glu Glu Thr
 45 50 55
 ggg cgt gtc tta agt att ggt gat ggt att gcc cgc gta cat ggg ctg 352
 Gly Arg Val Leu Ser Ile Gly Asp Gly Ile Ala Arg Val His Gly Leu
 60 65 70
 agg aat gtt caa gca gaa gaa atg gta gag ttt tct tca ggc tta aag 400
 Arg Asn Val Gln Ala Glu Glu Met Val Glu Phe Ser Ser Gly Leu Lys
 75 80 85 90
 ggt atg tcc ttg aac ttg gaa cct gac aat gtt ggt gtt gtc gtg ttt 448
 Gly Met Ser Leu Asn Leu Glu Pro Asp Asn Val Gly Val Val Val Phe
 95 100 105
 gga aat gat aaa cta att aag gaa gga gat ata gt 483
 Gly Asn Asp Lys Leu Ile Lys Glu Gly Asp Ile
 110 115

<210> 184
 <211> 259
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 92..259

<221> sig_peptide
 <222> 92..130
 <223> score 4.2
 seq MLSVRVAAAVVRA/LP

<400> 184
 cttcttgacc ttytttgagg ctgagccatt ttgtcccagt cagtccggag gctgaggctg 60
 cagaagtacc gcctgaggag taactgcaaa g atg ctg tcc gtg cgc gtt gct 112
 Met Leu Ser Val Arg Val Ala

-10

gcg gcc gtg gtc cgc gcc ctt cct cgg cgg gcc gga ctg gtc tcc aga	160
Ala Ala Val Val Arg Ala Leu Pro Arg Arg Ala Gly Leu Val Ser Arg	
-5 1 5 10	
aat gct ttg ggt tca tct ttc att gct gca agg aac ttc cat gcc tct	208
Asn Ala Leu Gly Ser Ser Phe Ile Ala Ala Arg Asn Phe His Ala Ser	
15 20 25	
aac act cat ctt caa aag act ggt aag tta tta ttt ctc agt cta cgc	256
Asn Thr His Leu Gln Lys Thr Gly Lys Leu Leu Phe Leu Ser Leu Arg	
30 35 40	
cgc	259
Arg	

<210> 185
 <211> 466
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 213..464

 <221> sig_peptide
 <222> 213..281
 <223> score 3.9
 seq GWAGSCFWQWSFC/PP

<400> 185

agaggagggg ccssaatgtc tgaggtggca acacttctct tcagccagac agcactggcc	60
agtttggagt nkgatccatcc tgcaggccac aagctctgga tgaggaactt gaggcaagtc	120
accagcccct gatcatttcg cctaaaagag caaggactag agttcctgac ctccaggcca	180
gtccctgac cctgacctaa tggtatcgcg ga atg atg ata tat gta tct acg	233
Met Met Ile Tyr Val Ser Thr	
-20	
ggg gcc tgg ggc tgg gcg ggc tcc tgc ttc tgg cag tgg tcc ttc tgt	281
Gly Ala Trp Gly Trp Ala Gly Ser Cys Phe Trp Gln Trp Ser Phe Cys	
-15 -10 -5	
ccg cct gcc tgt gtt ggc tgc atc gaa gag gcc cag ggc tcc tca gag	329
Pro Pro Ala Cys Val Gly Cys Ile Glu Glu Ala Gln Gly Ser Ser Glu	
1 5 10 15	
cag gaa stc cac tat gca tct ctg cag agg ctg cca gtg ccc agc agt	377
Gln Glu Xaa His Tyr Ala Ser Leu Gln Arg Leu Pro Val Pro Ser Ser	
20 25 30	
gag gga cct gac ctc agg ggc aga gac aag aga ggc acc aag gag gat	425
Glu Gly Pro Asp Leu Arg Gly Arg Asp Lys Arg Gly Thr Lys Glu Asp	
35 40 45	
cca aga gct gac tat gcc tgc att gct gag aac aaa ccc ac	466
Pro Arg Ala Asp Tyr Ala Cys Ile Ala Glu Asn Lys Pro	
50 55 60	

<210> 186
 <211> 486
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 197..484

<221> sig_peptide

<222> 197..292

<223> score 11.3

seq LLLAVVLLSACLC/WL

<400> 186

cacacaccca cccaggccca ggctccttcc cctccatcat ccccttacca gcacctagaa 60
ccatccaggg ctgaaaagtc ccctccaaac cacgtgatga ggaacttgag gcaagtcacc 120
agcccctgat catttcgcct aaaagagcaa ggactagagt tcctgacctc caggccagtc 180
cctgatccct gaccta atg tta tcg cgg aat gat gat ata tgt atc tac ggg 232

Met Leu Ser Arg Asn Asp Asp Ile Cys Ile Tyr Gly

-30

-25

ggc ctg ggg cts ggc ggg ctc ctg ctt ctg gca gtg gtc ctt ctg tcc 280
Gly Leu Gly Leu Gly Gly Leu Leu Leu Leu Ala Val Val Leu Leu Ser
-20 -15 -10 -5

gcc tgc ctg tgt tgg ctg cat cga aga gta aag agg ctg gag akg agc 328
Ala Cys Leu Cys Trp Leu His Arg Arg Val Lys Arg Leu Glu Xaa Ser

1

5

10

tgg gcc cag ggc tcc tca gag cag gaa ctc cac tat gca tct ctg cag 376
Trp Ala Gln Gly Ser Ser Glu Gln Glu Leu His Tyr Ala Ser Leu Gln

15

20

25

agg ctg cca gtg ccc agc agt gag gga cct gac ctc agg ggc aga gac 424
Arg Leu Pro Val Pro Ser Ser Glu Gly Pro Asp Leu Arg Gly Arg Asp
30 35 40

aag aga ggc acn aag gag gat cca aga gct gac tat gcc tgc att gct 472
Lys Arg Gly Thr Lys Glu Asp Pro Arg Ala Asp Tyr Ala Cys Ile Ala
45 50 55 60

gag aac aaa ccc ac 486
Glu Asn Lys Pro

<210> 187

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 106..540

<221> sig_peptide

<222> 106..180

<223> score 8.9

seq IIAVLMSAQESWA/IK

<400> 187

aatggtcaga ctctattaca cccacattc tcttttcttt tattcttgtc tggtctgcct 60

cactcccgag ctctactgac tcccaamaga ggcgccaaga agaaa atg gcc ata agt 117
Met Ala Ile Ser
-25

gga gtc cct gtg cta gga ttt ttc atc ata gct gtg ctg atg agc gct 165
Gly Val Pro Val Leu Gly Phe Phe Ile Ile Ala Val Leu Met Ser Ala
-20 -15 -10

cag gaa tca tgg gct atc aaa gaa gaa cat gtg atc atc cag gcc gag 213
Gln Glu Ser Trp Ala Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu
-5 1 5 10

ttc tat ctg aat cct gac caa tca ggc gag ttt atg ttt gac ttt gat 261
Phe Tyr Leu Asn Pro Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp
15 20 25

ggt gat gag att ttc cat gtg gat atg gca aag aag gag acg gtc tgg 309
Gly Asp Glu Ile Phe His Val Asp Met Ala Lys Lys Glu Thr Val Trp
30 35 40

cgg ctt gaa gaa ttt gga cga ttt gcc agc ttt gag gct caa ggt gca 357
Arg Leu Glu Glu Phe Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala
45 50 55

ttg gcc aac ata gct gtg gac aaa gcc aac ctg gaa atc atg aca aag 405
Leu Ala Asn Ile Ala Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys
60 65 70 75

cgc tcc aac tat act ccg atc acc aat gta cct cca gag gta act gtg 453
Arg Ser Asn Tyr Thr Pro Ile Thr Asn Val Pro Pro Glu Val Thr Val
80 85 90

ctc acg aac agc cct gtg gaa ctg aga gag ccc aac gtc ctc atc tgt 501
Leu Thr Asn Ser Pro Val Glu Leu Arg Glu Pro Asn Val Leu Ile Cys
95 100 105

ttc atm gac aag ttc acc cca cca gtg gtc aat gtc acg tg 542
Phe Ile Asp Lys Phe Thr Pro Pro Val Val Asn Val Thr
110 115 120

<210> 188
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..451

<221> sig_peptide
<222> 62..196
<223> score 5.8
seq ILVAFSFLFTVIT/FP

<400> 188
attcccgcg gctccgggtt tggcaacgag gacgggggag tgcgactgcg tctcgggcag 60
c atg gcc gag aag cgg cac aca cgg gac tcc gaa gcc cag cgg ctc ccc 109
Met Ala Glu Lys Arg His Thr Arg Asp Ser Glu Ala Gln Arg Leu Pro
-45 -40 -35 -30

gac tcc ttc aag gac agc ccc agt aag ggc ctt gga cct tgc gga tgg 157
Asp Ser Phe Lys Asp Ser Pro Ser Lys Gly Leu Gly Pro Cys Gly Trp
-25 -20 -15

004220 " 566T560

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att ttg gtg gcg ttc tca ttc tta ttc acc gtt ata act ttc cca atc      205
Ile Leu Val Ala Phe Ser Phe Leu Phe Thr Val Ile Thr Phe Pro Ile
      -10                      -5                      1
tca ata tgg atg tgc ata aag att ata aaa gag tat gaa aga gcc atc      253
Ser Ile Trp Met Cys Ile Lys Ile Ile Lys Glu Tyr Glu Arg Ala Ile
      5                      10                      15
atc ttt aga ttg gdw cgc att tta caa gga gsa gcc aaa gga cct ggt      301
Ile Phe Arg Leu Gly Arg Ile Leu Gln Gly Xaa Ala Lys Gly Pro Gly
      20                      25                      30                      35
ttg ttt ttt att ctg cca tgc act gac agc ttc atc aaa gtg gac atg      349
Leu Phe Phe Ile Leu Pro Cys Thr Asp Ser Phe Ile Lys Val Asp Met
      40                      45                      50
aga act att tca ttt gat att cct cct cag gag atc ctc aca aag gat      397
Arg Thr Ile Ser Phe Asp Ile Pro Pro Gln Glu Ile Leu Thr Lys Asp
      55                      60                      65
tca gtg aca att agc gtg gat ggt gtg gtc tat tac cgc gtt cag aat      445
Ser Val Thr Ile Ser Val Asp Gly Val Val Tyr Tyr Arg Val Gln Asn
      70                      75                      80
gca ccc tg
Ala Pro
      85

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<210> 189
 <211> 442
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 129..440

<221> sig_peptide
 <222> 129..173
 <223> score 4.8
 seq SLATAAPVPTTLA/QV

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<400> 189
aagtgggagg asgagccgga gtcggatggc ggctacggcg gctcattggt ttccgctgca      60
ggggtgctga aggggggacg cgggtcggac gcgtccggct gtggaagaga gcggcggccg      120
ctcacaac atg cac agc ctg gcg acg gct gcg cct gtg cct act aca ctg      170
      Met His Ser Leu Ala Thr Ala Ala Pro Val Pro Thr Thr Leu
      -15                      -10                      -5
gca caa gtg gat aga gaa aag atc tat cag tgg atc aat gag ctg tcc      218
Ala Gln Val Asp Arg Glu Lys Ile Tyr Gln Trp Ile Asn Glu Leu Ser
      1                      5                      10                      15
agt cct gag act agg gaa aat gct ttg ctg gag cta agt aag aag cga      266
Ser Pro Glu Thr Arg Glu Asn Ala Leu Leu Glu Leu Ser Lys Lys Arg
      20                      25                      30
gaa tct gtt cct gac ctt gca ccc atg ctg tgg cat tca ttt ggt act      314
Glu Ser Val Pro Asp Leu Ala Pro Met Leu Trp His Ser Phe Gly Thr
      35                      40                      45
att gca gca ctt tta cag gaa att gta aat att tat csr tct atc aac      362
Ile Ala Ala Leu Leu Gln Glu Ile Val Asn Ile Tyr Xaa Ser Ile Asn

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50	55	60	
cca ccc acc ttg aca gca cac cag tct aac aga gtt tgc aat gct ctg			410
Pro Pro Thr Leu Thr Ala His Gln Ser Asn Arg Val Cys Asn Ala Leu			
65	70	75	
gca tta ctg caa tgt gta gca tca cat cca ga			442
Ala Leu Leu Gln Cys Val Ala Ser His Pro			
80	85		

<210> 190
 <211> 332
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..332

<221> sig_peptide
 <222> 75..134
 <223> score 8.5
 seq WIGLISSVCCVFA/QT

<400> 190		
gagaggccca gcgggmgtcg cggaacagca ggcccagacc caccgcgccg ggccccggac		60
gccgcgcgga aaag atg aat tta caa cca att ttc tgg att gga ctg atc		110
Met Asn Leu Gln Pro Ile Phe Trp Ile Gly Leu Ile		
-20 -15 -10		
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Ser Ser Val Cys Cys Val Phe Ala Gln Thr Asp Xaa Asn Arg Cys Leu		
-5 1 5		
aaa gca aat gcc aaa tca tgt gga gaa tgt ata caa gca ggg cca aat		206
Lys Ala Asn Ala Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn		
10 15 20		
tgt ggg tgg tgc aca aat tca aca ttt tta cag gaa ggm atg cct act		254
Cys Gly Trp Cys Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr		
25 30 35 40		
tct gca cga tgt gat gat tta gaa gcc tta aaa aag aag ggt tgc cct		302
Ser Ala Arg Cys Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Pro		
45 50 55		
cca gat gac ata gaa aat ccc aga ggc tcc		332
Pro Asp Asp Ile Glu Asn Pro Arg Gly Ser		
60 65		

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 aggattctcc ttctgaaagc tcagaatatt tcttcccctt ccctatacac acagggctcg 180
 aagggttaga gaagaaaggc agacaacagc ttctgagctt tggactaatc acagcctctg 240
 ttctcagcag gagccccaac actgagacca gaaaag atg gtg cta tgc ttt cct 294
 Met Val Leu Cys Phe Pro
 -20 -15
 ctt ctt tta ctg ctg ctg gtt cta tgg gga cca gtg tgt cca ctt cat 342
 Leu Leu Leu Leu Leu Leu Val Leu Trp Gly Pro Val Cys Pro Leu His
 -10 -5 1
 gct tgg cct aag cgt ctc acc aag gct cac tgg ttt gaa att cag cat 390
 Ala Trp Pro Lys Arg Leu Thr Lys Ala His Trp Phe Glu Ile Gln His
 5 10 15
 ata cag cca agt cct ctc caa tgc aac agg gca atg agt ggc atc aac 438
 Ile Gln Pro Ser Pro Leu Gln Cys Asn Arg Ala Met Ser Gly Ile Asn
 20 25 30
 aat tat acc cag cac tgt aag cat caa aat acc ttt ctg cat gac t 484
 Asn Tyr Thr Gln His Cys Lys His Gln Asn Thr Phe Leu His Asp
 35 40 45

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 ctt gtc ctc ctt tct gtt acg gtc cag ggc aag gtc ttt gaa agg tgt 102
 Leu Val Leu Leu Ser Val Thr Val Gln Gly Lys Val Phe Glu Arg Cys
 -10 -5 1 5
 gag ttg gcc aga act ctg aaa aga ttg gga atg gat ggc tac agg gga 150
 Glu Leu Ala Arg Thr Leu Lys Arg Leu Gly Met Asp Gly Tyr Arg Gly
 10 15 20
 atc agc cta gca aac tgt aag tct act ctc cat aat tcc aga gaa tta 198
 Ile Ser Leu Ala Asn Cys Lys Ser Thr Leu His Asn Ser Arg Glu Leu
 25 30 35

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 Ala Thr Tyr Gly Thr Asp Thr Arg Arg Glu Gly Arg Arg Arg
 40 45 50

242

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 Met Ala Ile Arg Lys Lys
 -40
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 Ser Thr Lys Ser Pro Pro Val Leu Ser His Glu Phe Val Leu Gln Asn
 -35 -30 -25
 cac gcg gac atc gtc tcc tgt gtg gcg atg gtc ttc ctg ctg ggg ctc 211
 His Ala Asp Ile Val Ser Cys Val Ala Met Val Phe Leu Leu Gly Leu
 -20 -15 -10
 atg ttt gag ata acg gca aaa gct tct atc att ttt gtt act ctt cag 259
 Met Phe Glu Ile Thr Ala Lys Ala Ser Ile Ile Phe Val Thr Leu Gln
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 tac aat gtc acc ctc cca gca aca gaa gaa caa gct act gaa tca gtg 307
 Tyr Asn Val Thr Leu Pro Ala Thr Glu Glu Gln Ala Thr Glu Ser Val
 15 20 25
 tcc ctt tat tac tat ggc atc aaa gat ttg gct act gtt ttc ttc tac 355
 Ser Leu Tyr Tyr Tyr Gly Ile Lys Asp Leu Ala Thr Val Phe Phe Tyr
 30 35 40
 atg cta gtg gcg ata att att cat gcc gta att caa gag tat atg ttg 403
 Met Leu Val Ala Ile Ile Ile His Ala Val Ile Gln Glu Tyr Met Leu
 45 50 55
 gat aar att aac agg cga atg cnc ttc tcc aaa aca rna cac agc aag 451
 Asp Lys Ile Asn Arg Arg Met Xaa Phe Ser Lys Thr Xaa His Ser Lys
 60 65 70
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 Phe Asn Glu Ser Gly Gln Leu
 75 80

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<222> 90..173

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Met Ser His Gly Lys Gly Thr Asp
-25
atg ctc ccg gag atc gcc gcc gcc gtg ggc ttc ctc tcc agc ctc ctg 161
Met Leu Pro Glu Ile Ala Ala Ala Val Gly Phe Leu Ser Ser Leu Leu
-20 -15 -10 -5
agg acc cgg ggc tgc gtg agc gag cag agg ctt aag gtc ttc agc ggg 209
Arg Thr Arg Gly Cys Val Ser Glu Gln Arg Leu Lys Val Phe Ser Gly
1 5 10
gcg ctc cag gag gca ctc aca gag cac tac aaa cac cac tgg ttt ccc 257
Ala Leu Gln Glu Ala Leu Thr Glu His Tyr Lys His His Trp Phe Pro
15 20 25
gaa aag ccg tcc aag ggc tcc ggc tac cgc tgc att cgc atc aac cac 305
Glu Lys Pro Ser Lys Gly Ser Gly Tyr Arg Cys Ile Arg Ile Asn His
30 35 40
aag atg gac ccc atc atc agc agg gtg gcc agc cag atc gga ctc agc 353
Lys Met Asp Pro Ile Ile Ser Arg Val Ala Ser Gln Ile Gly Leu Ser
45 50 55 60
cag ccc cag ctg cac cag ctg ctg ccc agc gag ctg acc ctg tgg gtg 401
Gln Pro Gln Leu His Gln Leu Leu Pro Ser Glu Leu Thr Leu Trp Val
65 70 75
gac cct atg agg tgt cct acg cat tgg gag g 432
Asp Pro Met Arg Cys Pro Thr His Trp Glu
80 85

<210> 195

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<222> 30..95

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Val Phe Leu Leu Ala Leu Thr Ile Ile Ala Ser Thr Trp Ala Leu Thr		
	-10 -5 1	
ccc act cac tac ctc acc aag cat gac gtg grg aga cta aaa gcc tcg		149
Pro Thr His Tyr Leu Thr Lys His Asp Val Xaa Arg Leu Lys Ala Ser		
	5 10 15	
ctg gat cgc cct ttc aca aat ttg gaa tct gcc ttc tac tcc atc gtg		197
Leu Asp Arg Pro Phe Thr Asn Leu Glu Ser Ala Phe Tyr Ser Ile Val		
	20 25 30	
gga ctc agc agc ctt ggt gct cag gtg cca gat gca aag gta agg ctg		245
Gly Leu Ser Ser Leu Gly Ala Gln Val Pro Asp Ala Lys Val Arg Leu		
	35 40 45 50	
ctt ttg tcc tgg tgg tca ggg tgg ttc agg aga acc ttc atc cc		289
Leu Leu Ser Trp Trp Ser Gly Trp Phe Arg Arg Thr Phe Ile		
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aggaaaacaa aagctgctac tt atg gaa gat aca aag gag tct aac gtg aag		112
	Met Glu Asp Thr Lys Glu Ser Asn Val Lys	
	-35 -30	
aca ttt trc tcc arr aat atc cna gcc atc ctt ggc ntc ncy nct atc		160
Thr Phe Xaa Ser Xaa Asn Ile Xaa Ala Ile Leu Gly Xaa Xaa Xaa Ile		
	-25 -20 -15	
ata gct gtg ata gct ttg cnt gct gtg ggg ttg acc cag aac aaa gca		208
Ile Ala Val Ile Ala Leu Xaa Ala Val Gly Leu Thr Gln Asn Lys Ala		
	-10 -5 1	
ttg cca gaa aac gtt aag tat ggg att gtg ctg gat gcg ggt tct tct		256
Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser		
	5 10 15 20	
cac aca agt tta tac atc tat aag tgg cca gca gww aag gag aat gac		304
His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Xaa Lys Glu Asn Asp		
	25 30 35	
aca ggc gtg gan cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga		352
Thr Gly Val Xaa His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly		
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atc tca aaa ttt		364

Ile Ser Lys Phe
55

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cac gga tta ata ttt ctc cct gtc tta ctc agt tac ata ggc cca tca 100
His Gly Leu Ile Phe Leu Pro Val Leu Leu Ser Tyr Ile Gly Pro Ser
-15 -10 -5 1
att cct gag cac gcc crw ccc agt ggc agc aca gtg ggc aag aca cac 148
Ile Pro Glu His Ala Xaa Pro Ser Gly Ser Thr Val Gly Lys Thr His
5 10 15
gga tgc atc aag ccg cca ggg ctc aca gcc cag cag gaa aca aaa gga 196
Gly Cys Ile Lys Pro Pro Gly Leu Thr Ala Gln Gln Glu Thr Lys Gly
20 25 30
gag tca cta acc tct gaa aat gct ttg cag ccc 229
Glu Ser Leu Thr Ser Glu Asn Ala Leu Gln Pro
35 40

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<213> Homo sapiens

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gcattttcca ggataactgt gactccaggc ccgca atg gat gcc ctg caa cta 113
Met Asp Ala Leu Gln Leu

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                                -40
gca aat tcg gct ttt gcc gtt gat ctg ttc aaa caa cta tgt gaa aag      161
Ala Asn Ser Ala Phe Ala Val Asp Leu Phe Lys Gln Leu Cys Glu Lys
-35                                -30                                -25
gag cca ctg ggc aat gtc ctc ttc tct cca atc tgt ctc tcc acc tct      209
Glu Pro Leu Gly Asn Val Leu Phe Ser Pro Ile Cys Leu Ser Thr Ser
-20                                -15                                -10                                -5
ctg tca ctt gct caa gtg ggt gct aaa ggt gac act gca aat gaa att      257
Leu Ser Leu Ala Gln Val Gly Ala Lys Gly Asp Thr Ala Asn Glu Ile
1                                5                                10
gga cag gtt ctt cat ttt gaa aat gtc aaa gat gta ccc ttt gga ttt      305
Gly Gln Val Leu His Phe Glu Asn Val Lys Asp Val Pro Phe Gly Phe
15                                20                                25
caa aca gta aca tcg gat gta aac aaa ctt agt tcc ttt tac tca ctg      353
Gln Thr Val Thr Ser Asp Val Asn Lys Leu Ser Ser Phe Tyr Ser Leu
30                                35                                40
ara cta atc aag cgg ctc tac gta gac aaa tct ctg aat ctt tct aca      401
Xaa Leu Ile Lys Arg Leu Tyr Val Asp Lys Ser Leu Asn Leu Ser Thr
45                                50                                55                                60
gag ttc atc      410
Glu Phe Ile

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gtgctacttt gaactgcttt tcttttctcc tttttgcaca aagagtctca tgtctgatat      180
ttagac atg atg agc ttt gtg caa aag ggg agc tgg cta ctt ctc gct      228
      Met Met Ser Phe Val Gln Lys Gly Ser Trp Leu Leu Leu Ala
-20                                -15                                -10
ctg ctt cat ccc act att att ttg gca caa cag gaa gct gtt gaa gga      276
Leu Leu His Pro Thr Ile Ile Leu Ala Gln Gln Glu Ala Val Glu Gly
-5                                1                                5
gga tgt tcc cat ctt ggt cag tcc tat gcg gat aga gat gtc tgg aag      324
Gly Cys Ser His Leu Gly Gln Ser Tyr Ala Asp Arg Asp Val Trp Lys
10                                15                                20
cca gaa cca tgc caa ata tgt gtc tgt gac tca gga tcc gtt ctc tgc      372
Pro Glu Pro Cys Gln Ile Cys Val Cys Asp Ser Gly Ser Val Leu Cys
25                                30                                35
gat gac ata ata tgt gac gat caa gaa tta gac tgc ccc aac cca gaa      420

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Asp	Asp	Ile	Ile	Cys	Asp	Asp	Gln	Glu	Leu	Asp	Cys	Pro	Asn	Pro	Glu		
40					45					50					55		
att	cca	ttt	gga	gaa	tgt	tgt	gca	gtt	tgc	cca	cag	cct	cca	act	gct	468	
Ile	Pro	Phe	Gly	Glu	Cys	Cys	Ala	Val	Cys	Pro	Gln	Pro	Pro	Thr	Ala		
				60					65					70			
cct	act	cgc	cct	cct	aat	ggt	caa	gga	cct	caa	ggc	ccc	aag	gga	gat	516	
Pro	Thr	Arg	Pro	Pro	Asn	Gly	Gln	Gly	Pro	Gln	Gly	Pro	Lys	Gly	Asp		
			75					80					85				
cca	ggc	cct	cct	ggt	att	cct	ggg	aga	aat							546	
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	Met	Gly	Ser	Gly	Trp	Val	Pro	Trp	Val	Val	Ala	Leu	Leu	Val			
	-20						-15						-10				
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Asn	Leu	Thr	Arg	Leu	Asp	Ser	Ser	Met	Thr	Gln	Gly	Thr	Asp	Ser	Pro		
	-5					1				5							
gaa	gat	ttt	gtg	att	cag	gca	aag	gct	gac	tgt	tac	ttc	acc	aac	ggg	204	
Glu	Asp	Phe	Val	Ile	Gln	Ala	Lys	Ala	Asp	Cys	Tyr	Phe	Thr	Asn	Gly		
10				15				20						25			
aca	gaa	aag	gtg	cag	ttt	gtg	gtc	aga	ttc	atc	ttt	aac	ttg	gag	gag	252	
Thr	Glu	Lys	Val	Gln	Phe	Val	Val	Arg	Phe	Ile	Phe	Asn	Leu	Glu	Glu		
			30					35					40				
tat	gta	cgt	ttc	gac	agt	kat	gtg	ggg	atg	ttt	gtg	gca	ttg	acc	aag	300	
Tyr	Val	Arg	Phe	Asp	Ser	Xaa	Val	Gly	Met	Phe	Val	Ala	Leu	Thr	Lys		
			45				50					55					
ctg	ggg	cag	cca	gat	gct	gag	cag	tgg	aac	agc	cgg	ctg	gat	ctc	ttg	348	
Leu	Gly	Gln	Pro	Asp	Ala	Glu	Gln	Trp	Asn	Ser	Arg	Leu	Asp	Leu	Leu		
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gag	agg	agc														357	
Glu	Arg	Ser															
			75														

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<222> 87..476

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<222> 87..167

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                               Met Arg Lys Ser Pro Gly Leu Ser Asp
                               -25                               -20

tgt ctt tgg gcc tgg atc ctc ctt ctg agc aca ctg act gga aga agc      161
Cys Leu Trp Ala Trp Ile Leu Leu Leu Ser Thr Leu Thr Gly Arg Ser
                               -15                               -10                               -5

tat gga cag ccg tca tta caa gat gaa ctt aaa gac aat acc act gtc      209
Tyr Gly Gln Pro Ser Leu Gln Asp Glu Leu Lys Asp Asn Thr Thr Val
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Phe Thr Arg Ile Leu Asp Arg Leu Leu Asp Gly Tyr Asp Asn Arg Leu
15                               20                               25                               30

aga cca gga ttg gga gag cgt gta acc gaa gtg aag act gat atc ttc      305
Arg Pro Gly Leu Gly Glu Arg Val Thr Glu Val Lys Thr Asp Ile Phe
                               35                               40                               45

gtc acc agt ttc gga ccc gtt tca gac cat gat atg gaa tat aca ata      353
Val Thr Ser Phe Gly Pro Val Ser Asp His Asp Met Glu Tyr Thr Ile
                               50                               55                               60

gat gta ttt ttc cgt caa agc tgg aag gat gaa agg tta aaa ttt aaa      401
Asp Val Phe Phe Arg Gln Ser Trp Lys Asp Glu Arg Leu Lys Phe Lys
65                               70                               75

gga cct atg aca gtc ctc cgg tta aat aac cta atg gca agt aaa atc      449
Gly Pro Met Thr Val Leu Arg Leu Asn Asn Leu Met Ala Ser Lys Ile
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<222> 106..159

<223> score 16.3

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Met Gln Trp Thr
-15

tcc ctc ctg ctg ctg gca ggg ctc ttc tcc ctc tcc cag gcc cag tat 165
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gaa gat gac cct cat tgg tgg ttc cac tac ctc cgc agc cag cag tcc 213
Glu Asp Asp Pro His Trp Trp Phe His Tyr Leu Arg Ser Gln Gln Ser
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acc tac tac gat ccc tat gac cct tac ccg tat gag acc tac gag cct 261
Thr Tyr Tyr Asp Pro Tyr Asp Pro Tyr Pro Tyr Glu Thr Tyr Glu Pro
20 25 30

tac ccc tat ggg gtg gat gaa ggg cca gcc tac acc tac ggc tct cca 309
Tyr Pro Tyr Gly Val Asp Glu Gly Pro Ala Tyr Thr Tyr Gly Ser Pro
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tcc cct cca gat ccc cgc gac tgc ccc cag gaa tgc gac tgc cca ccc 357
Ser Pro Pro Asp Pro Arg Asp Cys Pro Gln Glu Cys Asp Cys Pro Pro
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Met Ala Ser Arg Leu Thr Leu Leu Thr Leu Leu Leu
-20 -15 -10

ctg ctg ctg gct ggg gat aga gcc tcc tca aat cca aat gct acc agc 160
Leu Leu Leu Ala Gly Asp Arg Ala Ser Ser Asn Pro Asn Ala Thr Ser
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tcc agc tcc cag gat cca gag agt ttg caa gac aga ggc gaa ggg aag 208
Ser Ser Ser Gln Asp Pro Glu Ser Leu Gln Asp Arg Gly Glu Gly Lys
10 15 20

gtc gca aca aca gtt atc tcc aag atg cta ttc gtt gaa ccc atc ctg 256

004220" 666E7560

Val	Ala	Thr	Thr	Val	Ile	Ser	Lys	Met	Leu	Phe	Val	Glu	Pro	Ile	Leu	
25					30					35					40	
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Glu	Val	Ser	Ser	Leu	Pro	Thr	Thr	Asn	Ser	Thr	Thr	Asn	Ser	Ala	Thr	
				45				50						55		
aaa	ata	aca	gct	aat	acc	act	gat	gaa	ccc	acc	aca	caa	ccc	acc	aca	352
Lys	Ile	Thr	Ala	Asn	Thr	Thr	Asp	Glu	Pro	Thr	Thr	Gln	Pro	Thr	Thr	
			60					65					70			
gag	ccc	acc	acc	can	cat	cc										372
Glu	Pro	Thr	Thr	Xaa	His											
			75													

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 <221> sig_peptide
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							Met	Ala									
							-20										
tcc	agg	ctg	acc	ctg	ctg	acc	ctc	ctg	ctg	ctg	ctg	ctg	gct	ggg	gat		106
Ser	Arg	Leu	Thr	Leu	Leu	Thr	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Gly	Asp		
			-15				-10						-5				
aga	gcc	tcc	tca	aat	cca	aat	gct	acc	agc	tcc	agc	tcc	cag	gat	cca		154
Arg	Ala	Ser	Ser	Asn	Pro	Asn	Ala	Thr	Ser	Ser	Ser	Ser	Gln	Asp	Pro		
	1			5						10							
gag	agt	ttg	caa	gac	aga	ggc	gaa	ggg	aag	gtc	gca	aca	aca	ggt	atc		202
Glu	Ser	Leu	Gln	Asp	Arg	Gly	Glu	Gly	Lys	Val	Ala	Thr	Thr	Val	Ile		
15			20					25						30			
tcc	aag	atg	cta	ttc	ggt	gaa	ccc	atc	ctg	gag	ggt	tcc	agc	ttg	ccg		250
Ser	Lys	Met	Leu	Phe	Val	Glu	Pro	Ile	Leu	Glu	Val	Ser	Ser	Leu	Pro		
			35					40					45				
aca	acc	aac	tca	aca	acc	aat	tca	gcc	acc	aaa	ata	aca	gct	aat	acc		298
Thr	Thr	Asn	Ser	Thr	Thr	Asn	Ser	Ala	Thr	Lys	Ile	Thr	Ala	Asn	Thr		
			50					55					60				
act	gat	gaa	ccc	acc	aca	caa	ccc	acc	aca	gag	ccc	ans	acc	caa	ccc		346
Thr	Asp	Glu	Pro	Thr	Thr	Gln	Pro	Thr	Thr	Glu	Pro	Xaa	Thr	Gln	Pro		
		65					70					75					
acc	atc	caa	c														356
Thr	Ile	Gln															
			80														

<210> 205

<211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 261..437

<221> sig_peptide
 <222> 261..362
 <223> score 4
 seq IAVLYLHLYDVFG/DP

<400> 205
 gcggggtgag aggccagggc cgagaagggc ttcaggacgc gggaggcgca cttgcttcaa 60
 gtcgcgggcg tgggaacggg gttgcaaaac ggggcctctt trtccgggct tgcttccggc 120
 gtcattggctc aaagggcctt cccgaatcct tatgctgatt ataacaatc cctggccgaa 180
 ngtactttga tgctgccggg aggctgactc ctgagttctc acaacgcttg accaataaga 240
 ttcgggagct tcttcagcaa atg gag aga ggc ctg aaa tca gca gac cct cgg 293
 Met Glu Arg Gly Leu Lys Ser Ala Asp Pro Arg
 -30 -25
 gat ggc acc ggt tac act ggc tgg gca ggt att gct gtg ctt tac tta 341
 Asp Gly Thr Gly Tyr Thr Gly Trp Ala Gly Ile Ala Val Leu Tyr Leu
 -20 -15 -10
 cat ctt tat gat gta ttt ggg gac cct gcc tac cta cag tta gca cat 389
 His Leu Tyr Asp Val Phe Gly Asp Pro Ala Tyr Leu Gln Leu Ala His
 -5 1 5
 ggc tat gta aag caa agt ctg aac tgc tta acc aag cgc tcc atc acc t 438
 Gly Tyr Val Lys Gln Ser Leu Asn Cys Leu Thr Lys Arg Ser Ile Thr
 10 15 20 25

<210> 206
 <211> 438
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 82..438

<221> sig_peptide
 <222> 82..207
 <223> score 7.4
 seq SLSVLVLLLTIIA/VT

<400> 206
 acccgcccc gtgcgctcat tggtcgggat gtgtcknctc agcagcctcc aacttctccc 60
 gaatcccact gattttaggt g atg ggc aag tca gaa agt cag atg gat ata 111
 Met Gly Lys Ser Glu Ser Gln Met Asp Ile
 -40 -35
 act gat atc awc act cca aag cca aag aag aaa cag cga kgg act cca 159
 Thr Asp Ile Xaa Thr Pro Lys Pro Lys Lys Lys Gln Arg Xaa Thr Pro

Ile	Xaa	Xaa	Met	Asp	Ala	Thr	Thr	Glu	Pro	Cys	Thr	Asp	Phe	Phe	Lys	
	30						35					40				
tat	gct	tgc	gga	ggc	tgg	ttg	aaa	cgt	aat	gtc	att	ccc	gag	acc	agc	462
Tyr	Ala	Cys	Gly	Gly	Trp	Leu	Lys	Arg	Asn	Val	Ile	Pro	Glu	Thr	Ser	
	45					50					55					
tcc	cgt	tac	ggn	acc	ttt	ggc	att	tta	aga	gat	gaa	cta	gaa	gtc	gtt	510
Ser	Arg	Tyr	Gly	Thr	Phe	Gly	Ile	Leu	Arg	Asp	Glu	Leu	Glu	Val	Val	
60					65					70					75	
ttg	aaa															516
Leu	Lys															

<210> 208
 <211> 311
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..311

<221> sig_peptide
 <222> 15..86
 <223> score 4.6
 seq QGMLLAILEXCGA/IP

<400> 208																	
tcctcaagtt	cttc	atg	gtc	aag	tcc	gtc	atc	ttt	ctt	tcc	ttc	tgg	caa				50
		Met	Val	Lys	Ser	Val	Ile	Phe	Leu	Ser	Phe	Trp	Gln				
						-20					-15						
ggc	atg	ctc	ctg	gcc	atc	ctg	gag	rag	tgt	ggg	gcc	atc	ccc	aaa	atc		98
Gly	Met	Leu	Leu	Ala	Ile	Leu	Glu	Xaa	Cys	Gly	Ala	Ile	Pro	Lys	Ile		
		-10				-5					1						
cac	tcg	gcc	cgc	gtg	tcg	gtg	ggc	gag	ggc	acc	gtg	gct	gcc	ggc	tac		146
His	Ser	Ala	Arg	Val	Ser	Val	Gly	Glu	Gly	Thr	Val	Ala	Ala	Gly	Tyr		
5				10					15					20			
cag	gac	ttc	atc	atc	tgt	gtg	gag	atg	ttc	ttt	gca	gcc	ctg	gcc	ctg		194
Gln	Asp	Phe	Ile	Ile	Cys	Val	Glu	Met	Phe	Phe	Ala	Ala	Leu	Ala	Leu		
				25				30					35				
cgg	cac	gcc	ttc	acc	tac	aag	gtc	tat	gct	gac	aag	agg	ctg	gac	gca		242
Arg	His	Ala	Phe	Thr	Tyr	Lys	Val	Tyr	Ala	Asp	Lys	Arg	Leu	Asp	Ala		
		40					45					50					
caa	gtg	cca	aca	tac	ggc	cct	tac	ggc	cgc	tgt	gcc	ccc	atg	aag	agc		290
Gln	Val	Pro	Thr	Tyr	Gly	Pro	Tyr	Gly	Arg	Cys	Ala	Pro	Met	Lys	Ser		
		55				60						65					
atc	tcc	agc	agc	ctc	aag	gag											311
Ile	Ser	Ser	Ser	Leu	Lys	Glu											
	70					75											

<210> 209
 <211> 435
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..433

<221> sig_peptide
 <222> 29..82
 <223> score 12.7
 seq LWVLLPLVTMAWG/QY

<400> 209
 gagattgttt gccaaaatcc caggcagc atg gac ctc agt ctt ctc tgg gta 52
 Met Asp Leu Ser Leu Leu Trp Val
 -15
 ctt ctg ccc cta gtc acc atg gcc tgg ggc cag tat ggc gat tat gga 100
 Leu Leu Pro Leu Val Thr Met Ala Trp Gly Gln Tyr Gly Asp Tyr Gly
 -10 -5 1 5
 tac cca tac cag cag tat cat gac tac agc gat gat ggg tgg gtg aat 148
 Tyr Pro Tyr Gln Gln Tyr His Asp Tyr Ser Asp Asp Gly Trp Val Asn
 10 15 20
 ttg aac cgg caa ggc ttc agc tac cag tgt ccc cag ggg cag gtg ata 196
 Leu Asn Arg Gln Gly Phe Ser Tyr Gln Cys Pro Gln Gly Gln Val Ile
 25 30 35
 gtg gcc gtg agg agc atc ttc agc aag aag gaa ggt tct gac aga caa 244
 Val Ala Val Arg Ser Ile Phe Ser Lys Lys Glu Gly Ser Asp Arg Gln
 40 45 50
 tgg aac tac gcc tgc atg ccc acr cca cag agc ctc ggg gaa ccc acg 292
 Trp Asn Tyr Ala Cys Met Pro Thr Pro Gln Ser Leu Gly Glu Pro Thr
 55 60 65 70
 gag tgc tgg tgg gag gag atc aac agg gct ggc atg gaa tgg tac cag 340
 Glu Cys Trp Trp Glu Glu Ile Asn Arg Ala Gly Met Glu Trp Tyr Gln
 75 80 85
 acg tgc tcc aac aat ggg ctg gtg gca gga ttc cag agc cgc tac ttc 388
 Thr Cys Ser Asn Asn Gly Leu Val Ala Gly Phe Gln Ser Arg Tyr Phe
 90 95 100
 gag tca gtg ctg gat cgg gag tgg cag ttt tac tgt tgt cgc tac ag 435
 Glu Ser Val Leu Asp Arg Glu Trp Gln Phe Tyr Cys Cys Arg Tyr
 105 110 115

<210> 210
 <211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 61..432
 <221> sig_peptide
 <222> 61..126
 <223> score 9.1
 seq LLLLSGALALTET/WA

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<400> 210
agtccccggtt ctaaagtccc cagtcaccca cccggactcr gattctccyc agacgccgag      60
atg cgg gtc ayg gcg ccc cga acc stc ctc ctg ctg ctc tcg ggr gcc      108
Met Arg Val Xaa Ala Pro Arg Thr Xaa Leu Leu Leu Leu Ser Gly Ala
      -20                      -15                      -10

ctg gcc ctg acc gag acc tgg gcc ggc tcc cac tcc atg agg tat ttc      156
Leu Ala Leu Thr Glu Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe
      -5                      1                      5                      10

tac acc kcc rtg tcc cgg ccc ggc cgc ggg gag ccc cgc ttc atc nca      204
Tyr Thr Xaa Xaa Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Xaa
      15                      20                      25

gtg ggc tac gtg gac gac acg cwg ttc gtg agg ttc gac agc gac gcc      252
Val Gly Tyr Val Asp Asp Thr Xaa Phe Val Arg Phe Asp Ser Asp Ala
      30                      35                      40

rcg agt ccg agg ang gmg ccs cgg gcg ccr tgg ata gag cag gag ggg      300
Xaa Ser Pro Arg Xaa Xaa Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly
      45                      50                      55

ccg gag tat tgg gac cgg ras aca cag atc tcc aag acc aac aca cag      348
Pro Glu Tyr Trp Asp Arg Xaa Thr Gln Ile Ser Lys Thr Asn Thr Gln
      60                      65                      70

act tac cga gag aac ctg cgc acc gcg ctc cgc tac tac aac cag agc      396
Thr Tyr Arg Glu Asn Leu Arg Thr Ala Leu Arg Tyr Tyr Asn Gln Ser
      75                      80                      85                      90

gag gcc ggg tct cac atc atc cag agg atg tac ggc      432
Glu Ala Gly Ser His Ile Ile Gln Arg Met Tyr Gly
      95                      100

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<210> 211
<211> 358
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 61..357

<221> sig_peptide
<222> 61..132
<223> score 9.4
      seq LLSGALALTETWA/XS

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<400> 211
agtccccggtt ctaaagtccc cagtcaccca cccggactcg gantctccyc agacgccgag      60
atg cgg gtc ayg gcg ccc cga acc stc ctc ctg ctg ctc tcg ggr gcc      108
Met Arg Val Xaa Ala Pro Arg Thr Xaa Leu Leu Leu Leu Ser Gly Ala
      -20                      -15                      -10

ctg gcc ctg acc gag acc tgg gcc kgc tcc cac tcc atg agg tat ttc      156
Leu Ala Leu Thr Glu Thr Trp Ala Xaa Ser His Ser Met Arg Tyr Phe
      -5                      1                      5

tac acc gcc gtg tcc cgg ccc ggc cgc ggr gag ccc cgc ttc atc kca      204
Tyr Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Xaa
      10                      15                      20

gtg ggc tac gtg gac gac acs cag ttc gtg agg ttc gac agc gac gcc      252

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Ser Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly
 110 115 120
 aag gat tac atc gcc ctg aaa gag gac ctg cgc tct
 Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser
 125 130

529

<210> 213
 <211> 424
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..423

<221> sig_peptide
 <222> 64..114
 <223> score 9.3
 seq SLLLLLSGALALT/DT

<400> 213
 aggttctaaa gtcccacgca ccccgcgga ctcattttt tcccagacgc ggaggttggg 60
 gtc atg gcg ccc cga agc ctc ctc ctg ctg ctc tca ggg gcc ctg gcc 108
 Met Ala Pro Arg Ser Leu Leu Leu Leu Leu Ser Gly Ala Leu Ala
 -15 -10 -5
 ctg acc gat act tgg gcg ggc tcc cac tcc ttg agg tat ttc agc acc 156
 Leu Thr Asp Thr Trp Ala Gly Ser His Ser Leu Arg Tyr Phe Ser Thr
 1 5 10
 gct gtg tcg cgg ccc ggc cgc ggg gag ccc cgc tac atc gcc gtg gag 204
 Ala Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Tyr Ile Ala Val Glu
 15 20 25 30
 tac gta gac gac acg caa ttc ctg cgg ttc gac agc gac gcc gcg att 252
 Tyr Val Asp Asp Thr Gln Phe Leu Arg Phe Asp Ser Asp Ala Ala Ile
 35 40 45
 ccg agg atg gag ccg cgg gag ccg tgg gtg gag caa gag ggg ccg cag 300
 Pro Arg Met Glu Pro Arg Glu Pro Trp Val Glu Gln Glu Gly Pro Gln
 50 55 60
 tat tgg gag tgg acc aca ggg tac gcc aag gcc aac gca cag act gac 348
 Tyr Trp Glu Trp Thr Thr Gly Tyr Ala Lys Ala Asn Ala Gln Thr Asp
 65 70 75
 cga gtg gcc ctg agg aac ctg ctc cgc cgc tac aac cag agc gag gct 396
 Arg Val Ala Leu Arg Asn Leu Leu Arg Arg Tyr Asn Gln Ser Glu Ala
 80 85 90
 ggg tct cac acc ctc cag gga atg aat g 424
 Gly Ser His Thr Leu Gln Gly Met Asn
 95 100

<210> 214
 <211> 435
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 24..434

<221> sig_peptide
 <222> 24..74
 <223> score 8.4
 seq TLLLLLSEALALT/QT

<400> 214
 ctcaggactc agaggctggg atc atg gta gat gga acc ctc ctt tta ctc ctc 53
 Met Val Asp Gly Thr Leu Leu Leu Leu
 -15 -10
 tcg gag gcc ctg gcc ctt acc cag acc tgg gcg ggc tcc cac tcc ttg 101
 Ser Glu Ala Leu Ala Leu Thr Gln Thr Trp Ala Gly Ser His Ser Leu
 -5 1 5
 aag tat ttc cac act tcc gtg tcc cgg ccc ggc cgc ggg gag ccc cgc 149
 Lys Tyr Phe His Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg
 10 15 20 25
 ttc atc tct gtg ggc tac gtg gac gac acc cag ttc gtg cgc ttc gac 197
 Phe Ile Ser Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp
 30 35 40
 aac gac gcc gcg agt ccg agg atg gtg ccg cgg gcg ccg tgg atg gag 245
 Asn Asp Ala Ala Ser Pro Arg Met Val Pro Arg Ala Pro Trp Met Glu
 45 50 55
 cag gag ggg tca gag tat tgg gac cgg gag aca cgg agc gcc agg gac 293
 Gln Glu Gly Ser Glu Tyr Trp Asp Arg Glu Thr Arg Ser Ala Arg Asp
 60 65 70
 acc gca cag att ttc cga gtg aac ctg cgg acg ctg cgc ggc tac tac 341
 Thr Ala Gln Ile Phe Arg Val Asn Leu Arg Thr Leu Arg Gly Tyr Tyr
 75 80 85
 aat cag agc gag gcc ggg tct cac acc ctg cag tgg atg cat ggc tgc 389
 Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln Trp Met His Gly Cys
 90 95 100 105
 gag ctg ggg ccc gaa ggc gct tcc tcc gcg ggt atg aca gtt cgc c 435
 Glu Leu Gly Pro Glu Gly Ala Ser Ser Ala Gly Met Thr Val Arg
 110 115 120

<210> 215
 <211> 301
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 100..300

<221> sig_peptide
 <222> 100..162
 <223> score 10.5
 seq VLGLCLLSVGWVG/QD

<400> 215

ctcctcccct cccagcctca ggtgcctgct tcagaaaatg aagtagtaag tctgctggcc 60
 tccgccatct tagtaaagta acagtcccat gaaacaaag atg cag tcg ggc act 114
 Met Gln Ser Gly Thr

-20

cac tgg aga gtt ctg ggc ctc tgc ctc tta tca gtt ggc gtt tgg ggg 162
 His Trp Arg Val Leu Gly Leu Cys Leu Leu Ser Val Gly Val Trp Gly
 -15 -10 -5

caa gat ggt aat gaa gaa atg ggt ggt att aca cag aca cca tat aaa 210
 Gln Asp Gly Asn Glu Glu Met Gly Gly Ile Thr Gln Thr Pro Tyr Lys
 1 5 10 15

gtc tcc atc tct gga acc aca gta ata ttg aca tgc cct cag tat cct 258
 Val Ser Ile Ser Gly Thr Thr Val Ile Leu Thr Cys Pro Gln Tyr Pro
 20 25 30

gga tct gaa ata cta tgg caa cac aat gat aaa aac ata ggc g 301
 Gly Ser Glu Ile Leu Trp Gln His Asn Asp Lys Asn Ile Gly
 35 40 45

<210> 216
 <211> 399
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 87..398

<221> sig_peptide
 <222> 87..146
 <223> score 7.4
 seq FGMVFSLLQVVSG/ES

<400> 216
 ttcctcccct cctcccttcc tcttactctc attcatttca tacacactgg ctacacatc 60
 tactctctct ctctatctct ctcaga atg aca att cta ggt aca act ttt ggc 113
 Met Thr Ile Leu Gly Thr Thr Phe Gly

-20 -15

atg gtt ttt tct tta ctt caa gtc gtt tct gga gaa agt ggc tat gct 161
 Met Val Phe Ser Leu Leu Gln Val Val Ser Gly Glu Ser Gly Tyr Ala
 -10 -5 1 5

caa aat gga gac ttg gaa gat gca gaa ctg gat gac tac tca ttc tca 209
 Gln Asn Gly Asp Leu Glu Asp Ala Glu Leu Asp Asp Tyr Ser Phe Ser
 10 15 20

tgc tat agc cag ttg gaa gtg aat gga tcg cag cac tca ctg acc tgt 257
 Cys Tyr Ser Gln Leu Glu Val Asn Gly Ser Gln His Ser Leu Thr Cys
 25 30 35

gct ttt gag gac cca gat gtc aac ayc acc aat ctg gaa ttt gaa ata 305
 Ala Phe Glu Asp Pro Asp Val Asn Xaa Thr Asn Leu Glu Phe Glu Ile
 40 45 50

tgt ggg gcc ctc gtg gag gta aag tgc ctg aat ttc agg aaa cta caa 353
 Cys Gly Ala Leu Val Glu Val Lys Cys Leu Asn Phe Arg Lys Leu Gln
 55 60 65

gag ata tat ttc atc gag aca aag aaa ttc tta ctg att gga aag a 399
 Glu Ile Tyr Phe Ile Glu Thr Lys Lys Phe Leu Leu Ile Gly Lys

70

75

80

<210> 217
 <211> 466
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..466

<221> sig_peptide
 <222> 20..91
 <223> score 3.8
 seq LLRLQLQSGRRVHS/VA

<400> 217
 aagtcctctt ccgggcaaa atg gcg atg gga cta atg tgc gga cgc cgg gag 52
 Met Ala Met Gly Leu Met Cys Gly Arg Arg Glu
 -20 -15
 ctt ctg cgc ttg cta cag tcc ggg cgt cgg gtc cac agc gtc gca ggg 100
 Leu Leu Arg Leu Leu Gln Ser Gly Arg Arg Val His Ser Val Ala Gly
 -10 -5 1
 ccc tcg caa tgg ctt ggg aaa ccg ctg acc aca cgg ctc cta ttc cca 148
 Pro Ser Gln Trp Leu Gly Lys Pro Leu Thr Thr Arg Leu Leu Phe Pro
 5 10 15
 gta gcc ccg tgc tgc tgt cgc cca cac tac ctc ttc ctt gcg gct tcc 196
 Val Ala Pro Cys Cys Cys Arg Pro His Tyr Leu Phe Leu Ala Ala Ser
 20 25 30 35
 ggc ccc cgc agc ctc agt acc tct gct atc tcn ntt gca gaa gtc cag 244
 Gly Pro Arg Ser Leu Ser Thr Ser Ala Ile Ser Xaa Ala Glu Val Gln
 40 45 50
 gtt cag gcc cct cct gtt gtt gct gca act ccc tca ccc aca gca gta 292
 Val Gln Ala Pro Pro Val Val Ala Ala Thr Pro Ser Pro Thr Ala Val
 55 60 65
 cct gag gtg gct tct gga gag act gca gat gta gtc caa act gct gca 340
 Pro Glu Val Ala Ser Gly Glu Thr Ala Asp Val Val Gln Thr Ala Ala
 70 75 80
 gag cag agc ttc gct gaa ctg ggg ctg ggg tca tac acc cca gtg gga 388
 Glu Gln Ser Phe Ala Glu Leu Gly Leu Gly Ser Tyr Thr Pro Val Gly
 85 90 95
 ctg atc cag aat tta ctg gaa ttt atg cat gtt gat ctg ggc cta cct 436
 Leu Ile Gln Asn Leu Leu Glu Phe Met His Val Asp Leu Gly Leu Pro
 100 105 110 115
 tgg tgg ggg gcc att gct gca tgt aca gtc 466
 Trp Trp Gly Ala Ile Ala Ala Cys Thr Val
 120 125

<210> 218
 <211> 271
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..270

<221> sig_peptide
 <222> 46..180
 <223> score 6.5
 seq LLLLVLHPSRXSA/VS

<400> 218
 ataaaatggc gcgtgctgca acccgcgccc gcttcggaga gagaa atg ctg ggg tgc 57
 Met Leu Gly Cys
 -45
 agc ttc aag ctt agg acc acc cac cat gcc tat cca ggt gct gaa ggg 105
 Ser Phe Lys Leu Arg Thr Thr His His Ala Tyr Pro Gly Ala Glu Gly
 -40 -35 -30
 cct gac cat cac tca ttn aag aac aga gga ggc tgc ctg tta ctc ctg 153
 Pro Asp His His Ser Xaa Lys Asn Arg Gly Gly Cys Leu Leu Leu Leu
 -25 -20 -15 -10
 gtg ttg cat ccc tcc aga cwc tct gct gtt tcc tgc cta ggc gtg gct 201
 Val Leu His Pro Ser Arg Xaa Ser Ala Val Ser Cys Leu Gly Val Ala
 -5 1 5
 gca gcc atg gct agg aaa gtg ctg cca ccc acc cac ctg ggc cag agc 249
 Ala Ala Met Ala Arg Lys Val Leu Pro Pro Thr His Leu Gly Gln Ser
 10 15 20
 tgg ttc tgc tcc tgc tgc agg g 271
 Trp Phe Cys Ser Cys Cys Arg
 25 30

<210> 219
 <211> 311
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 135..311

<221> sig_peptide
 <222> 135..185
 <223> score 8.9
 seq ILIIGILLPQSLA/HP

<400> 219
 gccagtcgc gccgccagcg ggctgagggt aggaagtagc cgctccgcag tggaggcgac 60
 tgggggctga agagcgcgcc gccctctcgt ccactttcc aggtgtgtga tcctgtaaaa 120
 ttaaattcttc caag atg atc tgg tat ata tta att ata gga att ctg ctt 170
 Met Ile Trp Tyr Ile Leu Ile Ile Gly Ile Leu Leu
 -15 -10
 ccc cag tct ttg gct cat cca ggc ttt ttt act tca att ggt cag atg 218
 Pro Gln Ser Leu Ala His Pro Gly Phe Phe Thr Ser Ile Gly Gln Met
 -5 1 5 10

act gat ttg atc cat act gag aaa gat ctg gtg act tct ctg aaa gat 266
 Thr Asp Leu Ile His Thr Glu Lys Asp Leu Val Thr Ser Leu Lys Asp
 15 20 25
 tat att aag gca gaa gag gac aag tta gaa caa ata aaa aaa tgg 311
 Tyr Ile Lys Ala Glu Glu Asp Lys Leu Glu Gln Ile Lys Lys Trp
 30 35 40

<210> 220
 <211> 813
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 182..811

<221> sig_peptide
 <222> 182..277
 <223> score 8.1
 seq FLLFFWLDRSVLA/KE

<400> 220
 aaaaaaattt acatgacatt atttacatac caaacctgcc ctacgcttcc tggaaacttt 60
 actacttatg agtgtggctc ctccttcctt ttcaatccct taattaaata gcttccctc 120
 tacaggcttt tgaagtggta gcagttctc ctaactcctg ccagaaacag ctctcctcaa 180
 c atg aga gct gca ccc ctc ctc ctg gcc agg gca gca agc ctt agc ctt 229
 Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
 -30 -25 -20
 ggc ttc ttg ttt ctg ctt ttt ttc tgg cta gac cga agt gta cta gcc 277
 Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
 -15 -10 -5
 aag gag ttg aag ttt gtg act ttg gtg ttt cgg cat gga gac cga agt 325
 Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
 1 5 10 15
 ccc att gac acc ttt ccc act gac ccc ata aag gaa tcc tca tgg cca 373
 Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
 20 25 30
 caa gga ttt ggc caa ctc acc cag ctg ggc atg gag cag cat tat gaa 421
 Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
 35 40 45
 ctt gga gag tat ata aga aag aga tat aga aaa ttc ttg aat gag tcc 469
 Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
 50 55 60
 tat aaa cat gaa cag gtt tat att cga agc aca gac gtt gac cgg act 517
 Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
 65 70 75 80
 ttg atg agt gct atg aca aac ctg gca gcc ctg ttt ccc cca gaa ggt 565
 Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly
 85 90 95
 gtc agc atc tgg aat cct atc cta ctc tgg cag ccc atc ccg gtg cac 613
 Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His
 100 105 110
 aca gtt cct ctt tct gaa gat cag ttg cta tac ctg cct ttc agg aac 661

Thr	Val	Pro	Leu	Ser	Glu	Asp	Gln	Leu	Leu	Tyr	Leu	Pro	Phe	Arg	Asn	
		115					120					125				
tgc	cct	cgt	ttt	caa	gaa	ctt	gag	agt	gag	act	ttg	aaa	tca	gag	gaa	709
Cys	Pro	Arg	Phe	Gln	Glu	Leu	Glu	Ser	Glu	Thr	Leu	Lys	Ser	Glu	Glu	
		130					135					140				
ttc	cag	aag	agg	ctg	cac	cct	tat	aag	gat	ttt	ata	gct	acc	ttg	gga	757
Phe	Gln	Lys	Arg	Leu	His	Pro	Tyr	Lys	Asp	Phe	Ile	Ala	Thr	Leu	Gly	
		145				150				155					160	
aaa	ctt	tca	gga	tta	cat	ggc	cag	gac	ctt	ttt	gga	att	tgg	agt	aaa	805
Lys	Leu	Ser	Gly	Leu	His	Gly	Gln	Asp	Leu	Phe	Gly	Ile	Trp	Ser	Lys	
				165					170					175		
gtc	tac	ga														813
Val	Tyr															

<210> 221
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 182..715
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 <222> 182..277
 <223> score 8.1
 seq FLLFFWLDRSVLA/KE

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aaaaaaattt acatgacatt atttacatac caaacctgcc ctacgcttcc tggaaacttt	60
actacttatg agtgtggctc ctccctccct ttcaatccct taattaaata gcttcccctc	120
tacaggcttt tgaagtggta gcagttcctc ctaactcctg ccagaaacag ctctcctcaa	180
c atg aga gct gca ccc ctc ctc ctg gcc agg gca gca agc ctt agc ctt	229
Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu	
-30 -25 -20	
ggc ttc ttg ttt ctg ctt ttt ttc tgg cta gac cga agt gta cta gcc	277
Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala	
-15 -10 -5	
aag gag ttg aag ttt gtg act ttg ctg ggc atg gag cag cat tat gaa	325
Lys Glu Leu Lys Phe Val Thr Leu Leu Met Glu Gln His Tyr Glu	
1 5 10 15	
ctt gga gag tat ata aga aag aga tat aga aaa ttc ttg aat gag tcc	373
Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser	
20 25 30	
tat aaa cat gna cag gtt tat att cga agc aca gac gtt gac cgg act	421
Tyr Lys His Xaa Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr	
35 40 45	
ttg atg agt gct atg aca aac ctg gca gcc ctg ttt ccc cca gaa ggt	469
Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly	
50 55 60	
gtc agc atc tgg aat cct atc cta ctc tgg cag ccc atc ccg gtg cac	517
Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His	
65 70 75 80	

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aca gtt cct ctt tct gaa gat cag ttg cta tac ctg cct ttc agg aac      565
Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn
      85                      90                      95
tgc cct cgt ttt caa gaa ctt gag agt gag act ttg aaa tca gag gaa      613
Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu
      100                      105                      110
ttc cag aag agg ctg cac cct tat aag gat ttt ata gct acc ttg gga      661
Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly
      115                      120                      125
aaa ctt tca gga tta cat ggc cag gac ctt ttt gga att tgg agt aaa      709
Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys
      130                      135                      140
gtc tac ga
Val Tyr
145

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<210> 222
<211> 237
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 78..236

<221> sig_peptide
<222> 78..137
<223> score 11.3
      seq VLLLWGILGAIQA/QQ

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actcggcgcc cgcgcctcgg gccgtcggga gcggasctcc tcgggaccag gacttcaggg      60
ccacaggtgc tgccaag atg ctc cag ggc acc tgc tcc gtg ctc ctg ctc      110
      Met Leu Gln Gly Thr Cys Ser Val Leu Leu Leu
      -20                      -15                      -10
tgg gga atc ctg ggg gcc atc cag gcc cag cag cag gag gtc atc tcg      158
Trp Gly Ile Leu Gly Ala Ile Gln Ala Gln Gln Gln Glu Val Ile Ser
      -5                      1                      5
ccg gac act acc gag aga aac aac aac tgc cca gag aag acc gac tgc      206
Pro Asp Thr Thr Glu Arg Asn Asn Asn Cys Pro Glu Lys Thr Asp Cys
      10                      15                      20
ccc atc cac gtg tac ttc gtg ctg gac acc t
Pro Ile His Val Tyr Phe Val Leu Asp Thr
      25                      30

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<210> 223
<211> 485
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 167..484

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<221> sig_peptide
 <222> 167..205
 <223> score 6.4
 seq MWGDLWLLPXASA/NP

<400> 223
 tttccggtgc tcgcccagagc aggggttgggg cgagtggacc gcgcctctaa aggcgcttgc 60
 cagtgaatc tggcgatcg cttcctgggtc ctgcctcct ccgctgtctc cctggagttc 120
 ttgcaagtcg gccaggatgt ctcagaccct tgtctgagac cgagct atg tgg ggc 175
 Met Trp Gly
 gac ctc tgg ctc ctc ccg cyt gcc tct gcc aat ccg ggc act ggg aca 223
 Asp Leu Trp Leu Leu Pro Xaa Ala Ser Ala Asn Pro Gly Thr Gly Thr
 -10 -5 1 5
 gag gct gag ttt gag aaa gct gca gag gag gtt agg cac ctt dag acc 271
 Glu Ala Glu Phe Glu Lys Ala Ala Glu Glu Val Arg His Leu Xaa Thr
 10 15 20
 aag cca tcg gat gag gag atg ctg ttc atc tat ggc cac tac aaa caa 319
 Lys Pro Ser Asp Glu Glu Met Leu Phe Ile Tyr Gly His Tyr Lys Gln
 25 30 35
 gca act gtg ggc gac ata aan kca gaa cgg ccc ggr nng ttg gac ttc 367
 Ala Thr Val Gly Asp Ile Xaa Xaa Glu Arg Pro Gly Xaa Leu Asp Phe
 40 45 50
 acg ggc aag gcc aag tgg gat gcc tgg aat gag ctg aaa ggg act tcc 415
 Thr Gly Lys Ala Lys Trp Asp Ala Trp Asn Glu Leu Lys Gly Thr Ser
 55 60 65 70
 aag gaa gat gcc aat gaa agc tta cat caa caa agt aga aga gct aaa 463
 Lys Glu Asp Ala Asn Glu Ser Leu His Gln Gln Ser Arg Arg Ala Lys
 75 80 85
 gaa aaa ata cgg gat aat gag a 485
 Glu Lys Ile Arg Asp Asn Glu
 90

<210> 224
 <211> 443
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 175..441

<221> sig_peptide
 <222> 175..234
 <223> score 11.6
 seq ILGLLTAVPPASC/QQ

<400> 224
 atccgacgcc cgtcttcgtg tctcctcctt ccctcgcctt cctccttctt agctcctctc 60
 ctccagggcc agactgagcc caggttgatt tcaggcggac accaatagac tccacagcag 120
 ctccaggagc ccagacaccg gcggccagaa gcaaggctag gagctgctgc agcc atg 177
 Met

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                                -20
tcg gcc ctc agc ctc ctc att ctg ggc ctg ctc acg gca gtg cca cct      225
Ser Ala Leu Ser Leu Leu Ile Leu Gly Leu Leu Thr Ala Val Pro Pro
                                -15          -10          -5
gcc agc tgt cag caa ggc ctg ggg aac ctt cag ccc tgg atg cag ggc      273
Ala Ser Cys Gln Gln Gly Leu Gly Asn Leu Gln Pro Trp Met Gln Gly
                                1          5          10
ctt atc gcg gtg gcc gtg ttc ctg gtc ctc gtt gca atc gcc ttt gca      321
Leu Ile Ala Val Ala Val Phe Leu Val Leu Val Ala Ile Ala Phe Ala
                                15          20          25
gtc nnc cac ttc tgg tgc cag gag gag ccg gag cct gca cac atg atc      369
Val Xaa His Phe Trp Cys Gln Glu Glu Pro Glu Pro Ala His Met Ile
                                30          35          40          45
ctg acc gtc gga aac aag gca gat gga gtc ctg gtg gga aac mga tgg      417
Leu Thr Val Gly Asn Lys Ala Asp Gly Val Leu Val Gly Asn Arg Trp
                                50          55          60
aaa ggt act ctt cga tgg cgg gcc ag      443
Lys Gly Thr Leu Arg Trp Arg Ala
                                65

<210> 225
<211> 397
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..396

<221> sig_peptide
<222> 106..156
<223> score 5.7
      seq LLYYALCFSLSKA/SA

<400> 225
agaacaaaga taaggcatca cggacaccac accgggcacg agctcacagg caagtcaagc      60
tgkgaggacc aaggccgggc agccgggagc acccaaggca ggaaa atg agg tgg ctg      117
                                Met Arg Trp Leu
                                -15
ctt ctc tat tat gct ctg tgc ttc tcc ctg tca aag gct tca gcc cac      165
Leu Leu Tyr Tyr Ala Leu Cys Phe Ser Leu Ser Lys Ala Ser Ala His
                                -10          -5          1
acc gtg gag cta aac aat atg ttt ggc cag atc cag tgc cct ggt tat      213
Thr Val Glu Leu Asn Asn Met Phe Gly Gln Ile Gln Ser Pro Gly Tyr
                                5          10          15
cca gac tcc tat ccc agt gat tca gag gtg act tgg aat atc act gtc      261
Pro Asp Ser Tyr Pro Ser Asp Ser Glu Val Thr Trp Asn Ile Thr Val
                                20          25          30          35
cca gat ggg ttt cgg atc aag ctt tac ttc atg cac ttc aac ttg gaa      309
Pro Asp Gly Phe Arg Ile Lys Leu Tyr Phe Met His Phe Asn Leu Glu
                                40          45          50
tcc tcc tac ctt tgt gaa tat gac tat gtg aag gtg aga ctc ctg atg      357
Ser Ser Tyr Leu Cys Glu Tyr Asp Tyr Val Lys Val Arg Leu Leu Met

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55 60 65 397
 tcc cta act ggg cca ggc tct ctt ctg gga ttt aga caa g
 Ser Leu Thr Gly Pro Gly Ser Leu Leu Gly Phe Arg Gln
 70 75 80

<210> 226
 <211> 204
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 44..202

<221> sig_peptide
 <222> 44..106
 <223> score 8.9
 seq VLLFSGFWGLAMG/AF

<400> 226 55
 agagagaaag agagagcgcg cgccagggag aggagaawag aag atg agg att att
 Met Arg Ile Ile
 -20
 tcc aga cag att gtc ttg tta ttt tct gga ttt tgg gga ctc gcc atg 103
 Ser Arg Gln Ile Val Leu Leu Phe Ser Gly Phe Trp Gly Leu Ala Met
 -15 -10 -5
 gga gcc ttt ccg agc agc gtg caa ata ggt ggt ctc ttc atc cga aac 151
 Gly Ala Phe Pro Ser Ser Val Gln Ile Gly Gly Leu Phe Ile Arg Asn
 1 5 10 15
 aca gat cag gaa tac act gct ttt cga tta gca att ttt ctt cat aac 199
 Thr Asp Gln Glu Tyr Thr Ala Phe Arg Leu Ala Ile Phe Leu His Asn
 20 25 30
 acc ag 204
 Thr

<210> 227
 <211> 502
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 114..500

<221> sig_peptide
 <222> 114..257
 <223> score 4.7
 seq LFTLSHITQLVLS/HN

<400> 227 60
 agggcgtggt cgctgttcag tgcsggtggt gcagggagtg agggcagctg gagtgcgttc 116
 tgccgaagct tgtggttgca cgcccatcgt ctaggggct accttccgtg acc atg

															Met	
tcc	aag	tct	ctg	aag	aag	ttg	gtg	gag	gag	agc	cgg	gag	aag	aac	cag	164
Ser	Lys	Ser	Leu	Lys	Lys	Leu	Val	Glu	Glu	Ser	Arg	Glu	Lys	Asn	Gln	
-45															-35	
ccc	gag	gtg	gac	atg	agt	gac	cgg	ggc	atc	tcc	aac	atg	ctg	gat	gtc	212
Pro	Glu	Val	Asp	Met	Ser	Asp	Arg	Gly	Ile	Ser	Asn	Met	Leu	Asp	Val	
-30															-20	
aac	ggc	ctc	ttt	acc	tta	tcc	cat	atc	aca	caa	ctg	gtm	ctc	agc	cat	260
Asn	Gly	Leu	Phe	Thr	Leu	Ser	His	Ile	Thr	Gln	Leu	Val	Leu	Ser	His	
-15															-5	1
aac	aag	cta	aca	atg	gtg	cca	ccg	aac	atc	gca	gaa	ctg	aag	aat	ttg	308
Asn	Lys	Leu	Thr	Met	Val	Pro	Pro	Asn	Ile	Ala	Glu	Leu	Lys	Asn	Leu	
5															10	15
gag	gtg	ctc	aac	ttt	ttt	aat	aac	caa	atc	gag	gag	ctg	ccc	aca	nag	356
Glu	Val	Leu	Asn	Phe	Phe	Asn	Asn	Gln	Ile	Glu	Glu	Leu	Pro	Thr	Xaa	
20															25	30
atc	agt	agc	ctt	cag	aaa	ctc	aaa	cac	ctg	aac	ctt	ggc	atg	aac	agg	404
Ile	Ser	Ser	Leu	Gln	Lys	Leu	Lys	His	Leu	Asn	Leu	Gly	Met	Asn	Arg	
35															40	45
ctg	aac	act	ttg	cca	cga	ggc	ttc	ggc	tcc	ctg	cca	gct	ctt	gag	gtt	452
Leu	Asn	Thr	Leu	Pro	Arg	Gly	Phe	Gly	Ser	Leu	Pro	Ala	Leu	Glu	Val	
50															55	60
ctg	gac	ttg	acg	tac	aac	aac	ttg	agc	gaa	aat	tct	ctt	cct	gga	aac	500
Leu	Asp	Leu	Thr	Tyr	Asn	Asn	Leu	Ser	Glu	Asn	Ser	Leu	Pro	Gly	Asn	
70															75	80
tt															502	

<221> sig_peptide
 <222> 190..285
 <223> score 11
 seq LGLLLSVLAATLA/QA

<400> 230
 aactttgctc aaagtcgctg gactctaagc tgtcggaggg accgctggac agacctggga 60
 actgacagag ggcctggagg gaaacaggcc aaagaccac aggcagagtt gacacggaac 120
 cccaaagcaa ggaggagggc tcgggcccga gaccgttcac ctccccttat ccctgttccc 180
 ctcttcagg atg gag ctg acc tca agg gaa aga ggg agg gga cag cct ctg 231
 Met Glu Leu Thr Ser Arg Glu Arg Gly Arg Gly Gln Pro Leu
 -30 -25 -20
 ccc tgg gaa ctt cga ctg ggc cta ctg cta agc gtg ctg gct gcc aca 279
 Pro Trp Glu Leu Arg Leu Gly Leu Leu Leu Ser Val Leu Ala Ala Thr
 -15 -10 -5
 ctg gca cag gcc cct gcc ccg gat gtg cct ggc tgt tcc agg gga agc 327
 Leu Ala Gln Ala Pro Ala Pro Asp Val Pro Gly Cys Ser Arg Gly Ser
 1 5 10
 tgc tac ccc gcc asg ggc gac ctg ctg gtg ggc cga gct gac aga ctg 375
 Cys Tyr Pro Ala Xaa Gly Asp Leu Leu Val Gly Arg Ala Asp Arg Leu
 15 20 25 30
 act gcc tca tcc act tgt ggc ctg aat ggc ccc agc cta ctg cat cgt c 424
 Thr Ala Ser Ser Thr Cys Gly Leu Asn Gly Pro Ser Leu Leu His Arg
 35 40 45

<210> 231
 <211> 503
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 124..501

<221> sig_peptide
 <222> 124..186
 <223> score 7.7
 seq GFVVLVLLQCCSA/YK

<400> 231
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 ctggcaccag gagccgtggg caagggaaga ggccacaccc tgccctgctc tgctgcagcc 120
 aga atg ggt gtg aag gcg tct caa aca ggc ttt gtg gtc ctg gtg ctg 168
 Met Gly Val Lys Ala Ser Gln Thr Gly Phe Val Val Leu Val Leu
 -20 -15 -10
 ctc cag tgc tgc tct gca tac aaa ctg gtc tgc tac tac acc agc tgg 216
 Leu Gln Cys Cys Ser Ala Tyr Lys Leu Val Cys Tyr Tyr Thr Ser Trp
 -5 1 5 10
 tcc cag tac cgg gaa ggc gat ggg agc tgc ttc cca gat gcc ctt gac 264
 Ser Gln Tyr Arg Glu Gly Asp Gly Ser Cys Phe Pro Asp Ala Leu Asp
 15 20 25

cgc ttc ctc tgt acc cac atc atc tac agc ttt gcc aat ata agc aac	312
Arg Phe Leu Cys Thr His Ile Ile Tyr Ser Phe Ala Asn Ile Ser Asn	
30 35 40	
gat cac atc gac acc tgg gag tgg aat gat gtg acg ctc tac ggc atg	360
Asp His Ile Asp Thr Trp Glu Trp Asn Asp Val Thr Leu Tyr Gly Met	
45 50 55	
ctc aac aca ctc aag aac agg aac ccc aac ctg aag act ctc ttg tct	408
Leu Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu Ser	
60 65 70	
gtc gga gga tgg aac ttt ggg tct caa aga ttt tcc aag ata gcc tcc	456
Val Gly Gly Trp Asn Phe Gly Ser Gln Arg Phe Ser Lys Ile Ala Ser	
75 80 85 90	
aac acc cag agt cgc cgg act ttc atc aag tca gta ccg cca ttt ct	503
Asn Thr Gln Ser Arg Arg Thr Phe Ile Lys Ser Val Pro Pro Phe	
95 100 105	

<210> 232
 <211> 539
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 99..539

<221> sig_peptide
 <222> 99..158
 <223> score 9.1
 seq LLLLLLVFPATVL/FR

<400> 232	
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cttagccgac ggaaactgga cactggaccg gcagcgcc atg aga ctc ctc ccc cgc	116
Met Arg Leu Leu Pro Arg	
-20 -15	
ttg ctg ctg ctt ctc tta ctc gtg ttc cct gcc act gtc ttg ttc cga	164
Leu Leu Leu Leu Leu Leu Leu Val Phe Pro Ala Thr Val Leu Phe Arg	
-10 -5 1	
ggc ggc ccc aga ggc tyg tta gca gtg gca caa gat ctt aca gag gat	212
Gly Gly Pro Arg Gly Xaa Leu Ala Val Ala Gln Asp Leu Thr Glu Asp	
5 10 15	
gaa gaa aca gta gaa gat tcc ata att gag gat gaa gat gat gaa gcc	260
Glu Glu Thr Val Glu Asp Ser Ile Ile Glu Asp Glu Asp Asp Glu Ala	
20 25 30	
gag gta gaa gaa gat gaa ccc aca gat ttg gta gaa gat aaa gag gaa	308
Glu Val Glu Glu Asp Glu Pro Thr Asp Leu Val Glu Asp Lys Glu Glu	
35 40 45 50	
gaa gat gtg tct ggt gaa cct gaa gct tca ccg agt gca gat aca act	356
Glu Asp Val Ser Gly Glu Pro Glu Ala Ser Pro Ser Ala Asp Thr Thr	
55 60 65	
ata ctg ttt gta aaa gga gaa gat ttt cca gca aat aac att gtg aag	404
Ile Leu Phe Val Lys Gly Glu Asp Phe Pro Ala Asn Asn Ile Val Lys	
70 75 80	

ttc ctg gta ggc ttt acc aac aag ggt aca gaa gat ttt att gtt gaa	452
Phe Leu Val Gly Phe Thr Asn Lys Gly Thr Glu Asp Phe Ile Val Glu	
85 90 95	
tcc tta gat gcc tca ttc cgt tat cct cag gac tac cag ttt tat atc	500
Ser Leu Asp Ala Ser Phe Arg Tyr Pro Gln Asp Tyr Gln Phe Tyr Ile	
100 105 110	
cag aat ttc aca gct ctt cct ctg aac act gta gtg cca	539
Gln Asn Phe Thr Ala Leu Pro Leu Asn Thr Val Val Pro	
115 120 125	

<210> 233
 <211> 567
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 273..566

<221> sig_peptide
 <222> 273..314
 <223> score 3.7
 seq GLTISSLFSRLFG/KK

<400> 233	
gtcgcgcgcgg ccgcgcgcgtg acgtggcaca gccagagcct aaaggctara agccgragct	60
gccgcgccag tcgcctagca ggtcctctac cggcttattc ctgtgccgga tcttcacgcg	120
cacagggggcc actgagacgt ttctgcctcc ctctttcttc ctccgctctt tctcttcct	180
ctcgtttagt ttgcctggga gcttgaaagg agaaagcacg gggtcgcccc aaaccccttc	240
tgcttctgcc catcacaagt gccactaccg cc atg ggc ctc act atc tcc tcc	293
Met Gly Leu Thr Ile Ser Ser	
-10	
ctc ttc tcc cga cta ttt ggc aag aag cag atg cgc att ttg atg gtt	341
Leu Phe Ser Arg Leu Phe Gly Lys Lys Gln Met Arg Ile Leu Met Val	
-5 1 5	
gga ttg gat gct gct ggc aag aca acc att ctg tat aaa ctg aag tta	389
Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu Tyr Lys Leu Lys Leu	
10 15 20 25	
ggg gag ata gtc acc acc att cct acc att ggt ttt aat gtg gaa aca	437
Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly Phe Asn Val Glu Thr	
30 35 40	
gta gaa tat aag aac att tgt ttc aca gta tgg gat gtt ggt ggt caa	485
Val Glu Tyr Lys Asn Ile Cys Phe Thr Val Trp Asp Val Gly Gly Gln	
45 50 55	
gat aga att agg cct ctc tgg aag cat tac ttc cag aat acc cag ggt	533
Asp Arg Ile Arg Pro Leu Trp Lys His Tyr Phe Gln Asn Thr Gln Gly	
60 65 70	
ctt att ttt gtg gta gat agc aac gat cgt gaa a	567
Leu Ile Phe Val Val Asp Ser Asn Asp Arg Glu	
75 80	

<210> 234
 <211> 407

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..407

<221> sig_peptide
<222> 87..146
<223> score 8.4
seq AVVGCLLVPPAEA/NK

<400> 234
aggagagggc ggggacaact gggctcttttg eggctgcagc gggctttag gtgtccggct 60
ttgctggccc agcaagcctg ataagc atg aag ctc tta tct ttg gtg gct gtg 113
Met Lys Leu Leu Ser Leu Val Ala Val
-20 -15
gtc ggg tgt ttg ctg gtg ccc cca gct gaa gcc aac aag agt tct gaa 161
Val Gly Cys Leu Leu Val Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu
-10 -5 1 5
gat atc egg tgc aaa tgc atc tgt cca cct tat aga aac atc agt ggg 209
Asp Ile Arg Cys Lys Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly
10 15 20
cac att tac aac cag aat gta tcc cag aag gac tgc aac tgc ctg cac 257
His Ile Tyr Asn Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His
25 30 35
gtg gtg gag ccc atg cna gtg cct ggc cat gac gtg gag gcc tac tgc 305
Val Val Glu Pro Met Xaa Val Pro Gly His Asp Val Glu Ala Tyr Cys
40 45 50
ctg ctg tgc gag tgc agg tac gag gag cgc asa cca cca cca tca agg 353
Leu Leu Cys Glu Cys Arg Tyr Glu Glu Arg Xaa Pro Pro Pro Ser Arg
55 60 65
tca tca ttg tca tct acc tgt ccg tgg tgg gtg cct gtt gct cta cat 401
Ser Ser Leu Ser Ser Thr Cys Pro Trp Trp Val Pro Val Ala Leu His
70 75 80 85
ggc ttc 407
Gly Phe

<210> 235
<211> 442
<212> DNA
<213> Homo sapiens

<220>
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<222> 87..440

<221> sig_peptide
<222> 87..200
<223> score 6.3
seq GLSISLRLTGSSA/QE

004220"66667550

<400> 235
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gaacgcagta gacgaaggcg gcggcg atg gcg gcg ggg ata gtg gct tct cgc 113
Met Ala Ala Gly Ile Val Ala Ser Arg
-35 -30
aga ctc cgc gac cta ctg acc cgg cga ctg aca ggc tcc aac tac ccg 161
Arg Leu Arg Asp Leu Leu Thr Arg Arg Leu Thr Gly Ser Asn Tyr Pro
-25 -20 -15
gga ctc agt att agc ctt cgc ctc act ggc tcc tct gca caa gag gcg 209
Gly Leu Ser Ile Ser Leu Arg Leu Thr Gly Ser Ser Ala Gln Glu Ala
-10 -5 1
gct tcc gga gta gcc ctc ggt gaa gcc cca gac cac agc tat gag tcc 257
Ala Ser Gly Val Ala Leu Gly Glu Ala Pro Asp His Ser Tyr Glu Ser
5 10 15
ctt cgt gtg acg tct gcg cag aaa cat gtt ctg cat gtc cag ctc aac 305
Leu Arg Val Thr Ser Ala Gln Lys His Val Leu His Val Gln Leu Asn
20 25 30 35
cgg ccc aac aag agg aat gcc atg aac aag gtc ttc tgg aga gag atg 353
Arg Pro Asn Lys Arg Asn Ala Met Asn Lys Val Phe Trp Arg Glu Met
40 45 50
gta gag tgc ttc aac aag att tcg aga gac gct gac tgt cgg gcg gtg 401
Val Glu Cys Phe Asn Lys Ile Ser Arg Asp Ala Asp Cys Arg Ala Val
55 60 65
gtg atc tct ggt gca gga aaa atg ttc act gca ggt att ga 442
Val Ile Ser Gly Ala Gly Lys Met Phe Thr Ala Gly Ile
70 75 80

<210> 236
<211> 445
<212> DNA
<213> Homo sapiens

<220>
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<222> 129..443

<221> sig_peptide
<222> 129..191
<223> score 9.5
seq LGLVLCIAQTIHT/QE

<400> 236
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gtctgctgca gagttctgtc cttgcattgg tgcgcctcag gccaggctgc actgctggga 120
cctggggc atg tct ccc cac ccc acc gcc ctc ctg ggc cta gtg ctc tgc 170
Met Ser Pro His Pro Thr Ala Leu Leu Gly Leu Val Leu Cys
-20 -15 -10
ctg gcc cag acc atc cac acg cag gag gaa gat ctg ccc aga ccc tcc 218
Leu Ala Gln Thr Ile His Thr Gln Glu Glu Asp Leu Pro Arg Pro Ser
-5 1 5
atc tcg gct gag cca ggc acc gtg atc ccc ctg ggg agc cat gtg act 266
Ile Ser Ala Glu Pro Gly Thr Val Ile Pro Leu Gly Ser His Val Thr
10 15 20 25

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..422

<221> sig_peptide
<222> 90..167
<223> score 8.9
seq GLLWAFCAPGARA/EE

<400> 238
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cgtctgcttc ggagaccgta aggatattg atg acc atg aga tcc ctg ctc aga 113
Met Thr Met Arg Ser Leu Leu Arg
-25 -20
acc ccc ttc ctg tgt ggc ctg ctc tgg gcc ttt tgt gcc cca ggc gcc 161
Thr Pro Phe Leu Cys Gly Leu Leu Trp Ala Phe Cys Ala Pro Gly Ala
-15 -10 -5
agg gct gag gag cct gca gcc agc ttc tcc caa ccc ggc agc atg ggc 209
Arg Ala Glu Glu Pro Ala Ala Ser Phe Ser Gln Pro Gly Ser Met Gly
1 5 10
ctg gat aag aac aca gtg cac gac caa gag cat atc atg gag cat cta 257
Leu Asp Lys Asn Thr Val His Asp Gln Glu His Ile Met Glu His Leu
15 20 25 30
gaa ggt gtc atc aac aaa cca gag gcg gag atg tgc cca caa gaa ttg 305
Glu Gly Val Ile Asn Lys Pro Glu Ala Glu Met Ser Pro Gln Glu Leu
35 40 45
cag ctc cat tac ttc aaa atg cat gat tat gat ggc aat aat ttg ctt 353
Gln Leu His Tyr Phe Lys Met His Asp Tyr Asp Gly Asn Asn Leu Leu
50 55 60
gat ggc tta gaa ctc tcc aca gcc atc act cat gtc cat aag gag gaa 401
Asp Gly Leu Glu Leu Ser Thr Ala Ile Thr His Val His Lys Glu Glu
65 70 75
ggg ast gaa cag gca cca cta a 423
Gly Xaa Glu Gln Ala Pro Leu
80 85

<210> 239
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..450

<221> sig_peptide
<222> 67..138
<223> score 3.8
seq VVALAGVLQSGFQ/EL

<400> 239
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 gttaag atg gcg tcc tca gcg gag ggg gac gag ggg act gtg gtg gcg 108
 Met Ala Ser Ser Ala Glu Gly Asp Glu Gly Thr Val Val Ala
 -20 -15
 ctg gcg ggg gtt ctg cag tcg ggt ttc cag gag ctg agc ctt aac aag 156
 Leu Ala Gly Val Leu Gln Ser Gly Phe Gln Glu Leu Ser Leu Asn Lys
 -10 -5 1 5
 ttg gcg acg tcc ctg ggc gcg tca gaa cag gcg ctg cgg ctg atc atc 204
 Leu Ala Thr Ser Leu Gly Ala Ser Glu Gln Ala Leu Arg Leu Ile Ile
 10 15 20
 tcc atc ttc ctg ggt tac ccc ttt gct ttg ttt tat cgg cat tac ctt 252
 Ser Ile Phe Leu Gly Tyr Pro Phe Ala Leu Phe Tyr Arg His Tyr Leu
 25 30 35
 ttc tac aag gag acc tac ctc atc cac ctc ttc cat acc ttt aca ggc 300
 Phe Tyr Lys Glu Thr Tyr Leu Ile His Leu Phe His Thr Phe Thr Gly
 40 45 50
 ctc tca att gct tat ttt aac ttt gga aac cag ctc tac cac tcc ctg 348
 Leu Ser Ile Ala Tyr Phe Asn Phe Gly Asn Gln Leu Tyr His Ser Leu
 55 60 65 70
 ctg tgt att gtg ctt cag ttc ctc atc ctt cga cta atg ggc cgc acc 396
 Leu Cys Ile Val Leu Gln Phe Leu Ile Leu Arg Leu Met Gly Arg Thr
 75 80 85
 atc act gcc gtc ctc act acc ttt tgc ttc cag atg gcc tam ctt ctg 444
 Ile Thr Ala Val Leu Thr Thr Phe Cys Phe Gln Met Ala Xaa Leu Leu
 90 95 100
 gct gga 450
 Ala Gly

<210> 240
 <211> 500
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 311..499

<221> sig_peptide
 <222> 311..415
 <223> score 5.1
 seq FLLFRSLPRXXFG/LV

<400> 240
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 gggcgtggga gtgaggtacc agattcagcc catttgggccc cgaygcctct gttctcggaa 120
 tccgggtgct gcggattgag gtcccgggtc ctaacgaatc tckkgctgga ttggccgtaa 180
 ccctgtcccc gagcgggctc acagggctct aaggccacgc atgaggcaaa ggtaaagttc 240
 tgagccaccc ggtgcctcct tcccaggact gcaagatgga ggaaggcggg aactaggagg 300
 cctgattaag atg gtc cat cta ctg gtc ttg tca ggt gcc tgg ggc atg 349
 Met Val His Leu Leu Val Leu Ser Gly Ala Trp Gly Met
 -35 -30 -25

caa atg tgg gtg acc ttc gtc tca ggc ttc ctg ctt ttc cga agc ctt	397
Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu	
-20 -15 -10	
ccc cga can rnc ttc gga cta gtg can ggc aaa ctc ttc ccc ttc tas	445
Pro Arg Xaa Xaa Phe Gly Leu Val Xaa Gly Lys Leu Phe Pro Phe Xaa	
-5 1 5 10	
ttm sac atc tcc atg ggc tgt gct tca tca acc tct gca tct tgg ctt	493
Xaa Xaa Ile Ser Met Gly Cys Ala Ser Ser Thr Ser Ala Ser Trp Leu	
15 20 25	
cac agc a	500
His Ser	

<210> 241
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 194..418
 <221> sig_peptide
 <222> 194..265
 <223> score 6.6
 seq KMVHLLVLSGAWG/MQ

<400> 241	
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gggcgtggga stsagaatct ctgctggatt ggccgtaacc ctgtccccga gcgggctcac	120
agggctctgaa ggccacgcat gacgcaaagg taaagttctg agccacccgg tgcctccttc	180
ccaggactgc aag atg gag gaa ggc ggg aac cta gga ggc ctg att aag	229
Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys	
-20 -15	
atg gtc cat cta ctg gtc ttg tca ggt gcc tgg ggc atg caa atg tgg	277
Met Val His Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp	
-10 -5 1	
gtg acc ttc gtc tca ggc ttc ctg ctt ttc cga agc ctt ccc cga cat	325
Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His	
5 10 15 20	
acc ttc gga cta gtg cag agc aaa ctc ttc ccc ttc tac ttc cac atc	373
Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile	
25 30 35	
tcc atg ggc tgt gct tca tca acc tct gca tct tgg ctt cac agc a	419
Ser Met Gly Cys Ala Ser Ser Thr Ser Ala Ser Trp Leu His Ser	
40 45 50	

<210> 242
 <211> 487
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 114..485

<221> sig_peptide

<222> 114..170

<223> score 7.4

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<400> 242

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ccagaaggta gcagacagac agacggatct aacctctctt ggatcctcca gcc atg 116
Met
agg ctg ctc tgg ggg ctg atc tgg gca tcc agc ttc ttc acc tta tct 164
Arg Leu Leu Trp Gly Leu Ile Trp Ala Ser Ser Phe Phe Thr Leu Ser
-15 -10 -5
ctg cag aag ccc agg ttg ctg ttg ttc tct cct tct gtg gtt cat ctg 212
Leu Gln Lys Pro Arg Leu Leu Phe Ser Pro Ser Val Val His Leu
1 5 10
ggg gtc ccc cta tcg gtg ggg gtg cag ctc cag gat gtg ccc cga gga 260
Gly Val Pro Leu Ser Val Gly Val Gln Leu Gln Asp Val Pro Arg Gly
15 20 25 30
cag gta gtg aaa gga tca gtg ttc ctg aga aac cca tct cgt aat aat 308
Gln Val Val Lys Gly Ser Val Phe Leu Arg Asn Pro Ser Arg Asn Asn
35 40 45
gtc ccc tgc tcc cca aag gtg gac ttc acc ctt agc tca gaa aga gac 356
Val Pro Cys Ser Pro Lys Val Asp Phe Thr Leu Ser Ser Glu Arg Asp
50 55 60
ttc gca ctc ctc agt ctc cag gtg ccc ttg aaa gat gcg aag agc tgt 404
Phe Ala Leu Leu Ser Leu Gln Val Pro Leu Lys Asp Ala Lys Ser Cys
65 70 75
ggc ctc cat caa ctc ctc aga ggc cct gag gtc cag ctg gtg gcc cat 452
Gly Leu His Gln Leu Leu Arg Gly Pro Glu Val Gln Leu Val Ala His
80 85 90
tcg cca tgg cta aag gac tct ctg tcc aga acg ac 487
Ser Pro Trp Leu Lys Asp Ser Leu Ser Arg Thr
95 100 105

<210> 243

<211> 365

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 71..364

<221> sig_peptide

<222> 71..187

<223> score 4.9

seq IILVGLLHMVLLS/IP

<400> 243

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agctggcagg atg aat gtg ggg gtg gca cac agc gaa gta aac ccc aac 109
 Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn
 -35 -30
 acc cga gtg atg aat agc cga ggc atc tgg ctg gcc tac atc atc ttg 157
 Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu
 -25 -20 -15
 gta gga ttg ctg cat atg gtt cta ctc agc atc ccc ttc ttc agc att 205
 Val Gly Leu Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile
 -10 -5 1 5
 cct gtt gtc tgg acc ctg acc aac gtc atc cat aac ctg gct acg tat 253
 Pro Val Val Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr
 10 15 20
 gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt gag act cct gac caa 301
 Val Phe Leu His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln
 25 30 35
 gga aag gct cgg cta ctg aca cac tgg gag caa atg gac tat ggg ctc 349
 Gly Lys Ala Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu
 40 45 50
 cag ttt act ctt ccc g 365
 Gln Phe Thr Leu Pro
 55

<210> 244
 <211> 490
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 215..490

<221> sig_peptide
 <222> 215..274
 <223> score 3.5
 seq IVLGTGLTECILS/GI

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 gtggcggtcg gtctgcgctt gtgcgcagct ccattttcct ctctttctct tcccctttcc 120
 ttgcgcgccca agagcgccct ccagcctcgt aggggtgtca cggagcccct gcgccttttc 180
 cttgctcggg tctgcgtcc gcgcctgccc cgcc atg aat gag gag tac gac gtg 235
 Met Asn Glu Glu Tyr Asp Val
 -20 -15
 atc gtg ctg ggc acc ggc ctg acg gaa tgt atc ctg tca ggt ata atg 283
 Ile Val Leu Gly Thr Gly Leu Thr Glu Cys Ile Leu Ser Gly Ile Met
 -10 -5 1
 tca gtg aat ggc aag aaa gtt ctt cat atg gat cga aac cct tac tac 331
 Ser Val Asn Gly Lys Lys Val Leu His Met Asp Arg Asn Pro Tyr Tyr
 5 10 15
 gga gga gag agt gca tct ata aca cca ttg gaa gat tta tac aaa aga 379
 Gly Gly Glu Ser Ala Ser Ile Thr Pro Leu Glu Asp Leu Tyr Lys Arg
 20 25 30 35
 ttt aaa ata cca gga tca cca mcc gag tca atg ggg aga gga aga gam 427

Phe Lys Ile Pro Gly Ser Pro Xaa Glu Ser Met Gly Arg Gly Arg Xaa
 40 45 50
 tgg aat gtt gac ttg att ccc aag ttc ctt atg gct aat ggt cag ctg 475
 Trp Asn Val Asp Leu Ile Pro Lys Phe Leu Met Ala Asn Gly Gln Leu
 55 60 65
 gtt aag atg ctg ctt 490
 Val Lys Met Leu Leu
 70

<210> 245
 <211> 508
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 245..508

<221> sig_peptide
 <222> 245..289
 <223> score 9.6
 seq EYVLLLFLALCSA/KP

<400> 245
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 acaccaggac tgtgttgaag ggtgtttttt ttcttttaaa tgtaatacct cctcatcttt 120
 tcttcttaca cagtgtctga gaacatttac attatagata agtagtacat ggtggataac 180
 ttctactttt aggaggacta ctctcttctg acagtcctag actggtcttc tacactaaga 240
 cacc atg aag gag tat gtg ctc cta tta ttc ctg gct ttg tgc tct gcc 289
 Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala
 -15 -10 -5
 aaa ccc ttc ttt agc cct tca cac atc gca ctg aag aat atg atg ctg 337
 Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met Leu
 1 5 10 15
 aag gat atg gaa gac aca gat gat gat gat gat gat gat gat gat 385
 Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp Asp Asp
 20 25 30
 gat gat gat gag gac aac tct ctt ttt cca aca aga gag cca aga agc 433
 Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu Pro Arg Ser
 35 40 45
 cat ttt ttt cca ttt gat ctg ttt cca atg tgt cca ttt gga tgt cag 481
 His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro Phe Gly Cys Gln
 50 55 60
 tgc tat tca cga gtt gta cat tgc tca 508
 Cys Tyr Ser Arg Val Val His Cys Ser
 65 70

<210> 246
 <211> 435
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
 <222> 45..434

<221> sig_peptide
 <222> 45..113
 <223> score 11.2
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 Met Asp Gly Trp
 -20
 aga agg atg cct cgc tgg gga ctg ctg ctg ctg ctc tgg ggc tcc tgt 104
 Arg Arg Met Pro Arg Trp Gly Leu Leu Leu Leu Trp Gly Ser Cys
 -15 -10 -5
 acc ttt ggt ctc ccg aca gac acc acc ttt aaa cgg atc ttc ctc 152
 Thr Phe Gly Leu Pro Thr Asp Thr Thr Thr Phe Lys Arg Ile Phe Leu
 1 5 10
 aag aga atg ccc tca atc cga gaa agc ctg aag gaa cga ggt gtg gac 200
 Lys Arg Met Pro Ser Ile Arg Glu Ser Leu Lys Glu Arg Gly Val Asp
 15 20 25
 atg gcc agg ctt ggt ccc gag tgg agc caa ccc atg aag agg ctg acm 248
 Met Ala Arg Leu Gly Pro Glu Trp Ser Gln Pro Met Lys Arg Leu Thr
 30 35 40 45
 ctt ggc aac acc acc tcc tcc gtg atc ctc acc aac tac atg gac acc 296
 Leu Gly Asn Thr Thr Ser Ser Val Ile Leu Thr Asn Tyr Met Asp Thr
 50 55 60
 cag tac tat ggc gag att ggc atc ggc acc cca ccc cag acc ttc aaa 344
 Gln Tyr Tyr Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Thr Phe Lys
 65 70 75
 gtc gtc ttt gac act ggt tgc tcc aat gtt tgg gtg ccc tcc tcc aag 392
 Val Val Phe Asp Thr Gly Ser Ser Asn Val Trp Val Pro Ser Ser Lys
 80 85 90
 tgc agc cgt ctc tac act gcc tgt gtg tat cac aag ctc ttc g 435
 Cys Ser Arg Leu Tyr Thr Ala Cys Val Tyr His Lys Leu Phe
 95 100 105

<210> 247
 <211> 615
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 269..613
 <221> sig_peptide
 <222> 269..364
 <223> score 5
 seq LCLLSLLPSGFMS/LD

<400> 247

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gcctttggga ccaaccagg gagctcaagt tagtagcagc caaggagagg cgctgccttg 120
ccaagactaa aaagggagg gagaaagag gaaaaaagca agaatcccc acccctctcc 180
cgggcggagg gggcgggaag agcgcgtcct ggccaagccg agtagtgtct tccactcgg 240
gcgtctctct aggagccgcg cggaagg atg ctg gtc cgc agg ggc gcg cgc 292
                                Met Leu Val Arg Arg Gly Ala Arg
                                -30                                -25
gca ggg ccc agg atg ccg cgg ggc tgg acc gcg ctt tgc ttg ctg agt 340
Ala Gly Pro Arg Met Pro Arg Gly Trp Thr Ala Leu Cys Leu Leu Ser
                                -20                                -15                                -10
ttg ctg cct tct ggg ttc atg agt ctt gac aac aac ggt act gct acc 388
Leu Leu Pro Ser Gly Phe Met Ser Leu Asp Asn Asn Gly Thr Ala Thr
                                -5                                1                                5
cca gag tta cct acc cag gga aca ttt tca aat gtt tct aca aat gta 436
Pro Glu Leu Pro Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val
                                10                                15                                20
tcc tac caa gaa act aca aca cct rgt acc ctt gga agt acc agc ctg 484
Ser Tyr Gln Glu Thr Thr Pro Xaa Thr Leu Gly Ser Thr Ser Leu
                                25                                30                                35                                40
cac cct gtg tct caa cat ggc aat gag gcc aca aca aac atc aca gaa 532
His Pro Val Ser Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu
                                45                                50                                55
acg aca gts sng ttc aca tct asc tct gtg ata asc tca gtt tat ggr 580
Thr Thr Val Xaa Phe Thr Ser Xaa Ser Val Ile Xaa Ser Val Tyr Gly
                                60                                65                                70
aac aca aac tct tct gtc cag tca cag acc tct gt 615
Asn Thr Asn Ser Ser Val Gln Ser Gln Thr Ser
                                75                                80

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<210> 248
 <211> 555
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 316..555

<221> sig_peptide
 <222> 316..420
 <223> score 3.6
 seq LEPLSSSAACNG/KE

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gaggccgggg taactggcag caggtaggaa actatgtgaa agaattcct gatgtcataa 180
tttccgggtg taccggaac atttgatcat cattccttg gcaattccag cttctgtgg 240
aaaggccagt agaaagcatt gatttattca cctctacagg aatcagactc agcctctttt 300
ggttttcagt gaagt atg cct ttt caa ttt gga acc cag cca agg agg ttt 351
                                Met Pro Phe Gln Phe Gly Thr Gln Pro Arg Arg Phe
                                -35                                -30                                -25
cca gtg gaa gga gga gat tct tca att gag ctg gaa cct ggg ctg agc 399

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Pro Val Glu Gly Gly Asp Ser Ser Ile Glu Leu Glu Pro Gly Leu Ser	
-20 -15 -10	
tcc agt gct gcc tgt aat ggg aag gag atg tca cca acc agg caa ctc	447
Ser Ser Ala Ala Cys Asn Gly Lys Glu Met Ser Pro Thr Arg Gln Leu	
-5 1 5	
cgg agg tgc cct gga agt cat tgc ctg aca ata act gat gtt ccc gtc	495
Arg Arg Cys Pro Gly Ser His Cys Leu Thr Ile Thr Asp Val Pro Val	
10 15 20 25	
act gtt tat gca aca acg aga aag cca cct gca caa agc agc aag gaa	543
Thr Val Tyr Ala Thr Thr Arg Lys Pro Pro Ala Gln Ser Ser Lys Glu	
30 35 40	
atg cat cct aaa	555
Met His Pro Lys	
45	

<210> 249
 <211> 430
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 188..430

<221> sig_peptide
 <222> 188..265
 <223> score 8.8
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<400> 249	
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cagcgcastt tggcggcgcc agcagcggag ccaacgcacc cgagtttggtg tttgaggcca	120
ccctgaggat cgggacagct gttccttttg gctgcagaaa ctccgctgag cagaacttgc	180
cgccaga atg ctc ctc ctg ttg ctg agt atc atc gtc ctc cac gtc gcg	229
Met Leu Leu Leu Leu Leu Ser Ile Ile Val Leu His Val Ala	
-25 -20 -15	
gtg ctg gtg ctg ctg ttc gtc tcc acg atc gtc agc caa tgg atc gtg	277
Val Leu Val Leu Leu Phe Val Ser Thr Ile Val Ser Gln Trp Ile Val	
-10 -5 1	
ggc aat gga cac gca act gat ctc tgg cag aac tgt agc acc tct tcc	325
Gly Asn Gly His Ala Thr Asp Leu Trp Gln Asn Cys Ser Thr Ser Ser	
5 10 15 20	
tca ggn aaa tgt cca cca ctg ttc ttc atc atc acc aaa cga atg gct	373
Ser Gly Lys Cys Pro Pro Leu Phe Phe Ile Ile Thr Lys Arg Met Ala	
25 30 35	
gca gtc tgt cca ggc cac cat gat cct gtc gat cat ctt cag cat tct	421
Ala Val Cys Pro Gly His His Asp Pro Val Asp His Leu Gln His Ser	
40 45 50	
gtc tct gta	430
Val Ser Val	
55	

<210> 250

<211> 240
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 88..240

<221> sig_peptide
 <222> 88..165
 <223> score 8.8
 seq AVLVLFLVSTIVS/QW

<400> 250
 ctccgctgct cggcccagtg cggtcggcct cagccccagc gctctcctcg caggcagaaa 60
 ctccgctgag cagaacttgc cgccaga atg ctc ctc ctg ttg ctg agt atc atc 114
 Met Leu Leu Leu Leu Leu Ser Ile Ile
 -25 -20
 gtc ctc cac gtc gcg gtg ctg gtg ctg ctg ttc gtc tcc acg atc gtc 162
 Val Leu His Val Ala Val Leu Val Leu Leu Phe Val Ser Thr Ile Val
 -15 -10 -5
 agc caa tgg atc gtg ggc aat gga cac gca act gat ctc tgg cag aac 210
 Ser Gln Trp Ile Val Gly Asn Gly His Ala Thr Asp Leu Trp Gln Asn
 1 5 10 15
 tgt agc acc tct tcc tca gga aat gcc cac 240
 Cys Ser Thr Ser Ser Ser Gly Asn Ala His
 20 25

<210> 251
 <211> 346
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 147..344

<221> sig_peptide
 <222> 147..194
 <223> score 10.5
 seq LWRLVSLLALSQA/LP

<400> 251
 actctctcca caaactgccc aggagtgagt agctgctttc ggtccgcccgg acacaccgga 60
 cagatagacg tgcggacggc ccaccacccc agcccnccaa ctagtacgcc tgcgcttggc 120
 gcctcccctc tccaggtcca tccgcc atg tgg ccc ctg tgg cgc ctc gtg tct 173
 Met Trp Pro Leu Trp Arg Leu Val Ser
 -15 -10
 ctg ctg gcc ctg agc cag gcc ctg ccc ttt gag cag aga ggc ttc tgg 221
 Leu Leu Ala Leu Ser Gln Ala Leu Pro Phe Glu Gln Arg Gly Phe Trp
 -5 1 5
 gac ttc acc ctg gac gat ggg cca ttc atg atg aac gat gag gaa gct 269

Asp	Phe	Thr	Leu	Asp	Asp	Gly	Pro	Phe	Met	Met	Asn	Asp	Glu	Glu	Ala		
10					15					20					25		
tcg	ggc	gct	gac	acc	tca	ggc	gtc	ntg	gac	ccg	gac	tct	gtc	aca	ccc		317
Ser	Gly	Ala	Asp	Thr	Ser	Gly	Val	Xaa	Asp	Pro	Asp	Ser	Val	Thr	Pro		
			30					35					40				346
acc	cat	ggt	act	ata	aac	tac	ctg	tat	tt								
Thr	His	Val	Thr	Ile	Asn	Tyr	Leu	Tyr									
			45					50									

<210> 252
 <211> 468
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..467

<221> sig_peptide
 <222> 30..89
 <223> score 6.6
 seq SALAARLLQPAHS/CS

<400> 252																	
ccctcccggc	gcagtcaccg	gcgcgggtct	atg	gct	gcg	act	tct	cta	atg	tct							53
			Met	Ala	Ala	Thr	Ser	Leu	Met	Ser							
			-20					-15									
gct	ttg	gct	gcc	cgg	ctg	ctg	cag	ccc	gcg	cac	agc	tgc	tcc	ctt	cgc		101
Ala	Leu	Ala	Ala	Arg	Leu	Leu	Gln	Pro	Ala	His	Ser	Cys	Ser	Leu	Arg		
	-10				-5							1					
ctt	cgc	cct	ttc	cac	ctc	gcg	gca	gnt	cga	aat	gaa	gct	ggt	gtc	att		149
Leu	Arg	Pro	Phe	His	Leu	Ala	Ala	Xaa	Arg	Asn	Glu	Ala	Val	Val	Ile		
5				10				15							20		
tct	gga	agg	aaa	ctg	gcc	cag	cag	atc	aag	cag	gaa	gtg	cgg	cag	gag		197
Ser	Gly	Arg	Lys	Leu	Ala	Gln	Gln	Ile	Lys	Gln	Glu	Val	Arg	Gln	Glu		
			25			30							35				
gta	gaa	gag	tgg	gtg	gcc	tca	ggc	aac	aaa	cgg	cca	cac	ctg	agt	gga		245
Val	Glu	Glu	Trp	Val	Ala	Ser	Gly	Asn	Lys	Arg	Pro	His	Leu	Ser	Gly		
	40				45							50					
tcc	tgg	ttg	gcg	aga	atc	ctg	caa	gtc	act	cct	atg	tcc	tca	aca	aaa		293
Ser	Trp	Leu	Ala	Arg	Ile	Leu	Gln	Val	Thr	Pro	Met	Ser	Ser	Thr	Lys		
	55				60							65					
ccc	agg	gcg	gct	gca	ggt	gtg	gga	atc	aac	agt	gag	aca	att	atg	aaa		341
Pro	Arg	Ala	Ala	Ala	Val	Val	Gly	Ile	Asn	Ser	Glu	Thr	Ile	Met	Lys		
	70				75						80						
cca	gct	tca	att	tca	gag	gaa	gaa	ttg	ttg	aat	tta	atc	aat	aaa	ctg		389
Pro	Ala	Ser	Ile	Ser	Glu	Glu	Glu	Leu	Leu	Asn	Leu	Ile	Asn	Lys	Leu		
	85				90					95					100		
aat	aat	gat	gat	aat	gta	gat	ggc	ctc	ctt	ggt	cag	ttg	cct	ctt	cca		437
Asn	Asn	Asp	Asp	Asn	Val	Asp	Gly	Leu	Leu	Val	Gln	Leu	Pro	Leu	Pro		
				105				110						115			
gag	cat	att	gat	gag	aga	agg	atc	tgc	aat	g							468
Glu	His	Ile	Asp	Glu	Arg	Arg	Ile	Cys	Asn								

120

125

<210> 253
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 134..349

<221> sig_peptide
 <222> 134..193
 <223> score 10.6
 seq LLLLLPLVHVSAT/TP

<400> 253
 ataaactgtc agaggcagcc gaagagttca caagtgtgaa gcctggaagc cggcgggtgc 60
 cgctgtgtag gaaagaagct aaagcacttc cagagcctgt ccggagctca gaggttcgga 120
 agacttatcg acc atg gag cgc gcg tcc tgc ttg ttg ctg ctg ctg ctg 169
 Met Glu Arg Ala Ser Cys Leu Leu Leu Leu Leu Leu
 -20 -15 -10
 ccg ctg gtg cac gtc tct gcg acc acg cca gaa cct tgt gag ctg gac 217
 Pro Leu Val His Val Ser Ala Thr Thr Pro Glu Pro Cys Glu Leu Asp
 -5 1 5
 gat gaa gat ttc cgc tgc gtc tgc aac ttc tcc gaa cct cag ccc gac 265
 Asp Glu Asp Phe Arg Cys Val Cys Asn Phe Ser Glu Pro Gln Pro Asp
 10 15 20
 tgg tcc gaa gcc ttc cag tgt gtg tct gca gta gag gtg gag atc cat 313
 Trp Ser Glu Ala Phe Gln Cys Val Ser Ala Val Glu Val Glu Ile His
 25 30 35 40
 gcc ggc ggt ctc aac cta gag ccg ttt cta aag cgc 349
 Ala Gly Gly Leu Asn Leu Glu Pro Phe Leu Lys Arg
 45 50

<210> 254
 <211> 364
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 53..364

<221> sig_peptide
 <222> 53..97
 <223> score 12.6
 seq WLLLLGLVALSEC/IM

<400> 254
 gcaccttcct cccatcttgc cttctccctc gagttgggac ccggaagaa cc atg aag 58
 Met Lys

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                                -15
tgg ctg ctg ctg ctg ggt ctg gtg gcg ctc tct gag tgc atc atg tac      106
Trp Leu Leu Leu Leu Gly Leu Val Ala Leu Ser Glu Cys Ile Met Tyr
                                -10          -5          1
aag gtc ccc ctc atc aga aag aag tcc ttg agg cgc acc ctg tcc gag      154
Lys Val Pro Leu Ile Arg Lys Lys Ser Leu Arg Arg Thr Leu Ser Glu
                                5          10          15
cgt ggc ctg ctg aag gac ttc ctg aag aag cac aac ctc aac cca gcc      202
Arg Gly Leu Leu Lys Asp Phe Leu Lys Lys His Asn Leu Asn Pro Ala
20          25          30          35
aga aag tac ttc ccc cag tgg gag gct ccc acc ctg gta gat gaa cag      250
Arg Lys Tyr Phe Pro Gln Trp Glu Ala Pro Thr Leu Val Asp Glu Gln
                                40          45          50
ccc ctg gag aac tac ctg gat atg gag tac ttc ggc act atc ggc atc      298
Pro Leu Glu Asn Tyr Leu Asp Met Glu Tyr Phe Gly Thr Ile Gly Ile
                                55          60          65
gga act cct gcc cag gat ttc acc gtc gtc ttt nac acc ggc tcm tcc      346
Gly Thr Pro Ala Gln Asp Phe Thr Val Val Phe Xaa Thr Gly Ser Ser
70          75          80
aac ctg tgg gtg ccc tca      364
Asn Leu Trp Val Pro Ser
85

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<210> 255
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 180..470

<221> sig_peptide
 <222> 180..236
 <223> score 5.9
 seq ALMYLGSLAFLGA/DT

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<400> 255
aactcagtgg tttcttggtg acactggata gaacagctca agccttgcca cttcgggctt      60
ctcactgcag ctgggcttgg acttcggagt tttgccattg ccagtgggac gtctgagact      120
ttctccttca agtacttggc agatcactct cttagcaggg tctgcgcttc gcagccggg      179
atg aag ctg gtt tcc gtc gcc ctg atg tac ctg ggt tcg ctc gcc ttc      227
Met Lys Leu Val Ser Val Ala Leu Met Tyr Leu Gly Ser Leu Ala Phe
                                -15          -10          -5
cta ggc gct gac acc gct cgg ttg gat gtc gcg tcg gag ttt cga aag      275
Leu Gly Ala Asp Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys
                                1          5          10
aag tgg aat aag tgg gct ctg agt cgt ggg aag agg gaa ctg cgg atg      323
Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met
15          20          25
tcc agc agc tac ccc acc ggg ctc gct gac gtg aag gcc ggg cct gcc      371
Ser Ser Ser Tyr Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala
30          35          40          45

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cag acc ctt att cgg ccc cag gac atg aag ggt gcc tct cga agc ccc 419
 Gln Thr Leu Ile Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro
 50 55 60
 gaa gac agc agt ccg gat gcc gcc cgc atc cga gtc aag cgc tac cgg 467
 Glu Asp Ser Ser Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg
 65 70 75
 ggr a 471
 Gly

<210> 256
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 67..315

<221> sig_peptide
 <222> 67..138
 <223> score 10.5
 seq LVLVSM LALGT LA/EA

<400> 256
 aaaatccggg gctcggggcgg cctctcatcc ctgactcggg gtcgcctttg gagcagagag 60
 gaggca atg gcc acc atg gag aac aag gtg atc tgc gcc ctg gtc ctg 108
 Met Ala Thr Met Glu Asn Lys Val Ile Cys Ala Leu Val Leu
 -20 -15
 gtg tcc atg ctg gcc ctc ggc acc ctg gcc gag gcc cag aca gag acg 156
 Val Ser Met Leu Ala Leu Gly Thr Leu Ala Glu Ala Gln Thr Glu Thr
 -10 -5 1 5
 tgt aca gtg gcc ccc cgt gaa aga cag aat tgt ggt ttt cct ggt gtc 204
 Cys Thr Val Ala Pro Arg Glu Arg Gln Asn Cys Gly Phe Pro Gly Val
 10 15 20
 acg ccc tcc cag tgt gca aat aag ggc tgc tgt ttc gac gac acc gtt 252
 Thr Pro Ser Gln Cys Ala Asn Lys Gly Cys Cys Phe Asp Asp Thr Val
 25 30 35
 cgt ggg gtc ccc tgg tgc ttc tat cct aat acc atc gac gtc cct cca 300
 Arg Gly Val Pro Trp Cys Phe Tyr Pro Asn Thr Ile Asp Val Pro Pro
 40 45 50
 gaa gag gag tgt gaa 315
 Glu Glu Glu Cys Glu
 55

<210> 257
 <211> 486
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 173..484

004220"656E7560

<221> sig_peptide
 <222> 173..256
 <223> score 5.3
 seq ASCLVLAARHASA/SS

<400> 257
 gaggaccccg ggctgggagc gcgcgcccgt tcgtctactc tttccttcag ccgcctcctt 60
 tcaaccttgt caaccgctcg gcgcggcctc tgggtgcagcg gcggcggtc ctgttctgc 120
 cgcagctctc tccctttctt acctcccccac cagatcccgg agatcgcccg cc atg gct 178
 Met Ala
 tta ctt act gcg gcc gcc cgg ctc ttg gga acc aag aat gca tct tgt 226
 Leu Leu Thr Ala Ala Ala Arg Leu Leu Gly Thr Lys Asn Ala Ser Cys
 -25 -20 -15
 ctt gtt ctt gca gcc cgg cat gcc agt gct tcc tcc acg aat ttg aaa 274
 Leu Val Leu Ala Ala Arg His Ala Ser Ala Ser Ser Thr Asn Leu Lys
 -10 -5 1 5
 gac ata ttg gct gac ctg ata cct aag gag cag gcc aga att aag act 322
 Asp Ile Leu Ala Asp Leu Ile Pro Lys Glu Gln Ala Arg Ile Lys Thr
 10 15 20
 ttc agg cag caa cat ggc aag acg gtg gtg ggc caa atc act gtg gac 370
 Phe Arg Gln Gln His Gly Lys Thr Val Val Gly Gln Ile Thr Val Asp
 25 30 35
 atg atg tat ggt ggc atg aga ggc atg aag gga ttg gtc tat gaa aca 418
 Met Met Tyr Gly Gly Met Arg Gly Met Lys Gly Leu Val Tyr Glu Thr
 40 45 50
 tca gtt ctt gat cct gat gag ggc atc cgt ttc cga ggc ttt agt atc 466
 Ser Val Leu Asp Pro Asp Glu Gly Ile Arg Phe Arg Gly Phe Ser Ile
 55 60 65 70
 cct gaa tgc cag aaa ctg ct 486
 Pro Glu Cys Gln Lys Leu
 75

<210> 258
 <211> 278
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..277

<221> sig_peptide
 <222> 83..133
 <223> score 11.5
 seq LLPILLLSGWAFQ/SQ

<400> 258
 acttctcttt tccctagact gcagccagcg gasccgcagc cggccccgagc caggaaccca 60
 ggtccggagc ctcaacttca gg atg ttg aca aca ttg ctg ccg ata ctg ctg 112
 Met Leu Thr Thr Leu Leu Pro Ile Leu Leu
 -15 -10
 ctg tct ggc tgg gcc ttt tgt agc caa gac gcc tca gat ggc ctc caa 160

Leu Ser Gly Trp Ala Phe Cys Ser Gln Asp Ala Ser Asp Gly Leu Gln
 -5 1 5
 aga ctt cat atg ctc cag atc tcc tac ttc cgc gac ccc tat cac gtg 208
 Arg Leu His Met Leu Gln Ile Ser Tyr Phe Arg Asp Pro Tyr His Val
 10 15 20 25
 tgg tac cag ggc aac gcg tcg ctg ggg gga cac cta acg cac gtg ctg 256
 Trp Tyr Gln Gly Asn Ala Ser Leu Gly Gly His Leu Thr His Val Leu
 30 35 40
 gaa ggc cca gac acc aac acc a 278
 Glu Gly Pro Asp Thr Asn Thr
 45

<210> 259
 <211> 338
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 133..336
 <221> sig_peptide
 <222> 133..213
 <223> score 5.7
 seq LVSLFCSCFLADP/LN

<400> 259
 accactaatt gagggagtga ggaagagagc agctcgcttc taactggact gcacgttggt 60
 gacagcgtcc caagctgggtg acagaccac tctgtaactt tcagctagat tcagccacca 120
 gatccagaa ac atg acc ctt gct gcc tac aaa gag aag atg aag gag ctc 171
 Met Thr Leu Ala Ala Tyr Lys Glu Lys Met Lys Glu Leu
 -25 -20 -15
 ccg ctg gtg tcc ttg ttc tgc tcc tgc ttc ctg gcc gat ccc ctg aat 219
 Pro Leu Val Ser Leu Phe Cys Ser Cys Phe Leu Ala Asp Pro Leu Asn
 -10 -5 1
 aag tcg tcc tac aaa tat gaa ggc tgg tgt ggg aga cag tgt agg agg 267
 Lys Ser Ser Tyr Lys Tyr Glu Gly Trp Cys Gly Arg Gln Cys Arg Arg
 5 10 15
 aag gat gaa agc cag cgg aaa gac agt gct gac tgg aga gaa nga aga 315
 Lys Asp Glu Ser Gln Arg Lys Asp Ser Ala Asp Trp Arg Glu Xaa Arg
 20 25 30
 gct cag gca gac acg gtg gac ct 338
 Ala Gln Ala Asp Thr Val Asp
 35 40

<210> 260
 <211> 499
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 112..498

<221> sig_peptide
 <222> 112..180
 <223> score 10.6
 seq CMLLLAFSSWSLC/SD

<400> 260
 atatagttca ctcactttca aagccagctg aaggaaagag gaagtgctag agagagcccc 60
 cttcagtgtg cttctgactt ttacggactt ggcttgtag aaggctgaaa g atg atg 117
 Met Met
 gca gga atg aaa atc cag ctt gta tgc atg cta ctc ctg gct ttc agc 165
 Ala Gly Met Lys Ile Gln Leu Val Cys Met Leu Leu Leu Ala Phe Ser
 -20 -15 -10
 tcc tgg agt ctg tgc tca gat tca gaa gag gaa atg aaa gca tta gaa 213
 Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala Leu Glu
 -5 1 5 10
 gca gat ttc ttg acc aat atg cat aca tca aag att agt aaa gca cat 261
 Ala Asp Phe Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys Ala His
 15 20 25
 gtt ccc tct tgg aag atg act ctg cta aat gtt tgc agt ctt gta aat 309
 Val Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu Val Asn
 30 35 40
 aat ttg aac agc cca gct gag gaa aca gga gaa gtt cat gaa gag gag 357
 Asn Leu Asn Ser Pro Ala Glu Glu Thr Gly Glu Val His Glu Glu Glu
 45 50 55
 ctt gtt gca aga agg aaa ctt cct act gct tta gat ggc ttt agc ttg 405
 Leu Val Ala Arg Arg Lys Leu Pro Thr Ala Leu Asp Gly Phe Ser Leu
 60 65 70 75
 gaa gca atg ttg aca ata tac cag ctc cac aaa ann tgt cac agc agg 453
 Glu Ala Met Leu Thr Ile Tyr Gln Leu His Lys Xaa Cys His Ser Arg
 80 85 90
 gct ttt caa cac tgg gag tta atc cag gaa gat att ctt gat act g 499
 Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp Thr
 95 100 105

<210> 261
 <211> 455
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..455

<221> sig_peptide
 <222> 63..155
 <223> score 11.5
 seq LLLFLLGPRLVLA/IS

<400> 261
 acgtgggtcc ccccggttcc ggcgcggttg aggccttcgg tggatgaacga gtctccagca 60
 cc atg tct ggt ttg tct ggc cca cca gcc cgg cgc ggc cct ttt ccg 107

Met Ser Gly Leu Ser Gly Pro Pro Ala Arg Arg Gly Pro Phe Pro
 -30 -25 -20
 tta gcg ttg ctg ctt ttg ttc ctg ctc ggc ccc aga ttg gtc ctt gcc 155
 Leu Ala Leu Leu Leu Leu Phe Leu Leu Gly Pro Arg Leu Val Leu Ala
 -15 -10 -5
 atc tcc ttc cat ctg ccc att aac tct cgc aag tgc ctc cgt gag gag 203
 Ile Ser Phe His Leu Pro Ile Asn Ser Arg Lys Cys Leu Arg Glu Glu
 1 5 10 15
 att cac aag gac ctg cta gtg act ggc gcg tac gag atc tcc gac cag 251
 Ile His Lys Asp Leu Leu Val Thr Gly Ala Tyr Glu Ile Ser Asp Gln
 20 25 30
 tct ggg ggc gct ggc ggc ctg cgc asc acc tca aga tca cag att ctg 299
 Ser Gly Gly Ala Gly Gly Leu Arg Xaa Thr Ser Arg Ser Gln Ile Leu
 35 40 45
 ctg gcc ata ttc tct act cca aag agg atg caa cca agg gga aat ttg 347
 Leu Ala Ile Phe Ser Thr Pro Lys Arg Met Gln Pro Arg Gly Asn Leu
 50 55 60
 cct tta cca ctg aag att atg aca tgt ttg aag tgt gtt ttg aga gca 395
 Pro Leu Pro Leu Lys Ile Met Thr Cys Leu Lys Cys Val Leu Arg Ala
 65 70 75 80
 agg gaa cag gga aca ggg cgg ata cct gac caa ctc gtg atc cta gac 443
 Arg Glu Gln Gly Thr Gly Arg Ile Pro Asp Gln Leu Val Ile Leu Asp
 85 90 95
 atg aag cat gga 455
 Met Lys His Gly
 100

 <210> 262
 <211> 352
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 32..352

 <221> sig_peptide
 <222> 32..70
 <223> score 3.5
 seq MAATLLAARGAGP/AP

 <400> 262
 agttgctttg aggcagtacc ggaggagaaa g atg gcg gct acc tta cta gct 52
 Met Ala Ala Thr Leu Leu Ala
 -10
 gct cgg gga gcc ggg cca gca ccg gct tgg ggg ccg gag ggt tca ctc 100
 Ala Arg Gly Ala Gly Pro Ala Pro Ala Trp Gly Pro Glu Gly Ser Leu
 -5 1 5 10
 cag act ggg aaa gcc gag aag ttt cca ctg ggr ycc tac atc gcc aat 148
 Gln Thr Gly Lys Ala Glu Lys Phe Pro Leu Gly Xaa Tyr Ile Ala Asn
 15 20 25
 cga gtg act gac aag ctg aca cct att cac gac cgc att ttc tgc tgt 196
 Arg Val Thr Asp Lys Leu Thr Pro Ile His Asp Arg Ile Phe Cys Cys

<211> 432
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 105..431

<221> sig_peptide
 <222> 105..161
 <223> score 8.1
 seq LLGVLVVSPDALG/ST

<400> 264
 agtcttgccc cagcctcggg aggtggtgga gtgacctggc cccagtgcctg cgtccttatc 60
 agccgagccg gtcccagctc ttgctcctgc ctgtttgcct ggaa atg gcc acg ctt 116
 Met Ala Thr Leu
 ctc ctt ctc ctt ggg gtg ctg gtg gta agc cca gac gct ctg ggg agc 164
 Leu Leu Leu Leu Gly Val Leu Val Val Ser Pro Asp Ala Leu Gly Ser
 -15 -10 -5 1
 aca aca gca gtg cag aca ccc acc tcc gga gag cct ttg gtc tct act 212
 Thr Thr Ala Val Gln Thr Pro Thr Ser Gly Glu Pro Leu Val Ser Thr
 5 10 15
 agc gag ccc ctg agc tca aag atg tac acc act tca ata aca agt gac 260
 Ser Glu Pro Leu Ser Ser Lys Met Tyr Thr Thr Ser Ile Thr Ser Asp
 20 25 30
 cct aag gcc gac agc act ggg gac cag acc tca gcc cta cct ccc tca 308
 Pro Lys Ala Asp Ser Thr Gly Asp Gln Thr Ser Ala Leu Pro Pro Ser
 35 40 45
 act tcc atc aat gag gga tcc cct ctt tgg act tcc att ggt gcc agc 356
 Thr Ser Ile Asn Glu Gly Ser Pro Leu Trp Thr Ser Ile Gly Ala Ser
 50 55 60 65
 act ggt tcc cct tta cct gag cca aca acc tac cag gaa gtt tcc atc 404
 Thr Gly Ser Pro Leu Pro Glu Pro Thr Thr Tyr Gln Glu Val Ser Ile
 70 75 80
 aag atg tca tsa gtg ccc cag gaa acc c 432
 Lys Met Ser Xaa Val Pro Gln Glu Thr
 85 90

<210> 265
 <211> 284
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 108..284

<221> sig_peptide
 <222> 108..170
 <223> score 11.2
 seq LLCLFSLLTQVTT/EP

<220>
 <221> CDS
 <222> 8..472

<221> sig_peptide
 <222> 8..115
 <223> score 10.1
 seq SFVVLALFAVTQA/EE

<400> 267
 ctttcgg atg ctg acg ctc tct tcc tgt ctt tgt ggc tcc gga aag gcg 49
 Met Leu Thr Leu Ser Ser Cys Leu Cys Gly Ser Gly Lys Ala
 -25
 -30
 -35
 ttt ggg atg cca acg atg agg ctg ctg tca ttt gtg gtg ttg gct cta 97
 Phe Gly Met Pro Thr Met Arg Leu Leu Ser Phe Val Val Leu Ala Leu
 -10
 -15
 -20
 ttt gct gtc act caa gca gag gaa gga gcc agg ctt ttg gct tcc aaa 145
 Phe Ala Val Thr Gln Ala Glu Glu Gly Ala Arg Leu Leu Ala Ser Lys
 10
 -5
 1
 5
 tca ctg ctg aac aga tac gcc gtg gag gga cga gac ctg acc ttg cag 193
 Ser Leu Leu Asn Arg Tyr Ala Val Glu Gly Arg Asp Leu Thr Leu Gln
 25
 15
 20
 tac aac atc tac aat gtt ggc tca agt gct gca tta gac gtg gaa cta 241
 Tyr Asn Ile Tyr Asn Val Gly Ser Ser Ala Ala Leu Asp Val Glu Leu
 40
 30
 35
 tct gat gat tcc ttc cct cca gaa gac ttt ggc att gtg tct gga atg 289
 Ser Asp Asp Ser Phe Pro Pro Glu Asp Phe Gly Ile Val Ser Gly Met
 55
 45
 50
 ctc aat gtc aaa tgg gac cgg att gcc cct gct agc aat gtc tcc cac 337
 Leu Asn Val Lys Trp Asp Arg Ile Ala Pro Ala Ser Asn Val Ser His
 70
 65
 60
 act gtg gtc ctg cgc cct ctc aag gct ggt tat ttc aac ttc acc tcg 385
 Thr Val Val Leu Arg Pro Leu Lys Ala Gly Tyr Phe Asn Phe Thr Ser
 90
 80
 85
 75
 gca aca att act tac ctg gcc cag gag gat ggg ccc gtt gtg att ggc 433
 Ala Thr Ile Thr Tyr Leu Ala Gln Glu Asp Gly Pro Val Val Ile Gly
 105
 95
 100
 tct acc agt gca ctg gac agg gag gaa tcc tgg ctc agc g 473
 Ser Thr Ser Ala Leu Asp Arg Glu Glu Ser Trp Leu Ser
 110
 115

<210> 268
 <211> 453
 <212> DNA
 <213> Homo sapiens

<220>
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<221> sig_peptide
 <222> 8..115
 <223> score 10.1

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Met Leu Thr Leu Ser Ser Cys Leu Cys Gly Ser Gly Lys Ala
-35 -30 -25
ttt ggg atg cca acg atg agg ctg ctg tca ttt gtg gtg ttg gct cta 97
Phe Gly Met Pro Thr Met Arg Leu Leu Ser Phe Val Val Leu Ala Leu
-20 -15 -10
ttt gct gtc act caa gca gag gaa gga gcc agg ctt ttg gct tcc aaa 145
Phe Ala Val Thr Gln Ala Glu Glu Gly Ala Arg Leu Leu Ala Ser Lys
-5 1 5 10
tca ctg ctg aac aga tac gcc gtg gag gga cga gac ctg acc ttg cag 193
Ser Leu Leu Asn Arg Tyr Ala Val Glu Gly Arg Asp Leu Thr Leu Gln
15 20 25
tac aac atc tac aat gtt ggc tca agt gct gca tta gac gtg gaa cta 241
Tyr Asn Ile Tyr Asn Val Gly Ser Ser Ala Ala Leu Asp Val Glu Leu
30 35 40
tct gat gat tcc ttc cct cca gaa gac ttt ggc att gtg tct gga atg 289
Ser Asp Asp Ser Phe Pro Pro Glu Asp Phe Gly Ile Val Ser Gly Met
45 50 55
ctc aat gtc aaa tgg gac cgg att gcc cct gct agc aat gtc tcc cac 337
Leu Asn Val Lys Trp Asp Arg Ile Ala Pro Ala Ser Asn Val Ser His
60 65 70
act gtg gtc ctg cgc cct ctc aag gcc ctg gga atc cca ctg cac ttg 385
Thr Val Val Leu Arg Pro Leu Lys Ala Leu Gly Ile Pro Leu His Leu
75 80 85 90
gcc tac aat tcc agc ctg gtc acc ttc caa gag ccc ccg ggg gtc aac 433
Ala Tyr Asn Ser Ser Leu Val Thr Phe Gln Glu Pro Pro Gly Val Asn
95 100 105
acc aca gag ctg cca tcc tt 453
Thr Thr Glu Leu Pro Ser
110

<210> 269
<211> 364
<212> DNA
<213> Homo sapiens

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<222> 105..362

<221> sig_peptide
<222> 105..227
<223> score 3.9
seq ALFLCGCYVVALG/AH

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gagattgctg cctatgcaaa gcaggtaaga agccgaactc tgaggcctct cgccattgtc 60
tccgagtcgg ccagctggag cgttttcggg gctgtaaagg gaga atg gcg cat gcg 116
Met Ala His Ala

004220" 666E T560

cat att cag ggc gga agg cgc gct aag agc aga ttt gtg gtc tgc att	-40	
His Ile Gln Gly Gly Arg Arg Ala Lys Ser Arg Phe Val Val Cys Ile		164
-35	-30	
atg tct gga gcc aga agt aag ctt gct ctt ttc ctc tgc ggc tgt tac	-25	
Met Ser Gly Ala Arg Ser Lys Leu Ala Leu Phe Leu Cys Gly Cys Tyr		212
-20	-15	
gtg gtt gcc ctg gga gcc cac acc ggg gag gag agc gtg gct gac cat	-10	
Val Val Ala Leu Gly Ala His Thr Gly Glu Glu Ser Val Ala Asp His		260
-5	1	
cac gag gct gaa tat tat gtg gct gcc gtg tat gag cat cca tcc atc	5	
His Glu Ala Glu Tyr Tyr Val Ala Ala Val Tyr Glu His Pro Ser Ile	10	308
15	20	
ctg agt ctg aac cct ctg gct ctc atc agc cgc caa gag gcc ttg gag	25	
Leu Ser Leu Asn Pro Leu Ala Leu Ile Ser Arg Gln Glu Ala Leu Glu		356
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ctc atg aa	40	
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agcgacacgg atatggcccc gcgggcgggg ttttaggcccc aagtgggtgtc ggagcagcgc		120
ctattagtgt catctcacc gtcacggccg gcgcctcttc ctggattcat tcaactcgctc		180
ttttcattca cgaaggtagt gaggcctagt ggaaagcc atg gag agc gct ctc ccc		236
Met Glu Ser Ala Leu Pro		
-15		
gcc gcc ggc ttc ctg tac tgg gtc ggc gcg gcc acc gtg gcc tac cta		284
Ala Ala Gly Phe Leu Tyr Trp Val Gly Ala Gly Thr Val Ala Tyr Leu		
-10	-5	
gcc ctg cgt att tcg tac tcg ctc ttc acg gcc ctc cgg gtc tgg gga	1	
Ala Leu Arg Ile Ser Tyr Ser Leu Phe Thr Ala Leu Arg Val Trp Gly	5	332
10	15	
gtg ggg aat gag gcg ggg gtc gcc cgg ggc tcg gag aat ggg cag ttg	20	
Val Gly Asn Glu Ala Gly Val Gly Arg Gly Ser Glu Asn Gly Gln Leu		380
25	30	
tca cag gta gta ctg a	35	
Ser Gln Val Val Leu		396
40		

<210> 271
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 108..413

<221> sig_peptide
 <222> 108..197
 <223> score 7.3
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 aaagccggcc agctgatcgt cgtgtgttgc caccattca tgtcaag atg act aag 116
 Met Thr Lys
 -30
 ttt gga ttt ttg cga ttg tcc tat gag aag cag gac aca ctt ttg aag 164
 Phe Gly Phe Leu Arg Leu Ser Tyr Glu Lys Gln Asp Thr Leu Leu Lys
 -25 -20 -15
 ctt ctc att ctg tca atg gct gct gta tta tcc ttc tcc act cgt ctg 212
 Leu Leu Ile Leu Ser Met Ala Ala Val Leu Ser Phe Ser Thr Arg Leu
 -10 -5 1 5
 ttt gct gtc ctg aga ttt gaa agt gtt atc cat gag ttt gat ccg tac 260
 Phe Ala Val Leu Arg Phe Glu Ser Val Ile His Glu Phe Asp Pro Tyr
 10 15 20
 ttt aat tat cgg act acc agg ttc ctg gct gag gag ggg ttt tat aaa 308
 Phe Asn Tyr Arg Thr Thr Arg Phe Leu Ala Glu Glu Gly Phe Tyr Lys
 25 30 35
 ttc cat aac tgg ttt gat gac cga gcc tgg tac cct ttg gga cga atc 356
 Phe His Asn Trp Phe Asp Asp Arg Ala Trp Tyr Pro Leu Gly Arg Ile
 40 45 50
 att gga gga aca att tac cca ggt tta atg atc acc tct gct gca atc 404
 Ile Gly Gly Thr Ile Tyr Pro Gly Leu Met Ile Thr Ser Ala Ala Ile
 55 60 65
 tac cat gta c 414
 Tyr His Val
 70

<210> 272
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 55..288

<221> sig_peptide
 <222> 55..153

<223> score 9.5
seq LLLGLVMPLAIIA/QV

<400> 272
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Met
ggg acc atg aag acc caa agg gat ggc cac tcc ctg ggg cgg tgg tca 105
Gly Thr Met Lys Thr Gln Arg Asp Gly His Ser Leu Gly Arg Trp Ser
-30 -25 -20
ctg gtg ctc ctg ctg ctg ggc ctg gtg atg cct ctg gcc atc att gcc 153
Leu Val Leu Leu Leu Leu Gly Leu Val Met Pro Leu Ala Ile Ile Ala
-15 -10 -5
cag gtc ctc agc tac aag gaa gct gtg ctt cgt gct ata gat ggc atc 201
Gln Val Leu Ser Tyr Lys Glu Ala Val Leu Arg Ala Ile Asp Gly Ile
1 5 10 15
aac cag cgg tcc tcg gat gct aac ctc tac cgc ctc ctg gac ctg gac 249
Asn Gln Arg Ser Ser Asp Ala Asn Leu Tyr Arg Leu Leu Asp Leu Asp
20 25 30
ccc agg ccc acg atg gtg agc ttt ggg gga cat tct gct 288
Pro Arg Pro Thr Met Val Ser Phe Gly Gly His Ser Ala
35 40 45

<210> 273
<211> 454
<212> DNA
<213> Homo sapiens

<220>
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<222> 100..453

<221> sig_peptide
<222> 100..180
<223> score 7.2
seq VLWLSGLSEPGAA/RQ

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cgcgattggg acagtcgcca gggatggctg agcgtgaag atg cag cgg gtg tcc 114
Met Gln Arg Val Ser
-25
ggg ctg ctc tcc tgg acg ctg agc aga gtc ctg tgg ctc tcc ggc ctc 162
Gly Leu Leu Ser Trp Thr Leu Ser Arg Val Leu Trp Leu Ser Gly Leu
-20 -15 -10
tct gag cgg gga gct gcc cgg cag ccc cgg atc atg gaa gag aaa gcg 210
Ser Glu Pro Gly Ala Ala Arg Gln Pro Arg Ile Met Glu Glu Lys Ala
-5 1 5 10
cta gag gtt tat gat ttg att aga act atc cgg gac cca gaa aag ccc 258
Leu Glu Val Tyr Asp Leu Ile Arg Thr Ile Arg Asp Pro Glu Lys Pro
15 20 25
aat act tta gaa gaa ctg gaa gtg gtc tcg gaa agt tgt gtg gaa gtt 306
Asn Thr Leu Glu Glu Leu Glu Val Val Ser Glu Ser Cys Val Glu Val

	30		35		40	
cag gag ata aat gaa gam gaa tat ctg gtt ann atc agg ttc acg cca						354
Gln Glu Ile Asn Glu Xaa Glu Tyr Leu Val Xaa Ile Arg Phe Thr Pro						
	45		50		55	
rca gta cct cat tgc tct ttg gcg act ctt att ggg ctg tgc tta aga						402
Xaa Val Pro His Cys Ser Leu Ala Thr Leu Ile Gly Leu Cys Leu Arg						
	60		65		70	
gta aaa ctt cag cga tgt tta cca ttt aaa cat aag ttg gaa atc tac						450
Val Lys Leu Gln Arg Cys Leu Pro Phe Lys His Lys Leu Glu Ile Tyr						
75	80		85		90	
att t						454
Ile						

<210> 274
 <211> 399
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 81..398

 <221> sig_peptide
 <222> 81..152
 <223> score 10
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ggagcaggag caggaggggg atg gag agg aga agg ctc ctg ggt ggc atg gcg	113
Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala	
	-20 -15
ctc ctg ctc ctc cag gcg ctg ccc agc ccc ttg tca gcc agg gct gaa	161
Leu Leu Leu Leu Gln Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu	
	-10 -5 1
ccc ccg cag gat aag gaa gcc tgt gtg ggt acc aac aat caa agc tac	209
Pro Pro Gln Asp Lys Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr	
	5 10 15
atc tgt gac aca gga cac tgc tgt gga cag tct cag tgc tgy aac tac	257
Ile Cys Asp Thr Gly His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr	
	20 25 30 35
tac tat gaa ctc tgg tgg ttc tgg ctg gtg tgg acc atc atc atc atc	305
Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile	
	40 45 50
ctg agc tgc tgc tgt gtt tgc cac cac cgc cga gcc aag cac cgc ctt	353
Leu Ser Cys Cys Cys Val Cys His His Arg Arg Ala Lys His Arg Leu	
	55 60 65
cag gcc cag cag cgg caa cat gaa atc aac ctg atc gct tac cga g	399
Gln Ala Gln Gln Arg Gln His Glu Ile Asn Leu Ile Ala Tyr Arg	
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<210> 275
 <211> 272

<212> DNA
<213> Homo sapiens

<220>
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<222> 118..270

<221> sig_peptide
<222> 118..180
<223> score 14.3
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gtggtggcag aggcgaaggc gacagctcta ggggttggca ccggccccga gaggagg 117
atg cgg gtc cgg ata ggg ctg acg ctg ctg ctg tgt gcg gtg ctg ctg 165
Met Arg Val Arg Ile Gly Leu Thr Leu Leu Leu Cys Ala Val Leu Leu
-20 -15 -10
agc ttg gcc tcg gcg tcc tcg ggt cag tat ccg ccc cct cgg gct gaa 213
Ser Leu Ala Ser Ala Ser Ser Gly Gln Tyr Pro Pro Pro Arg Ala Glu
-5 1 5 10
ggc cca gag cct ccg ccc ccc agc ctc tac agc cgg cgg ggc cgt ggg 261
Gly Pro Glu Pro Pro Pro Pro Ser Leu Tyr Ser Arg Arg Gly Arg Gly
15 20 25
gac tcc agg ct 272
Asp Ser Arg
30

<210> 276
<211> 448
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..446

<221> sig_peptide
<222> 15..155
<223> score 7.1
seq SLLFLLMGLRASG/KD

<400> 276
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Met Val Ala Pro Lys Ser His Thr Asp Asp Trp Ala
-45 -40
cct ggg cct ttc tcc agt aag cca cag agg agt cag ctg caa ata ttc 98
Pro Gly Pro Phe Ser Ser Lys Pro Gln Arg Ser Gln Leu Gln Ile Phe
-35 -30 -25 -20
tct tct gtt cta cag acc tct ctc ctc ttc ctg ctc atg gga cta aga 146
Ser Ser Val Leu Gln Thr Ser Leu Leu Phe Leu Leu Met Gly Leu Arg
-15 -10 -5

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gcc tct gga aag gac tca gcc cca aca gtg gtg tca ggg atc cta ggg      194
Ala Ser Gly Lys Asp Ser Ala Pro Thr Val Val Ser Gly Ile Leu Gly
      1              5              10

ggt tcc gtg act ctc ccc cta aac atc tca gta gac aca gag att gag      242
Gly Ser Val Thr Leu Pro Leu Asn Ile Ser Val Asp Thr Glu Ile Glu
      15              20              25

aac gtc atc tgg att ggt ccc aaa aat gct ctt gct ttc gca cgt ccc      290
Asn Val Ile Trp Ile Gly Pro Lys Asn Ala Leu Ala Phe Ala Arg Pro
      30              35              40              45

aaa gaa aat gta acc att atg gtc aaa agc tac ctg ggc cga cta gac      338
Lys Glu Asn Val Thr Ile Met Val Lys Ser Tyr Leu Gly Arg Leu Asp
      50              55              60

atc acc aag tgg agt tac tcc ctg tgc atc agc aat ctg act ctg aat      386
Ile Thr Lys Trp Ser Tyr Ser Leu Cys Ile Ser Asn Leu Thr Leu Asn
      65              70              75

gat gca gga tcc tas aaa gcc cag ata aac caa rgg aat ttt gaa gtc      434
Asp Ala Gly Ser Xaa Lys Ala Gln Ile Asn Gln Xaa Asn Phe Glu Val
      80              85              90

acc act gag gag ga      448
Thr Thr Glu Glu
      95

<210> 277
<211> 552
<212> DNA
<213> Homo sapiens

<220>
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<222> 207..551

<221> sig_peptide
<222> 207..284
<223> score 10
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accaattgag gagagacaca tgggtgggaa attgcaataa aaagacggcc cacagcaggc      120
tgcattccca tggetggcca gaggaggaac gctttgtgtt ctcacgag ctgcatggga      180
agtctgcata cagcaaagtg acctgc atg cct cac ctt atg gaa agg atg gtg      233
      Met Pro His Leu Met Glu Arg Met Val
      -25              -20

ggc tct ggc ctc ctg tgg ctg gcc ttg gtc tcc tgc att ctg acc cag      281
Gly Ser Gly Leu Leu Trp Leu Ala Leu Val Ser Cys Ile Leu Thr Gln
      -15              -10              -5

gca tct gca gtg cag cga gac cca tcc act gtg gag gac aag tgt gag      329
Ala Ser Ala Val Gln Arg Asp Pro Ser Thr Val Glu Asp Lys Cys Glu
      1              5              10              15

aag gcc tgc cgc ccc gag gag gag tgc ctt gcc ctc aac agc acc tgg      377
Lys Ala Cys Arg Pro Glu Glu Glu Cys Leu Ala Leu Asn Ser Thr Trp
      20              25              30

ggc tgt ttc tgc aga cag gac ctc aat agt tct gat gtc cac agt ttg      425

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004220"666T560

Gly	Cys	Phe	Cys	Arg	Gln	Asp	Leu	Asn	Ser	Ser	Asp	Val	His	Ser	Leu	
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cag	cct	cag	cta	gac	tgt	ggg	ccc	agg	gag	atc	aag	gtg	aag	gtg	gac	473
Gln	Pro	Gln	Leu	Asp	Cys	Gly	Pro	Arg	Glu	Ile	Lys	Val	Lys	Val	Asp	
		50				55					60					
aaa	tgt	ttg	ctg	gga	ggc	ctg	ggt	ttg	ggg	gag	gag	gtc	atg	cct	acc	521
Lys	Cys	Leu	Leu	Gly	Gly	Leu	Gly	Leu	Gly	Glu	Glu	Val	Met	Pro	Thr	
	65				70					75						
tgc	gag	acc	caa	ctg	cag	cag	cat	ctt	gca	g						552
Cys	Glu	Thr	Gln	Leu	Gln	Gln	His	Leu	Ala							
80					85											

<210> 278
 <211> 503
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 207..503

 <221> sig_peptide
 <222> 207..284
 <223> score 10
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tgcattccca	tggtggcca	gaggaggaac	gctttgtgtt	ctcatcggag	ctgcatggga											180	
agtctgcata	cagcaaagtg	acctgc	atg	cct	cac	ctt	atg	gaa	agg	atg	gtg					233	
			Met	Pro	His	Leu	Met	Glu	Arg	Met	Val						
			-25				-20										
ggc	tct	ggc	ctc	ctg	tgg	ctg	gcc	ttg	gtc	tcc	tgc	att	ctg	acc	cag	281	
Gly	Ser	Gly	Leu	Leu	Trp	Leu	Ala	Leu	Val	Ser	Cys	Ile	Leu	Thr	Gln		
		-15				-10					-5						
gca	tct	gca	gtg	cag	cga	ggy	wat	gga	rac	ccc	att	gaa	gcc	agt	atg	329	
Ala	Ser	Ala	Val	Gln	Arg	Gly	Xaa	Gly	Xaa	Pro	Ile	Glu	Ala	Ser	Met		
	1			5				10						15			
tat	ggg	ctg	gac	ctg	gac	tcc	gga	gct	cct	ggc	acc	cca	gag	gct	cat	377	
Tyr	Gly	Leu	Asp	Leu	Asp	Ser	Gly	Ala	Pro	Gly	Thr	Pro	Glu	Ala	His		
		20					25				30						
gtc	tgt	ttt	gac	ccc	tgt	cag	aat	tac	acc	atc	ctg	gat	gaa	ccc	ttc	425	
Val	Cys	Phe	Asp	Pro	Cys	Gln	Asn	Tyr	Thr	Ile	Leu	Asp	Glu	Pro	Phe		
		35				40				45							
cga	agc	aca	gag	aac	tca	gca	ggg	ggg	gtg	cga	tna	aaa	cat	gag	cgg	473	
Arg	Ser	Thr	Glu	Asn	Ser	Ala	Gly	Gly	Val	Arg	Xaa	Lys	His	Glu	Arg		
		50				55				60							
ctg	gta	ccg	ctt	tgt	agg	gga	agg	rgg	agt							503	
Leu	Val	Pro	Leu	Cys	Arg	Gly	Arg	Xaa	Ser								
	65				70												

<210> 279

<211> 416
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 262..414

<221> sig_peptide
 <222> 262..306
 <223> score 6.4
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 aggggtgtccg ctgctgcttt ccttcggaat ccagtgttc cacagagaat tagcctgtag 180
 cttatatttg acattcttca ctgtctgttg tttacctacc gtagcttttt accgttcact 240
 tccccctcca actatgtcca g atg tgc agg ctc ctc ctc tct gga ctt tct 291
 Met Cys Arg Leu Leu Leu Ser Gly Leu Ser
 -15 -10
 cca aag gca ctg acc ctc ggc ctc tac ttt gtc ccc tca cct cca ccc 339
 Pro Lys Ala Leu Thr Leu Gly Leu Tyr Phe Val Pro Ser Pro Pro Pro
 -5 1 5 10
 cct cct gtc acc ggc ctt gtg aca ttc act cag aga aga cca cac caa 387
 Pro Pro Val Thr Gly Leu Val Thr Phe Thr Gln Arg Arg Pro His Gln
 15 20 25
 gga ggc ggc cgc tgg cca gga gag aac ac 416
 Gly Gly Gly Arg Trp Pro Gly Glu Asn
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<210> 280
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 <212> DNA
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<220>
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 <222> 68..343

<221> sig_peptide
 <222> 68..136
 <223> score 9.1
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<400> 280
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 Met Glu Arg Met Leu Pro Leu Leu Xaa Leu Gly Leu Leu Ala
 -20 -15 -10
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 Ala Gly Phe Cys Pro Ala Val Leu Cys His Pro Asn Ser Pro Leu Asp


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          90          95          100
aat cag tcc agc gat gag ctg cag ctg rgt atg gga aaa tgc cat gwy      493
Asn Gln Ser Ser Asp Glu Leu Gln Leu Xaa Met Gly Lys Cys His Xaa
      105          110          115
tgt yna aga gca act cag tct gct gga cag gtt cac gga gga tgc caa      541
Cys Xaa Arg Ala Thr Gln Ser Ala Gly Gln Val His Gly Gly Cys Gln
120          125          130          135
gag gct gta tgg c      554
Glu Ala Val Trp

<210> 282
<211> 435
<212> DNA
<213> Homo sapiens

<220>
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<222> 160..435

<221> sig_peptide
<222> 160..228
<223> score 9.1
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gcagcagcct ggagtgtgtg gagtgtgagg gagttgaga atg gag aga atg tta      174
                               Met Glu Arg Met Leu
                               -20

cct ctc ctg act ctg ggg ctc ttg gcg gct ggg ttc tgc cct gct gtc      222
Pro Leu Leu Thr Leu Gly Leu Leu Ala Ala Gly Phe Cys Pro Ala Val
      -15          -10          -5
ctc tgc cac cct aac agc cca ctt gac gag gag aat ctg acc cag gag      270
Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu
      1          5          10
aac caa gac cga ggg aca cac gtg gac ctc gga tta gcc tcc gcc aac      318
Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly Leu Ala Ser Ala Asn
15          20          25          30
gtg gac ttc gct ttc agc ctg tac aag ctg gga gtc cgc ctc agg gat      366
Val Asp Phe Ala Phe Ser Leu Tyr Lys Leu Gly Val Arg Leu Arg Asp
      35          40          45
cgt gga gtt ctg ggt aga tgg gaa gcc cag ggt gag gaa gag tct gaa      414
Arg Gly Val Leu Gly Arg Trp Glu Ala Gln Gly Glu Glu Glu Ser Glu
50          55          60
gaa ggg ata cac tgt ggg ggc      435
Glu Gly Ile His Cys Gly Gly
      65

<210> 283
<211> 646
<212> DNA
<213> Homo sapiens

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<220>
 <221> CDS
 <222> 160..645

<221> sig_peptide
 <222> 160..228
 <223> score 9.1
 seq GLLAAGFCPAVLC/HP

<400> 283
 ccactactcc agacagacgg ctttggaatc caccagctac atccagctcc ctgagggcagg 60
 taatccatga tgttttacat cctgggagcg gaggaatctg tttttccagg akagtttttag 120
 gcagcagcct ggagtgtgtg gagtgtgagg gagttgaga atg gag aga atg tta 174
 Met Glu Arg Met Leu
 -20
 cct ctc ctg act ctg ggg ctc ttg gcg gct ggg ttc tgc cct gct gtc 222
 Pro Leu Leu Thr Leu Gly Leu Leu Ala Ala Gly Phe Cys Pro Ala Val
 -15 -10 -5
 ctc tgc cac cct aac agc cca ctt gac gag gag aat ctg acc cag gag 270
 Leu Cys His Pro Asn Ser Pro Leu Asp Glu Glu Asn Leu Thr Gln Glu
 1 5 10
 aac caa gac cga ggg aca cac gtg gac ctc gga tta gcc tcc gcc aac 318
 Asn Gln Asp Arg Gly Thr His Val Asp Leu Gly Leu Ala Ser Ala Asn
 15 20 25 30
 gtg gac ttc gct ttc agc ctg tac aag cag tta gtc ctg aag gcc cct 366
 Val Asp Phe Ala Phe Ser Leu Tyr Lys Gln Leu Val Leu Lys Ala Pro
 35 40 45
 gat aag aat gtc atc ttc tcc cca ctg agc atc tcc acc gcc ttg gcc 414
 Asp Lys Asn Val Ile Phe Ser Pro Leu Ser Ile Ser Thr Ala Leu Ala
 50 55 60
 ttc ctg tct ctg ggg gcc cat aat acc acc ctg aca gag att ctc aaa 462
 Phe Leu Ser Leu Gly Ala His Asn Thr Thr Leu Thr Glu Ile Leu Lys
 65 70 75
 ggc ctc aag ttc aac ctc acg gag act tct gag gca gaa att cac cag 510
 Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu Ala Glu Ile His Gln
 80 85 90
 agc ttc cag cac ctc ctg cgc acc ctc aat cag tcc agc gat gag ctg 558
 Ser Phe Gln His Leu Leu Arg Thr Leu Asn Gln Ser Ser Asp Glu Leu
 95 100 105 110
 cag ctg rgt atg gga aaa tgc cat gwy tgt yna aga gca act cag tct 606
 Gln Leu Xaa Met Gly Lys Cys His Xaa Cys Xaa Arg Ala Thr Gln Ser
 115 120 125
 gct gga cag gtt cac gga gga tgc caa gag gct gta tgg c 646
 Ala Gly Gln Val His Gly Gly Cys Gln Glu Ala Val Trp
 130 135

<210> 284
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 168..383

<221> sig_peptide
<222> 168..224
<223> score 9.8
seq LLILQALLPSLA/DG

<400> 284
acatgaccca aggggagggc tcccgggaca gccctcgag aaactgcatc atcctcacta 60
atgatccact tcctcctcag ggaataaagg ctcagggacc ggcagttcta ctctagagcc 120
caccagcctc tcagagcctc cgggtgactgg cctgtgtctc cccctgg atg gac atg 176
Met Asp Met
tgg acg gcg ctg ctc atc ctg caa gcc ttg ttg cta ccc tcc ctg gct 224
Trp Thr Ala Leu Leu Ile Leu Gln Ala Leu Leu Leu Pro Ser Leu Ala
-15 -10 -5
gat ggt gcc acc cct gcc ctg cgc ttt gta gcc gtg ggt gac tgg gga 272
Asp Gly Ala Thr Pro Ala Leu Arg Phe Val Ala Val Gly Asp Trp Gly
1 5 10 15
ggg gtc ccc aat gcc cca ttc cac acg gcc cgg gaa atg gcc aat gcc 320
Gly Val Pro Asn Ala Pro Phe His Thr Ala Arg Glu Met Ala Asn Ala
20 25 30
aag gag atc gct cgg act gtg cag atc ctg ggt gca gac ttc atc ctg 368
Lys Glu Ile Ala Arg Thr Val Gln Ile Leu Gly Ala Asp Phe Ile Leu
35 40 45
tct cta ggg gac aat 383
Ser Leu Gly Asp Asn
50

<210> 285
<211> 440
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 101..439

<221> sig_peptide
<222> 101..235
<223> score 6.8
seq IMVLVVAESVWG/DE

<400> 285
agtacctggt ggcataaggc agacacgcct gcagacattc tctgggaaag ggcagcagca 60
gccagggtgtg gcagtgcacag ggaggtgtga atgaggcagg atg aac tgg aca ggt 115
Met Asn Trp Thr Gly
-45
ttg tac acc ttg ctc agt ggc gtg aac cgg cat tct act gcc att ggc 163
Leu Tyr Thr Leu Leu Ser Gly Val Asn Arg His Ser Thr Ala Ile Gly
-40 -35 -30 -25
cga gta tgg ctc tcg gtc atc ttc atc ttc aga atc atg gtg ctg gtg 211

004220 656E7560

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Arg Val Trp Leu Ser Val Ile Phe Ile Phe Arg Ile Met Val Leu Val
      -20                      -15                      -10
gtg gct gca gag agt gtg tgg ggt gat gag aaa tct tcc ttc atc tgc    259
Val Ala Ala Glu Ser Val Trp Gly Asp Glu Lys Ser Ser Phe Ile Cys
      -5                      1                      5
aac aca ctc cag cct ggc tgc aac agc gtt tgc tat gac caa ttc ttc    307
Asn Thr Leu Gln Pro Gly Cys Asn Ser Val Cys Tyr Asp Gln Phe Phe
      10                      15                      20
ccc atc tcc cat gtg cgg ctg tgg tcc ctg cag ctc atc cta gtt tcc    355
Pro Ile Ser His Val Arg Leu Trp Ser Leu Gln Leu Ile Leu Val Ser
      25                      30                      35                      40
acc cca gct ctc ctc gtg gcc atg cac gtg gct cac cag caa cac ata    403
Thr Pro Ala Leu Leu Val Ala Met His Val Ala His Gln Gln His Ile
      45                      50                      55
gag aag aaa atg cta cgg ctt gag ggc atg ggg acc c    440
Glu Lys Lys Met Leu Arg Leu Glu Gly Met Gly Thr
      60                      65

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<210> 286
 <211> 315
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 143..313

<221> sig_peptide
 <222> 143..190
 <223> score 3.7
 seq VVIGAGVIGLSTA/LC

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<400> 286
gcactccagt ccgggctggc ggacagaggg ctggaaacaa gacgctccag aatcaggagc    60
ttcccctcag gaaatagcat cctgtgtccc cgcactgcag ttgtctggtc tctccagcag    120
tttggctactt ccggctgctg ca atg cgt gtg gtg gtg att gga gca gga gtc    172
                      Met Arg Val Val Val Ile Gly Ala Gly Val
                      -15                      -10
atc ggg ctg tcc acc gcc ctc tgc atc cat gag cgc tac cac tca gtc    220
Ile Gly Leu Ser Thr Ala Leu Cys Ile His Glu Arg Tyr His Ser Val
      -5                      1                      5                      10
ctg cag cca ctg gac ata aag gtc tac gcg gac cgc ttc acc cma ctc    268
Leu Gln Pro Leu Asp Ile Lys Val Tyr Ala Asp Arg Phe Thr Xaa Leu
      15                      20                      25
acc acc acc gac gtg gct gcc ggc ctc tgg cag ccc tac stt tct ga    315
Thr Thr Thr Asp Val Ala Ala Gly Leu Trp Gln Pro Tyr Xaa Ser
      30                      35                      40

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<210> 287
 <211> 402
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 40..402

<221> sig_peptide
 <222> 40..105
 <223> score 6.5
 seq SLLFLQLPLLGVG/LN

<400> 287
 aacagacaga ctacaccag ggaatgaaga gcaagcgcc atg ttg aag cca tca 54
 Met Leu Lys Pro Ser
 -20
 tta cca ttc aca tcc ctc tta ttc ctg cag ctg ccc ctg ctg gga gtg 102
 Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu Pro Leu Leu Gly Val
 -15 -10 -5
 ggg ctg aac acg aca att ctg acg ccc aat ggg aat gaa gac acc aca 150
 Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp Thr Thr
 1 5 10 15
 gct gat ttc ttc ctg acc act atg ccc act gac tcc ctc agt gtt tcc 198
 Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser Leu Ser Val Ser
 20 25 30
 act ctg ccc ctc cca gag gtt cag tgt ttt gtg ttc aat gtc gag tac 246
 Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr
 35 40 45
 atg aat tgc act tgg aac agc agc tct gag ccc cag cct acc aac ctc 294
 Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu
 50 55 60
 act ctg cat tat tgg tac aag aac tcg gat aat gat aaa gtc cag aag 342
 Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys
 65 70 75
 tgc agc cac tat cta ttc tct gaa gaa atc act tct ggc tgt cag ttg 390
 Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu
 80 85 90 95
 caa aaa aag gag 402
 Gln Lys Lys Glu

<210> 288
 <211> 434
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 201..434
 <221> sig_peptide
 <222> 201..263
 <223> score 8.6
 seq FTLCLLLSEMASG/GN

<400> 288

aaatgacacc aggggttagt gattagaagt tcacccttga ctgtggcacc tcccttcagt 60
 tccgtcgacg aggttggtgca atccaccagt cttataaata cagtgcgct ccagcctctg 120
 gaagcctctg tcagctcagc ctccaaagra gccagcctct cccagttcc tgaaatcctg 180
 ggtgttgccct gccagtcgcc atg aga act tcc tac ctt ctg ctg ttt act ctc 233
 Met Arg Thr Ser Tyr Leu Leu Leu Phe Thr Leu

-20 -15
 tgc tta ctt ttg tct gag atg gcc tca ggt ggt aac ttt ctc aca ggc 281
 Cys Leu Leu Leu Ser Glu Met Ala Ser Gly Gly Asn Phe Leu Thr Gly
 -10 -5 1 5

ctt ggc cac aga tct gat cat tac aat tgc gtc agc agt gga ggg caa 329
 Leu Gly His Arg Ser Asp His Tyr Asn Cys Val Ser Ser Gly Gly Gln
 10 15 20

tgt ctc tat tct gcc tgc ccg atc ttt acc aaa att caa ggc acc tgt 377
 Cys Leu Tyr Ser Ala Cys Pro Ile Phe Thr Lys Ile Gln Gly Thr Cys
 25 30 35

tac gag gga agg cca agt gct gca agt gag ctg gga gtg acc aga aga 425
 Tyr Glu Gly Arg Pro Ser Ala Ala Ser Glu Leu Gly Val Thr Arg Arg
 40 45 50

aat gac gca 434
 Asn Asp Ala
 55

<210> 289
 <211> 305
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 144..305

<221> sig_peptide
 <222> 144..197
 <223> score 7.7
 seq AFLFLLGVLGALT/EM

<400> 289
 aattgcaggc atggaggatt aatcagtgac aggaagctgc gtctctcgga gcggtgacca 60
 gctgtggtca ggagagcctc agcagggcca gccccaggag tctttcccga ttcttgctca 120
 ctgctcacc accgtgctgct gcc atg agg cac ctt ggg gcc ttc ctc ttc ctt 173
 Met Arg His Leu Gly Ala Phe Leu Phe Leu

-15 -10
 ctg ggg gtc ctg ggg gcc ctc act gag atg tgt gaa ata cca gag atg 221
 Leu Gly Val Leu Gly Ala Leu Thr Glu Met Cys Glu Ile Pro Glu Met
 -5 1 5

gac agc cat ctg gta gag aag ttg ggc cag cac ctc tta cct tgg atg 269
 Asp Ser His Leu Val Glu Lys Leu Gly Gln His Leu Leu Pro Trp Met
 10 15 20

gac cgg ctt tcn ctg gag cac ttg aac ccc agc atc 305
 Asp Arg Leu Ser Leu Glu His Leu Asn Pro Ser Ile
 25 30 35

<210> 290

<211> 448
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 234..446

<221> sig_peptide
 <222> 234..281
 <223> score 7.4
 seq VLLSVSLRRTEA/HL

<400> 290
 aacgccttcg cccaggggta gttggagcgg tgcaggttcc caggctccag gtactgggcg 60
 ccttacgagc tgggaggtgg tgccctctcac ccagctaatt gctctctagc ccttggcctt 120
 cacaggtggt ggtgcctgcc gtgaacgcat tctgacctgg gccgtatctg tctcccaaga 180
 ctttgtgcct atggttgggg acagagtgag gtcgttgctt tgacgacgac agc atg 236
 Met
 cgg ccc gtg gtc ctc cta agt gtg agc ttg cgg cgg acc gag gcc cac 284
 Arg Pro Val Val Leu Leu Ser Val Ser Leu Arg Arg Thr Glu Ala His
 -15 -10 -5 1
 ctg cct ccc tgc ctg ctt cgc cct gga ctc gtg act gcg tcc gca gaa 332
 Leu Pro Pro Cys Leu Leu Arg Pro Gly Leu Val Thr Ala Ser Ala Glu
 5 10 15
 gaa atc aca aca gcg ctg gaa ttt gct agt ttg cta ggc agc atc ttt 380
 Glu Ile Thr Thr Ala Leu Glu Phe Ala Ser Leu Leu Gly Ser Ile Phe
 20 25 30
 tgg acc tgc gaa cca tat gca ttt cac ctc aaa ttt gtt tcc aag ttg 428
 Trp Thr Cys Glu Pro Tyr Ala Phe His Leu Lys Phe Val Ser Lys Leu
 35 40 45
 aaa atc ttt ggg tct ttc ta 448
 Lys Ile Phe Gly Ser Phe
 50 55

<210> 291
 <211> 452
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 25..450

<221> sig_peptide
 <222> 25..96
 <223> score 5.3
 seq CLPVLAAGRARG/RA

<400> 291
 aatcagcgag ggattcacgg cgaa atg aga ctg ttc gtg agt gat ggc gtc 51
 Met Arg Leu Phe Val Ser Asp Gly Val

-20

ccg ggt tgc ttg ccg gtg ctg gcc gcc gcc ggg aga gcc cgg ggc aga	99
Pro Gly Cys Leu Pro Val Leu Ala Ala Ala Gly Arg Ala Arg Gly Arg	
-15 -10 -5 1	
gca gag gtg ctc atc agc act gta ggc ccg gaa gat tgt gtg gtc ccg	147
Ala Glu Val Leu Ile Ser Thr Val Gly Pro Glu Asp Cys Val Val Pro	
5 10 15	
ttc ctg acc cgg cct aag gtc cct gtc ttg cag ctg gat agc ggc aac	195
Phe Leu Thr Arg Pro Lys Val Pro Val Leu Gln Leu Asp Ser Gly Asn	
20 25 30	
tac ctc ttc tcc act agt gca atc tgc cga tat ttt ttt ttg tta tct	243
Tyr Leu Phe Ser Thr Ser Ala Ile Cys Arg Tyr Phe Phe Leu Leu Ser	
35 40 45	
ggc tgg gag caa gat gac ctc act aac cag tgg ctg gaa tgg gaa gcg	291
Gly Trp Glu Gln Asp Asp Leu Thr Asn Gln Trp Leu Glu Trp Glu Ala	
50 55 60 65	
aca gag ctg cag cca gct ttg tct gct gcc ctg tac tat tta gtg gtc	339
Thr Glu Leu Gln Pro Ala Leu Ser Ala Ala Leu Tyr Tyr Leu Val Val	
70 75 80	
caa ggc aag aag ggg gaa gat gtt ctt ggt tca rtg cgg aga gcc ctg	387
Gln Gly Lys Lys Gly Glu Asp Val Leu Gly Ser Xaa Arg Arg Ala Leu	
85 90 95	
act cac att gac cac agc ttg agt cgt cag act gtc ctt tcc tgg ctg	435
Thr His Ile Asp His Ser Leu Ser Arg Gln Thr Val Leu Ser Trp Leu	
100 105 110	
ggg aga cag aat ctc ta	452
Gly Arg Gln Asn Leu	
115	

<210> 292
 <211> 391
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 90..389

<221> sig_peptide
 <222> 90..146
 <223> score 5.7
 seq GLLVLTTPLASLA/PR

<400> 292	
ttctccgtta gtgcttccgg gttgcagcca gggaagcctc cgcggtggtg caagtggaac	60
ccaagccttg aggtttcagc ctgggcagc atg gcc gta ttc cgg tcg ggt ctc	113
Met Ala Val Phe Arg Ser Gly Leu	
-15	
ctg gtg ctg acg acg ccg ctg gcc tcc cta gcc cct cgc ctg gcc tcc	161
Leu Val Leu Thr Thr Pro Leu Ala Ser Leu Ala Pro Arg Leu Ala Ser	
-10 -5 1 5	
atc ctg acc tcg gcg gcc ccg ctg gtg aat cac aca ctc tat gtt cac	209
Ile Leu Thr Ser Ala Ala Arg Leu Val Asn His Thr Leu Tyr Val His	

004220"666F560

	10		15		20	
ctg cag ccg ggc atg agc ctg gag ggc ccg gct cag ccc cag tmc agc						257
Leu Gln Pro Gly Met Ser Leu Glu Gly Pro Ala Gln Pro Gln Xaa Ser						
	25		30		35	
ccc gtg cag gcc acg ttt gag gtt ctt gat ttc atc acg cac ctc tat						305
Pro Val Gln Ala Thr Phe Glu Val Leu Asp Phe Ile Thr His Leu Tyr						
	40		45		50	
gct ggc gcc gac gtc cac agg cac ttg gac gtc aga atc cta ctg acc						353
Ala Gly Ala Asp Val His Arg His Leu Asp Val Arg Ile Leu Leu Thr						
	55		60		65	
aat atc cga acc aag agc acc ttt ctc cct ccc ctg cc						391
Asn Ile Arg Thr Lys Ser Thr Phe Leu Pro Pro Leu						
70	75		80			

<210> 293
 <211> 412
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 125..412

 <221> sig_peptide
 <222> 125..172
 <223> score 7.7
 seq TLLLSLLGAVGLA/AV

<400> 293	
acaccgcggg gmccaggagg cacgctgggt ttccggggcc gctccatcgc gccttcctcc	60
tgcgctcgc ttctccgggtc cagccgccat ctctctttcc gcacaggggc cgccgagcgg	120
ggcc atg cag cca acg ctg ctt ctc agc ctc ctg gga gcc gtg ggg ctg	169
Met Gln Pro Thr Leu Leu Ser Leu Leu Gly Ala Val Gly Leu	
-15 -10 -5	
gcg gct gtc aat tcc atg cca gtg gat aac agg aac cac aat gaa gga	217
Ala Ala Val Asn Ser Met Pro Val Asp Asn Arg Asn His Asn Glu Gly	
1 5 10 15	
atg gtg act cgc tgc atc att gag gtc ctc tca aat gcc ttg tgc aag	265
Met Val Thr Arg Cys Ile Ile Glu Val Leu Ser Asn Ala Leu Ser Lys	
20 25 30	
tcc agc gct cca ccc atc acc cct gag tgc cgc caa gtc ctg aag acg	313
Ser Ser Ala Pro Pro Ile Thr Pro Glu Cys Arg Gln Val Leu Lys Thr	
35 40 45	
agt aga aaa gac gtc aaa gac aaa gag aca act gaa aat gaa aac aca	361
Ser Arg Lys Asp Val Lys Asp Lys Glu Thr Thr Glu Asn Glu Asn Thr	
50 55 60	
aag ttt gaa gta aga ttg tta aga gac cca gct gat gcc acg gaa gcc	409
Lys Phe Glu Val Arg Leu Leu Arg Asp Pro Ala Asp Ala Thr Glu Ala	
65 70 75	
cac	412
His	
80	

004420" 666T560

<210> 294
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 157..432

<221> sig_peptide
<222> 157..195
<223> score 3.8
seq MAHCVTLVQLSIS/CD

<400> 294
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ggaagccgtt cgggctgggg ctgtcggccg cggggcggag gcactcgcgc ggggggtaat 120
tcgggggtctg ggttctgggt cgcgcgrstt tccccg atg gcc cac tgc gtg acc 174
Met Ala His Cys Val Thr
-10
ttg gtt cag ctg tcc att tcc tgt gac cat ctc att gac aag gac atc 222
Leu Val Gln Leu Ser Ile Ser Cys Asp His Leu Ile Asp Lys Asp Ile
-5 1 5
ggc tcc aag tct gac cca ctc tgc gtc ctt tta cag gat gtg gga ggg 270
Gly Ser Lys Ser Asp Pro Leu Cys Val Leu Leu Gln Asp Val Gly Gly
10 15 20 25
ggc agc tgg gct gag ctt ggc cgg act gaa cgg gtg cgg aac tgc tca 318
Gly Ser Trp Ala Glu Leu Gly Arg Thr Glu Arg Val Arg Asn Cys Ser
30 35 40
agc cct gag ttc tcc aag act cta cag ctt gag tac cgc ttt gag aca 366
Ser Pro Glu Phe Ser Lys Thr Leu Gln Leu Glu Tyr Arg Phe Glu Thr
45 50 55
gtc cag aag cta cgc ttt gga atc tat gac ata gac aac aag acg cca 414
Val Gln Lys Leu Arg Phe Gly Ile Tyr Asp Ile Asp Asn Lys Thr Pro
60 65 70
gag ctg agg gat gat gac t 433
Glu Leu Arg Asp Asp Asp
75

<210> 295
<211> 435
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 197..433

<221> sig_peptide
<222> 197..241
<223> score 5.2
seq WSCLVTGAGLLG/QR

<400> 295
aagggtgag acacaagcca cagagcataa agctccagtc cntcctccag ggatgaggca 60
gtaaggactt ggactcctct gtccagcttt taacaatcta agttacgcc tcttctgggt 120
cacgctagaa tcagatctgc tctccagcat cttctgtttc ctggcaagtg tttcctgcta 180
ctttggattg gccacg atg ggc tgg agc tgc ctt gtg aca gga gca gga ggg 232
Met Gly Trp Ser Cys Leu Val Thr Gly Ala Gly Gly
-15 -10 -5
ctt ctg ggt cag agg atc gtc cgc ctg ttg gtg gaa gag aag gaa ctg 280
Leu Leu Gly Gln Arg Ile Val Arg Leu Leu Val Glu Glu Lys Glu Leu
1 5 10
aag gag atc agg gcc ttg gac aag gcc ttc aga cca gaa ttg aga gag 328
Lys Glu Ile Arg Ala Leu Asp Lys Ala Phe Arg Pro Glu Leu Arg Glu
15 20 25
gaa ttt tct aag ctc cag aac agg acc aag ctg act gta ctt gaa gga 376
Glu Phe Ser Lys Leu Gln Asn Arg Thr Lys Leu Thr Val Leu Glu Gly
30 35 40 45
gac att ctg gat gag cca ttc ctg aaa aga gsw tgc cag gac gtc tcg 424
Asp Ile Leu Asp Glu Pro Phe Leu Lys Arg Xaa Cys Gln Asp Val Ser
50 55 60
gtc gtc atc ca 435
Val Val Ile

<210> 296
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 11..406
<221> sig_peptide
<222> 11..73
<223> score 13.2
seq VLLLSLFLGGQA/QH

<400> 296
ttcattacag atg tgc agc acc atg agg gcc ctg gtg ctt ctg ctg tcc 49
Met Cys Ser Thr Met Arg Ala Leu Val Leu Leu Leu Ser
-20 -15 -10
ctg ttc ctg ctg ggt ggc cag gcc cag cat gtg tct gac tgg acc tac 97
Leu Phe Leu Leu Gly Gly Gln Ala Gln His Val Ser Asp Trp Thr Tyr
-5 1 5
tca gaa ggg gca ctg gac gaa gcg cac tgg cca cag cac tac ccc gcc 145
Ser Glu Gly Ala Leu Asp Glu Ala His Trp Pro Gln His Tyr Pro Ala
10 15 20
tgt ggg ggc cag aga cag tcg cct atc aac cta cag agg acg aag gtg 193
Cys Gly Gly Gln Arg Gln Ser Pro Ile Asn Leu Gln Arg Thr Lys Val
25 30 35 40
cgg tac aac ccc tcc ttg aag ggg ctc aat atg aca ggc tat gag acc 241
Arg Tyr Asn Pro Ser Leu Lys Gly Leu Asn Met Thr Gly Tyr Glu Thr
45 50 55

cag gca ggg gag ttc ccc atg gtc aac aat ggc cac aca gtg cag atc	289
Gln Ala Gly Glu Phe Pro Met Val Asn Asn Gly His Thr Val Gln Ile	
60 65 70	
agc ctg ccc tcc acc atg cgc atg aca gtg gct gac ggc act gta tac	337
Ser Leu Pro Ser Thr Met Arg Met Thr Val Ala Asp Gly Thr Val Tyr	
75 80 85	
ata gcc cag cag atg cac ttt cac tgg gga ggt gcg tcc tcg gag atc	385
Ile Ala Gln Gln Met His Phe His Trp Gly Gly Ala Ser Ser Glu Ile	
90 95 100	
agc ggc tct gag cac acc gtg ga	408
Ser Gly Ser Glu His Thr Val	
105 110	

<210> 297
 <211> 385
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 196..384

 <221> sig_peptide
 <222> 196..255
 <223> score 5.1
 seq FILLWSAVGIKA/AK

<400> 297	
aaascatkgc tatcaactgy gaacccagag agnccctcctt agccaacacg ctaactccga	60
agcctccctt acgccccga accaccgaag cggcgacacc tgattcagcg cacaaacaca	120
ggtcccttct gtcccgata caattacgcg gcagacacac actcagactc gcgcggggca	180
gccaaagagac gagct atg aag tct tac act cca tat ttc att ctc ctg tgg	231
Met Lys Ser Tyr Thr Pro Tyr Phe Ile Leu Leu Trp	
-20 -15 -10	
agt gct gtt ggg ata gcg aag gct gcc aaa atc atc atc gtg ccg cca	279
Ser Ala Val Gly Ile Ala Lys Ala Ala Lys Ile Ile Ile Val Pro Pro	
-5 1 5	
att atg ttt gaa agc cat atg tac att ttc aag acg cta gcc tca gcc	327
Ile Met Phe Glu Ser His Met Tyr Ile Phe Lys Thr Leu Ala Ser Ala	
10 15 20	
ttg cac gag aga ggc cac cat aca gtg ttc ctc ctc tct gaa ggc aga	375
Leu His Glu Arg Gly His His Thr Val Phe Leu Leu Ser Glu Gly Arg	
25 30 35 40	
gac atc gcc c	385
Asp Ile Ala	

<210> 298
 <211> 322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 72..320

<221> sig_peptide

<222> 72..134

<223> score 7.6

seq LTPLLCVLHGACP/RA

<400> 298

```
acttcttatt tctcgtcctg tctctttgca aagtatgggc ttttttggtt ttgtttttta 60
agggaaacga a atg gaa ttc gaa ggg acc ttt tca cta acc cca ctt ctg 110
      Met Glu Phe Glu Gly Thr Phe Ser Leu Thr Pro Leu Leu
      -20 -15 -10
tgt gtt ctg cat ggc gcc tgc ccc agg gca tct gcc aac tcc agt atc 158
Cys Val Leu His Gly Ala Cys Pro Arg Ala Ser Ala Asn Ser Ser Ile
      -5 1 5
agc tct cac agt gta ctt ggt acc atc cct ggg ctc tgc tgg cga gac 206
Ser Ser His Ser Val Leu Gly Thr Ile Pro Gly Leu Cys Trp Arg Asp
      10 15 20
gaa aca gct gta gag atg aaa aca ggc tgc aga ggc tgg cac agc tgg 254
Glu Thr Ala Val Glu Met Lys Thr Gly Cys Arg Gly Trp His Ser Trp
      25 30 35 40
ccg gct ttt ctc cat ctg ggg aac art cct act cca aga aca ctg cac 302
Pro Ala Phe Leu His Leu Gly Asn Xaa Pro Thr Pro Arg Thr Leu His
      45 50 55
acc agc tcc tca cac aga tc 322
Thr Ser Ser Ser His Arg
      60
```

<210> 299

<211> 426

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 66..425

<221> sig_peptide

<222> 66..122

<223> score 7.6

seq LPVLLVPFLLCQA/LV

<400> 299

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attaattggt cggcgatcgc tggctgccgg gacttttctc gcgctggtct cttcgggtggt 60
caggg atg gcg cgg aag tcg aac ttg cct gtg ctt ctc gtg ccg ttt ctg 110
      Met Ala Arg Lys Ser Asn Leu Pro Val Leu Leu Val Pro Phe Leu
      -15 -10 -5
ctc tgc cag gcc cta gtg cgc tgc tcc agc cct ctg ccc ctg gtc gtc 158
Leu Cys Gln Ala Leu Val Arg Cys Ser Ser Pro Leu Pro Leu Val Val
      1 5 10
aac act tgg ccc ttt aag aat gca acc gaa gca gcg tgg agg gca tta 206
Asn Thr Trp Pro Phe Lys Asn Ala Thr Glu Ala Ala Trp Arg Ala Leu
```

004220" 656E560

15	20	25	
gca tct gga ggc tct gcc ctg gat gca gtg gag agc ggc tgt gcc atg			254
Ala Ser Gly Gly Ser Ala Leu Asp Ala Val Glu Ser Gly Cys Ala Met			
30	35	40	
tgt gag aga gag cag tgt gac ggc tct gta ggc ttt gga gga agt cct			302
Cys Glu Arg Glu Gln Cys Asp Gly Ser Val Gly Phe Gly Gly Ser Pro			
45	50	55	60
gat gaa ctt gga gaa acc aca cta gat gcc atg atc atg gat ggc act			350
Asp Glu Leu Gly Glu Thr Thr Leu Asp Ala Met Ile Met Asp Gly Thr			
65	70	75	
act atg gat gta gga gca gta gga gat ctc aga cga atk aaa aat gct			398
Thr Met Asp Val Gly Ala Val Gly Asp Leu Arg Arg Xaa Lys Asn Ala			
80	85	90	
att ggt gtg gca cgg aaa gta ctg gaa c			426
Ile Gly Val Ala Arg Lys Val Leu Glu			
95	100		

<210> 300
 <211> 237
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 78..236

<221> sig_peptide
 <222> 78..170
 <223> score 4.5
 seq LLSLPSWASLAYS/YL

<400> 300	
tgccctagggt tgcccgtgtg ggcctgctcc cagggagcaa cagagaggcc accaagcaga	60
ggcccgtggg gctgagg atg gag ccg ccc cca gcc gac tcc aag ccc gca	110
Met Glu Pro Pro Pro Ala Asp Ser Lys Pro Ala	
-30	-25
gag ggc aga cgc cac cct gga ctg ctc tcc ctg ccc agc tgg gcc tct	158
Glu Gly Arg Arg His Pro Gly Leu Leu Ser Leu Pro Ser Trp Ala Ser	
-20	-15
ctg gcc tat tcc tac ctt cca ggc cca ctg cac tcc tgt ctg gga ggc	206
Leu Ala Tyr Ser Tyr Leu Pro Gly Pro Leu His Ser Cys Leu Gly Gly	
1	5
cct tat gag ggc agc cca gcc ccc gca ccc a	237
Pro Tyr Glu Gly Ser Pro Ala Pro Ala Pro	
15	20

<210> 301
 <211> 394
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 166..393

<221> sig_peptide

<222> 166..282

<223> score 4.8

seq IILFSAIVGFIYG/YV

<400> 301

```
gtcggagmyt ccgcttccgg ggccgccgcc atcgctctcc cgggcttaga agggccgggt      60
actgacgcgc agtgccagac cttaccctc acggtcctta agtctcggtc gccctcgcc      120
cgcagcctgc caccgcgct cagctgccc ctcctcagc cagcc atg ctg gag cat      177
                                Met Leu Glu His
ctg agc tcg ctg ccc acg cag atg gat tac aag ggc cag aag cta gct      225
Leu Ser Ser Leu Pro Thr Gln Met Asp Tyr Lys Gly Gln Lys Leu Ala
-35                                -30                                -25                                -20
gaa cag atg ttt cag gga att att ctt ttt tct gca ata gtt gga ttt      273
Glu Gln Met Phe Gln Gly Ile Ile Leu Phe Ser Ala Ile Val Gly Phe
                                -15                                -10                                -5
atc tac ggg tac gtg gct gaa cag ttc ggg tgg act gtc tat ata gtt      321
Ile Tyr Gly Tyr Val Ala Glu Gln Phe Gly Trp Thr Val Tyr Ile Val
                                1                                5                                10
atg gcc gga ttt gct ttt tca tgt ttg ctg aca ctt cct cca tgg ccc      369
Met Ala Gly Phe Ala Phe Ser Cys Leu Leu Thr Leu Pro Pro Trp Pro
                                15                                20                                25
atc tat crc cgg cat cct ctg aag t      394
Ile Tyr Xaa Arg His Pro Leu Lys
30                                35
```

<210> 302

<211> 359

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..357

<221> sig_peptide

<222> 22..144

<223> score 4.3

seq RVVSWLFSIVVFG/SI

<400> 302

```
aaccgcgcgg gtgcagccac g atg gaa ggg ggt gcg tac gga gcg ggc aaa      51
                                Met Glu Gly Gly Ala Tyr Gly Ala Gly Lys
                                -40                                -35
gcc ggg ggc gcc ttc gac ccc tac acc ctg gtc cgg cag ccg cac acc      99
Ala Gly Gly Ala Phe Asp Pro Tyr Thr Leu Val Arg Gln Pro His Thr
-30                                -25                                -20
atc ctg cgc gtc gtg tct tgg ctg ttc tcc ata gtg gtg ttc ggc tcc      147
Ile Leu Arg Val Val Ser Trp Leu Phe Ser Ile Val Val Phe Gly Ser
-15                                -10                                -5                                1
```

```

atc gtg aac gag ggc tac ctc aac agc gcc tcc gag ggg gag gag ttc      195
Ile Val Asn Glu Gly Tyr Leu Asn Ser Ala Ser Glu Gly Glu Glu Phe
      5                      10                      15
tgc atc tac aac cgc aac ccc aac gcc tgc agc tat ggc gtg gcc gtg      243
Cys Ile Tyr Asn Arg Asn Pro Asn Ala Cys Ser Tyr Gly Val Ala Val
      20                      25                      30
ggc gtg ctc gcc ttc ctc acc tgc ctg ctg tac ctg gcc ctg gac gtg      291
Gly Val Leu Ala Phe Leu Thr Cys Leu Leu Tyr Leu Ala Leu Asp Val
      35                      40                      45
tac ttc ccg cag atc agc agc gtc aag gac cgc aag aaa gcc gtc ctg      339
Tyr Phe Pro Gln Ile Ser Ser Val Lys Asp Arg Lys Lys Ala Val Leu
      50                      55                      60                      65
tcc gac atc ggt gtc tcg gc
Ser Asp Ile Gly Val Ser
      70

```

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<210> 303
<211> 310
<212> DNA
<213> Homo sapiens

```

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<220>
<221> CDS
<222> 105..308

<221> sig_peptide
<222> 105..149
<223> score 7
      seq LLFLLPLVMQGVVS/RA

```

```

<400> 303
acacagaccc cggtagcgga agtgacgtaa ggccggggct ggagggcagc gctgggctgg      60
tcccgacgag ctcgggggtg gagccagcga ccgtcggtag cagc atg gct ctc ctc      116
                                     Met Ala Leu Leu
                                     -15
ttt ctc cta ccc ctt gtc atg cag ggt gtg agc agg gct gag atg ggc      164
Phe Leu Leu Pro Leu Val Met Gln Gly Val Ser Arg Ala Glu Met Gly
      -10                      -5                      1                      5
acc gcg gat ctg ggg ccg tcc tca gtg cct aca cca act aat gtt aca      212
Thr Ala Asp Leu Gly Pro Ser Ser Val Pro Thr Pro Thr Asn Val Thr
      10                      15                      20
att gaa tcc tat aac atg aac cct atc gta tat tgg gag tac cag atc      260
Ile Glu Ser Tyr Asn Met Asn Pro Ile Val Tyr Trp Glu Tyr Gln Ile
      25                      30                      35
atg cca cag gtc cct gtt ttt acc gta gag gta aag aac tat ggt gtt      308
Met Pro Gln Val Pro Val Phe Thr Val Glu Val Lys Asn Tyr Gly Val
      40                      45                      50
aa

```

```

<210> 304
<211> 250
<212> DNA
<213> Homo sapiens

```

<220>

<221> CDS

<222> 46..249

<221> sig_peptide

<222> 46..144

<223> score 11.5

seq LLSLCCLLPSCLP/AG

<400> 304

gagtgcgagc tgaaagmwgc tggagagtga gcagccctag caggg atg gac atg atg 57
Met Asp Met Met
-30

ctg ttg gtg cag ggt gct tgt tgc tcg aac cag tgg ctg gcg gcg gtg 105
Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln Trp Leu Ala Ala Val
-25 -20 -15

ctc ctc agc ctg tgc tgc ctg cta ccc tcc tgc ctc ccg gct gga cag 153
Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser Cys Leu Pro Ala Gly Gln
-10 -5 1

agt gtg gac ttc ccc tgg gcg gcc gtg gac aac atg atg gtc aga aaa 201
Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn Met Met Val Arg Lys
5 10 15

ggg gac acg gcg gtg ctt agg tgt tat ttg gaa gat gga gct tca aag g 250
Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu Glu Asp Gly Ala Ser Lys
20 25 30 35

<210> 305

<211> 397

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 151..396

<221> sig_peptide

<222> 151..291

<223> score 6.8

seq PLGLLRLLQLVST/CV

<400> 305

tcagaccctt ccagctgccg ctgtcgtctt tgcctcagcc gcagtcgcca ctggctgcct 60
gagtgctct tacagcctgt tccaagtgtg gcttaatccg tctccaccac cagatcttcc 120
tccgtggatt cctctgctaa gaccgtgcc atg cca gtg acg gta acc cgc acc 174
Met Pro Val Thr Val Thr Arg Thr
-45 -40

acc atc aca acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg 222
Thr Ile Thr Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met
-35 -30 -25

atc gtg ggg tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc 270
Ile Val Gly Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg

	-20		-15		-10		
ctg	ctg	cag	ctg	gtg	tct	acc	tgc
Leu	Leu	Gln	Leu	Val	Ser	Thr	Cys
	-5						1
gtg	ggc	gcc	tgg	acg	ggg	tcc	atg
Val	Gly	Ala	Trp	Thr	Gly	Ser	Met
10					15		
tgc	ttc	tgc	ttc	tcn	gtg	acc	ctg
Cys	Phe	Cys	Phe	Ser	Val	Thr	Leu
					30		35

318

366

397

<210> 306
 <211> 299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 83..298

<221> sig_peptide
 <222> 83..127
 <223> score 11.7
 seq SLVLLLCCLAQLWG/CH

<400> 306	
ctacctttcc cagcagagca cctgggttgg tcccgaagcc tccaaccacc tgcacgcctg	60
ccagggcctc tctggggcag cc atg aag tcc ctc gtc ctg ctc ctt tgt ctt	112
Met Lys Ser Leu Val Leu Leu Leu Cys Leu	
-15	-10
gct cag ctc tgg ggc tgc cac tca gcc cca cat ggc cca ggg ctg att	160
Ala Gln Leu Trp Gly Cys His Ser Ala Pro His Gly Pro Gly Leu Ile	
-5	1
tat aga caa ccg aac tgc gat gat cca gaa act gag gaa gca gct ctg	208
Tyr Arg Gln Pro Asn Cys Asp Asp Pro Glu Thr Glu Glu Ala Ala Leu	
15	20
gtg gct ata gac tac atc aat caa aac ctt cct tgg gga tac aaa cac	256
Val Ala Ile Asp Tyr Ile Asn Gln Asn Leu Pro Trp Gly Tyr Lys His	
30	35
acc ttg aac cag att gat gaa gta aag gtg tgg cct cag cag c	299
Thr Leu Asn Gln Ile Asp Glu Val Lys Val Trp Pro Gln Gln	
45	50

<210> 307
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 208..414

<221> sig_peptide

<222> 208..264
 <223> score 5.4
 seq LSHLLPSLRQVIQ/EP

<400> 307
 tgtttgattg gtgtgcctga aagtgaaggg gagaatgaaa acatctgccca gctccgccga 60
 cccggccccc gcggccctcc cagctcggct ccggctcagt ggacaggaac cactgaagtt 120
 tgcctgacac catcaaccag gccctagtca cctggctttg cctttgccct gctgtgtgat 180
 cttagctccc tgcccaggcc cacagcc atg gcc atg gcc cag aaa ctc agc cac 234
 Met Ala Met Ala Gln Lys Leu Ser His

-15
 ctc ctg ccg agt ctg cgg cag gtc atc cag gag cct cag cta tct ctg 282
 Leu Leu Pro Ser Leu Arg Gln Val Ile Gln Glu Pro Gln Leu Ser Leu
 -10 -5 1 5
 cag cca gag myg gtc ttc acg gtg gat cga gct gag gtg ccg ccg ctc 330
 Gln Pro Glu Xaa Val Phe Thr Val Asp Arg Ala Glu Val Pro Pro Leu
 10 15 20
 ttc tgg aag ccg tac atc tat gcg ggc tam ccg ccg ctg cat cag acc 378
 Phe Trp Lys Pro Tyr Ile Tyr Ala Gly Xaa Arg Pro Leu His Gln Thr
 25 30 35
 tgg cgc ttc tat ttc cgc acg ctg ttc cag cag cac 414
 Trp Arg Phe Tyr Phe Arg Thr Leu Phe Gln Gln His
 40 45 50

<210> 308
 <211> 279
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 30..278
 <221> sig_peptide
 <222> 30..98
 <223> score 7.9
 seq LGLWSLCWSLAIA/TP

<400> 308
 gagctgtcct gtggcctctg cagctcagc atg gct agg gta ctg gga gca ccc 53
 Met Ala Arg Val Leu Gly Ala Pro
 -20
 gtt gca ctg ggg ttg tgg agc cta tgc tgg tct ctg gcc att gcc acc 101
 Val Ala Leu Gly Leu Trp Ser Leu Cys Trp Ser Leu Ala Ile Ala Thr
 -15 -10 -5 1
 cct ctt cct ccg act agt gcc cat ggg aat gtt gct gaa ggc gag acc 149
 Pro Leu Pro Pro Thr Ser Ala His Gly Asn Val Ala Glu Gly Glu Thr
 5 10 15
 aag cca gac cca gac gtg act gaa cgc tgc tca gat ggc tgg agc ttt 197
 Lys Pro Asp Pro Asp Val Thr Glu Arg Cys Ser Asp Gly Trp Ser Phe
 20 25 30
 gat gct acc acc ctg gat gac aat gga acc atg ctg ttt ttt aaa ggg 245

Asp Ala Thr Thr Leu Asp Asp Asn Gly Thr Met Leu Phe Phe Lys Gly
 35 40 45
 gag tkt gtg tgg aag agt cac aaa tgg gac cgg g
 Glu Xaa Val Trp Lys Ser His Lys Trp Asp Arg
 50 55 60

279

<210> 309
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..302

<221> sig_peptide
 <222> 54..110
 <223> score 7.6
 seq FALFSLFGICDA/VT

<400> 309
 aatttattcc actgggatag aagcggcagg agcagcgcttg gcaccggcga acc atg 56
 Met
 gct ggg att ttc tat ttc gcc cta ttt tgc tgt ctc ttc ggg att tgc 104
 Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile Cys
 -15 -10 -5
 gac gct gtc aca ggt tcc agg gta tac ccc gcg aat gaa gtt acc tta 152
 Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr Leu
 1 5 10
 ttg gat tcc aga tct gtt cag gga gaa ctt ggg tgg ata gca agc cct 200
 Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro
 15 20 25 30
 ctg gaa gga ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat aca 248
 Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn Thr
 35 40 45
 cca atc cga acc tac ctg ggg ggt tgt tgc ttt gag gga agt tac gct 296
 Pro Ile Arg Thr Tyr Leu Gly Gly Cys Cys Phe Glu Gly Ser Tyr Ala
 50 55 60
 tat ttt t 303
 Tyr Phe

<210> 310
 <211> 417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 149..415

<221> sig_peptide
 <222> 149..265
 <223> score 11.6

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gag gaa tgt ccc aag cct ttg agt agg gta agc atc atg gct ggc agc 220
Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser Ile Met Ala Gly Ser
-30 -25 -20

-15 -10 -5

cgc ccc tgc atc cct aaa agc ttc ggc tac agc tcg gtg gtg tgt gtc 316
Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val
5 10 15

20
 ctt ggt acc ttc agc cgc tat gag agt aca cgc agt ggc gac gga tgg 412
 Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Asp Gly Trp
 35 40 45

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<210> 311
<211> 246
<212> DNA
<213> Homo sapiens
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```
<221> sig_peptide
<222> 42..152
<223> score 5
      seq PACLSPSPHLSSA/AN
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acc atg gat ctg act gcc atc tac gag gtg agt ccc cgc cgc acg gca 104
Thr Met Asp Leu Thr Ala Ile Tyr Glu Val Ser Pro Arg Arg Thr Ala
-30 -25 -20 150

[illegible]

Ala Asn Ser Ser Pro Gly Arg Leu Pro Pro Phe Ser Asn Trp Gly Ser
 1 5 10 15
 cta gcg ccg cgc cct cca gcc tgg ggc ccc tgc ctc ccg ctc aga c 246
 Leu Ala Pro Arg Pro Pro Ala Trp Gly Pro Cys Leu Pro Leu Arg
 20 25 30

<210> 312
 <211> 441
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 34..441

<221> sig_peptide
 <222> 34..84
 <223> score 8.7
 seq RLVCAFLLAACCC/CP

<400> 312
 actcacttgg ctctcgccct ccggccggga agc atg ggg ctt ccc agg ctg gtc 54
 Met Gly Leu Pro Arg Leu Val
 -15
 tgc gcc ttc ttg ctc gcc gcc tgc tgc tgc tgt cct cgc gtc gcg ggt 102
 Cys Ala Phe Leu Leu Ala Ala Cys Cys Cys Cys Pro Arg Val Ala Gly
 -10 -5 1 5
 gtg ccc gga gag gct gag cag cct gcg cct gag ctg gtg gag gtg gaa 150
 Val Pro Gly Glu Ala Glu Gln Pro Ala Pro Glu Leu Val Glu Val Glu
 10 15 20
 gtg ggc agc aca gcc ctt ctg aag tgc ggc ctc tcc cag tcc caa ggc 198
 Val Gly Ser Thr Ala Leu Leu Lys Cys Gly Leu Ser Gln Ser Gln Gly
 25 30 35
 aac ctc agc cat gtc gac tgg ttt tct gtc cac aag gag aag cgg acg 246
 Asn Leu Ser His Val Asp Trp Phe Ser Val His Lys Glu Lys Arg Thr
 40 45 50
 ctc atc ttc cgt gtg cgc cag ggc cag ggc cag agc gaa cct ggg gag 294
 Leu Ile Phe Arg Val Arg Gln Gly Gln Gly Gln Ser Glu Pro Gly Glu
 55 60 65 70
 tac gag cag cgg ctc agc ctc cag gac aga ggg gct act ctg gcc ctg 342
 Tyr Glu Gln Arg Leu Ser Leu Gln Asp Arg Gly Ala Thr Leu Ala Leu
 75 80 85
 act caa gtc acc ccc caa gac gag cgc atc ttc ttg tgc ang tnr naa 390
 Thr Gln Val Thr Pro Gln Asp Glu Arg Ile Phe Leu Cys Xaa Xaa Xaa
 90 95 100
 gcg ccc tcg gtc cca gga gta ccg cat cca gct ccg cgt cta caa agc 438
 Ala Pro Ser Val Pro Gly Val Pro His Pro Ala Pro Arg Leu Gln Ser
 105 110 115
 tcc 441
 Ser

<210> 313
 <211> 185

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 9..185

<221> sig_peptide
<222> 9..71
<223> score 4
seq AACTAAAPLQAHG/AD

<400> 313
agtgatgg atg atg aga acg aca gcg aga gtc gct gcg tgt act gct gca 50
Met Met Arg Thr Thr Ala Arg Val Ala Ala Cys Thr Ala Ala
-20 -15 -10
gcc cca ttg caa gcc cac ggt gca gac att cag cag gat cca gac agc 98
Ala Pro Leu Gln Ala His Gly Ala Asp Ile Gln Gln Asp Pro Asp Ser
-5 1 5
ctc tgc tct aga agg ctc agc aga gaa gga ctt tct gca rgg cga mtg 146
Leu Cys Ser Arg Arg Leu Ser Arg Glu Gly Leu Ser Ala Xaa Arg Xaa
10 15 20 25
cac caa agc gaa aca gaa gct gaa ctg gaa gcc ccg ggt 185
His Gln Ser Glu Thr Glu Ala Glu Leu Glu Ala Pro Gly
30 35

<210> 314
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..455

<221> sig_peptide
<222> 87..146
<223> score 3.5
seq IVLGTGLTECILS/GI

<400> 314
atctttggc cagtgcggtg gcggcggcga ctgctgcggt gaaggaggag gaggagccga 60
gcgggcgctg gcaccgaggc ctgacc atg gac gag gaa tac gat gtg atc gtg 113
Met Asp Glu Glu Tyr Asp Val Ile Val
-20 -15
ctg ggg acc ggt ctc acc gaa tgc atc ctg tcg ggc atc atg tct gtg 161
Leu Gly Thr Gly Leu Thr Glu Cys Ile Leu Ser Gly Ile Met Ser Val
-10 -5 1 5
aac ggg aag aag gtg ctg cac atg gac cgg aac ccc tac tac ggg ggc 209
Asn Gly Lys Lys Val Leu His Met Asp Arg Asn Pro Tyr Tyr Gly Gly
10 15 20
gag agc tcc tcc atc aca ccc ctg gag gag ctg tat aag cgt ttt cag 257

<220>
 <221> CDS
 <222> 12..206

 <221> sig_peptide
 <222> 12..140
 <223> score 4.1
 seq VLITQLCLGKGQS/EP

<400> 316
 tcaatccttg a atg ctc tgg gag act gat ttg agt acc aat aaa act cca 50
 Met Leu Trp Glu Thr Asp Leu Ser Thr Asn Lys Thr Pro
 -40 -35
 gtc tcc tgc aca gct ggc tct gcg tgt gct ctt tct cta ttg caa ttc 98
 Val Ser Cys Thr Ala Gly Ser Ala Cys Ala Leu Ser Leu Leu Gln Phe
 -30 -25 -20 -15
 cct gtc ttg ata act cag ctc tgt cta ggc aaa ggg caa agt gaa ccc 146
 Pro Val Leu Ile Thr Gln Leu Cys Leu Gly Lys Gly Gln Ser Glu Pro
 -10 -5 1
 att ggg cca tta caa gat ttt gtg tct ttg gaa agc act tca cat ttt 194
 Ile Gly Pro Leu Gln Asp Phe Val Ser Leu Glu Ser Thr Ser His Phe
 5 10 15
 tat tct ttt ttt t 207
 Tyr Ser Phe Phe
 20

<210> 317
 <211> 391
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 149..391

 <221> sig_peptide
 <222> 149..196
 <223> score 6
 seq LTALPLFWIMISA/SR

<400> 317
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 tgagtccaag ttgtctggcg gcttcaggtg gaccagaag acgtcccaa ctcagggaga 120
 ttcagcgatc actcactcgc tgtacaga atg ata ttc ctc acg gca ctg cct 172
 Met Ile Phe Leu Thr Ala Leu Pro
 -15 -10
 ctg ttc tgg att atg att tca gcc tcc cga ggg ggt cac tgg ggt gcc 220
 Leu Phe Trp Ile Met Ile Ser Ala Ser Arg Gly Gly His Trp Gly Ala
 -5 1 5
 tgg atg ccc tcg tcc atc tcg gcc ttc gaa ggc acg tgc gtc tcc atc 268
 Trp Met Pro Ser Ser Ile Ser Ala Phe Glu Gly Thr Cys Val Ser Ile

10	15	20	
ccc tgc cgc ttt gac ttc ccg gat gag ctg cgg ccc gct gtg gtg cat			316
Pro Cys Arg Phe Asp Phe Pro Asp Glu Leu Arg Pro Ala Val Val His			
25	30	35	40
ggt gtc tgg tac ttc aat agc ccc tac ccc aag aac tac ccc ccg gtg			364
Gly Val Trp Tyr Phe Asn Ser Pro Tyr Pro Lys Asn Tyr Pro Pro Val			
45	50	55	
gtc ttc aag tcg cgc acc caa gta gtc			391
Val Phe Lys Ser Arg Thr Gln Val Val			
60	65		

<210> 318
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 203..457

<221> sig_peptide
 <222> 203..256
 <223> score 11.9
 seq ALLFLILANGAQA/FR

<400> 318	
agcctcttcc tctttttttt cccctcctag ccctattcag gcaggagctg ctcttctggg	60
gtatcgcat ccacttaagg atgaggcaga cttgggtgaca agctgggtctg agcagcgtt	120
ccagagccag aactgagccc agtgagagcg caccctgggg cagcctggat tcttgggggtg	180
wccccggcag ccacacacag cc atg cac tac cca act gca ctc ctc ttc ctc	232
Met His Tyr Pro Thr Ala Leu Leu Phe Leu	
-15	-10
atc ctg gcc aat ggg gcc cag gcc ttt cgc atc tgc gcc ttc aat gcc	280
Ile Leu Ala Asn Gly Ala Gln Ala Phe Arg Ile Cys Ala Phe Asn Ala	
-5	1
cag cgg ctg aca ctg gcc aag gtg gcc agg gag cag gtg atg gac acc	328
Gln Arg Leu Thr Leu Ala Lys Val Ala Arg Glu Gln Val Met Asp Thr	
10	15
tta gtt cgg ata ctg gct cgc tgt gac atc atg gtg ctg cag gag gtg	376
Leu Val Arg Ile Leu Ala Arg Cys Asp Ile Met Val Leu Gln Glu Val	
25	30
gtg gac tct tcc ggc agc gcc atc ccg ctc ctg ctt cga gaa ctc aat	424
Val Asp Ser Ser Gly Ser Ala Ile Pro Leu Leu Leu Arg Glu Leu Asn	
45	50
cga ttt gat ggc tct ggg ccc tac agc acc ctg a	458
Arg Phe Asp Gly Ser Gly Pro Tyr Ser Thr Leu	
60	65

<210> 319
 <211> 429
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 99..428

<221> sig_peptide
 <222> 99..152
 <223> score 9.9
 seq SLLLAALLLLLSG/DG

<400> 319
 agctattttca aggcgcgcgc ctcgtggtgg actcaccgct agcccgcagc gctcggtttc 60
 ctggtaattc ttcacctctt ttctcagctc cctgcagc atg ggt gct ggg ccc tcc 116
 Met Gly Ala Gly Pro Ser
 -15
 ttg ctg ctc gcc gcc ctc ctg ctg ctt ctc tcc ggc gac ggc gcc gtg 164
 Leu Leu Leu Ala Ala Leu Leu Leu Leu Ser Gly Asp Gly Ala Val
 -10 -5 1
 cgy tgc gac aca cct gcc aac tgc acc tat ctt gac ctg ctg ggc acc 212
 Arg Cys Asp Thr Pro Ala Asn Cys Thr Tyr Leu Asp Leu Leu Gly Thr
 5 10 15 20
 tgg gtc ttc cag gtg ggc tcc agc ggt tcc cag cgc gat gtc aac tgc 260
 Trp Val Phe Gln Val Gly Ser Ser Gly Ser Gln Arg Asp Val Asn Cys
 25 30 35
 tcg gtt atg gga cca caa gaa aaa aaa gta gtg gtg tay ctt cag aag 308
 Ser Val Met Gly Pro Gln Glu Lys Lys Val Val Val Tyr Leu Gln Lys
 40 45 50
 ctg gat aca gca tat gat gac ctt ggc aat tct ggc cat ttc acc atc 356
 Leu Asp Thr Ala Tyr Asp Asp Leu Gly Asn Ser Gly His Phe Thr Ile
 55 60 65
 att tac aac caa ggc ttt gag att gtg ttg aat gac tac aag tgg ttt 404
 Ile Tyr Asn Gln Gly Phe Glu Ile Val Leu Asn Asp Tyr Lys Trp Phe
 70 75 80
 gcc ttt ttt aag tat aaa gaa gag g 429
 Ala Phe Phe Lys Tyr Lys Glu Glu
 85 90

<210> 320
 <211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 86..325
 <221> sig_peptide
 <222> 86..133
 <223> score 4.6
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<400> 320
 aatttccgcc tctggcgaat ggctcgtctg tagtgcacgc cgcgggcca gctgcgaccc 60

001220" 666E550

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cggccccgcc cccgggaccc cggcc atg gac gaa ctg ttc ccc ctc atc ttc      112
                               Met Asp Glu Leu Phe Pro Leu Ile Phe
                               -15                               -10

ccg gca gag cca gcc cag gcc tct ggc ccc tat gtg gag atc att gag      160
Pro Ala Glu Pro Ala Gln Ala Ser Gly Pro Tyr Val Glu Ile Ile Glu
      -5                               1                               5

cag ccc aag cag cgg ggc atg cgc ttc cgc tac aag tgc gag ggg cgc      208
Gln Pro Lys Gln Arg Gly Met Arg Phe Arg Tyr Lys Cys Glu Gly Arg
10                               15                               20                               25

tcc gcg ggc agc atc cca ggc gag agg agc aca gat acc acc aag acc      256
Ser Ala Gly Ser Ile Pro Gly Glu Arg Ser Thr Asp Thr Thr Lys Thr
      30                               35                               40

cas ccc asc ats aag atc aat ggc tac aca ggn cca ggg aca gtg cgc      304
Xaa Pro Xaa Xaa Lys Ile Asn Gly Tyr Thr Gly Pro Gly Thr Val Arg
      45                               50                               55

atc tmc ctg gtc acc aag gac cc      327
Ile Xaa Leu Val Thr Lys Asp
      60

<210> 321
<211> 442
<212> DNA
<213> Homo sapiens

<220>
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<222> 119..442

<221> sig_peptide
<222> 119..214
<223> score 7.2
      seq YMLVSLLLIGVAA/WG

<400> 321
gtattgggty tggctggcct cgatttaaag agacagaagc tgtcggggtc ctggaagacg      60
gtccccaata ccctccccc aagtccttgg gaccacttgg gtccccagag ctggrgag      118
atg gtt tgt ggc ggc ttt gcc tgc tcc aag aat gcg ctt tgc gct ctc      166
Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Ala Leu Cys Ala Leu
      -30                               -25                               -20

aac gtg gtc tac atg ctg gtg agc ttg ttg ctc att gga gtg gct gct      214
Asn Val Val Tyr Met Leu Val Ser Leu Leu Leu Ile Gly Val Ala Ala
      -15                               -10                               -5

tgg ggc aag ggc ctg ggt ctg gtg tcc agc atc cac atc atc ggc gga      262
Trp Gly Lys Gly Leu Gly Leu Val Ser Ser Ile His Ile Ile Gly Gly
1                               5                               10                               15

gtc att gct gtg gga gtc ttc ctt stc ckt att gca gtg gct gga ctg      310
Val Ile Ala Val Gly Val Phe Leu Xaa Xaa Ile Ala Val Ala Gly Leu
      20                               25                               30

gtg ggt gct gtc aac cac cam caa gtc ctg ctg ttc ttt tac atg atc      358
Val Gly Ala Val Asn His Xaa Gln Val Leu Leu Phe Phe Tyr Met Ile
      35                               40                               45

atc ctt ggt ttg gtc ttc atc ttc caa ttt gta atc tct tgc tca tgt      406
Ile Leu Gly Leu Val Phe Ile Phe Gln Phe Val Ile Ser Cys Ser Cys

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50 55 60 442
 ctg gct att aac gaa gca aac aga cag atg tca tca
 Leu Ala Ile Asn Glu Ala Asn Arg Gln Met Ser Ser
 65 70 75

<210> 322
 <211> 375
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..375

<221> sig_peptide
 <222> 160..282
 <223> score 4.3
 seq VASFFHLFFRVSA/II

<400> 322
 aaaagcggag gtagggccgg actgaggctc ttacagtggc ccctgctggc ccttggtgac 60
 gggtcgcgtc agttccgacc cggacccgta cgctgctgcg ctgacgtggc tccygggaagy 120
 agggctggcg tagggccgcc atgttgcagc aggatagta atg atg aca ctg aag 174
 Met Met Thr Leu Lys
 -40
 atg ttt cac tgt ttt gat gcg gaa gag gag acg act aat aga cca aga 222
 Met Phe His Cys Phe Asp Ala Glu Glu Glu Thr Thr Asn Arg Pro Arg
 -35 -30 -25
 aaa gcc aaa atc aga cat cca gta gca tcg ttt ttc cac tta ttc ttt 270
 Lys Ala Lys Ile Arg His Pro Val Ala Ser Phe Phe His Leu Phe Phe
 -20 -15 -10 -5
 cga gtc agt gca atc atc gtc tat ctt ctc tgt ggg ttg ctc agc agc 318
 Arg Val Ser Ala Ile Ile Val Tyr Leu Leu Cys Gly Leu Leu Ser Ser
 1 5 10
 agc ttt att acc tgt atg gtg aca att atc ttg ttg ttg tcg tgt gac 366
 Ser Phe Ile Thr Cys Met Val Thr Ile Ile Leu Leu Leu Ser Cys Asp
 15 20 25
 ttt tgg gca 375
 Phe Trp Ala
 30

<210> 323
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 141..302

<221> sig_peptide
 <222> 141..227
 <223> score 3.6

seq VMLLVALPCFLQN/CP

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cagtagcaga gtaagcacia ggttttaatc gagttgcata agacaccttt gcatagctat 60
ttaattgccc aatgtaaaac tttaatgcca tttctaatac tkttattcat ttttgaagta 120
tgagtttgta gggacaaaaga atg tat gtt atc gta gac aag acc ccc aga gac 173
Met Tyr Val Ile Val Asp Lys Thr Pro Arg Asp
-25 -20
tct ttt cag cag aaa gtt atg ctt cta gtt gcc tta cca tgt ttc ttg 221
Ser Phe Gln Gln Lys Val Met Leu Leu Val Ala Leu Pro Cys Phe Leu
-15 -10 -5
caa aac tgt cca tgg tcc tca agg gtg ttg gaa aca tta tgt tta tta 269
Gln Asn Cys Pro Trp Ser Ser Arg Val Leu Glu Thr Leu Cys Leu Leu
1 5 10
aat ggg cct ctt ttc ctt tgc tgt gca ctt gat g 303
Asn Gly Pro Leu Phe Leu Cys Cys Ala Leu Asp
15 20 25

<210> 324
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 124..432

<221> sig_peptide
<222> 124..195
<223> score 4.3
seq LXFLGMFLSGMVA/QI

<400> 324
ggscctttgga ttggawagag gagctgggca ggaggcaggg caaggagaaa gctgttcggg 60
ggtcttgtct ggattttgtg tgcctcctcc aatgttcttc tacctctact acaaggatgg 120
gtc atg ttt gtg tct gka aca rcg ttt ttc ttt kcg ctc ckc ttt ctg 168
Met Phe Val Ser Xaa Thr Xaa Phe Phe Phe Xaa Leu Xaa Phe Leu
-20 -15 -10
ggc atg ttc ctc tct ggc atg gtg gct caa att gat gct aac tgg aac 216
Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala Asn Trp Asn
-5 1 5
ttc ctg gat ttt gcc tac cat ttt aca gta ttt gtc ttc tat ttt gga 264
Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe Tyr Phe Gly
10 15 20
gcc ttt tta ttg gaa gca gca gcc aca tcc ctg cat gat ttg cat tgc 312
Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp Leu His Cys
25 30 35
aat aca acc ata acc rgg cag cca ctc ctg agt gat aac cag tat aac 360
Asn Thr Thr Ile Thr Xaa Gln Pro Leu Leu Ser Asp Asn Gln Tyr Asn
40 45 50 55
ata aac gta gca gcc tca att ttt gcc ttt atg acg aca gct tgt tat 408
Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr Ala Cys Tyr

60 65 70 434
 ggt tgc agt ttg ggt ctg gct tta cg
 Gly Cys Ser Leu Gly Leu Ala Leu
 75

<210> 325
 <211> 452
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 277..450

<221> sig_peptide
 <222> 277..333
 <223> score 9.6
 seq FCILLAAVSGAEG/WG

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 aagagcggag gaccaggaac cagagagaga gasagagaaa agagagagga gagacagagc 120
 gcttgggggc gaaaggagag agggagggaa ggggtgggtaa ggaggagaga gcggtctgct 180
 gcaaacccca ggaggagakc ttggagccca agccagaact cgagccctag ccggagccgt 240
 tcacaggagag gcggctgccg agaccgtcag ccctgc atg atg cat ctc cgg ctc 294
 Met Met His Leu Arg Leu
 -15
 ttc tgc atc ctg ctc gcc gcg gtc tca gga gcc gag ggc tgg ggc tac 342
 Phe Cys Ile Leu Leu Ala Ala Val Ser Gly Ala Glu Gly Trp Gly Tyr
 -10 -5 1
 tac ggc tgc nac gag gag ctk gtg ggt ccc ctg tat gca cgc tcc ctg 390
 Tyr Gly Cys Xaa Glu Glu Leu Val Gly Pro Leu Tyr Ala Arg Ser Leu
 5 10 15
 ggc gcc tcc tcc tac tac agt ctc ctt act gcg ccg cga ttc gcc agg 438
 Gly Ala Ser Ser Tyr Tyr Ser Leu Leu Thr Ala Pro Arg Phe Ala Arg
 20 25 30 35
 ctg cac ggc ata ag 452
 Leu His Gly Ile

<210> 326
 <211> 476
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 200..475

<221> sig_peptide
 <222> 200..283
 <223> score 5.5
 seq FLAIVYFCTIVQG/QV

<400> 326
 agaaggagag ggagagagaa agagagagag gctaattaaa aaaggataact ccgaggggaag 60
 agagcaaggg cggtgcgccg ccaaggacca actagcggcg gasttcgatac ttgcctaggc 120
 gcggagagct cccaacctgg gctggaacct tgcccagcac atgtggctgc tacaccccat 180
 gtaaaaagcg gaaaataaaa atg aag att ttc cag cgc aag atg cgg tac tgg 232
 Met Lys Ile Phe Gln Arg Lys Met Arg Tyr Trp
 -25 -20

ttg cnt cca cct ttt ttg gca att gtt tat ttc tgc acc att gtc caa 280
 Leu Xaa Pro Pro Phe Leu Ala Ile Val Tyr Phe Cys Thr Ile Val Gln
 -15 -10 -5
 ggt caa gtg gct cca ccc aca agg tta aga tat aat gta ata tct cat 328
 Gly Gln Val Ala Pro Pro Thr Arg Leu Arg Tyr Asn Val Ile Ser His
 1 5 10 15
 gac agt ata cag att tca tgg aag gct cca aga ggg aaa ttt ggt ggt 376
 Asp Ser Ile Gln Ile Ser Trp Lys Ala Pro Arg Gly Lys Phe Gly Gly
 20 25 30
 tac aaa ctt ctt gtg act cca act tca ggt gga aaa act aac cag ctg 424
 Tyr Lys Leu Leu Val Thr Pro Thr Ser Gly Gly Lys Thr Asn Gln Leu
 35 40 45
 aat ctg cag aac act gca act aaa gca att att caa ggc ctt atg cca 472
 Asn Leu Gln Asn Thr Ala Thr Lys Ala Ile Ile Gln Gly Leu Met Pro
 50 55 60
 gac c 476
 Asp

<210> 327
 <211> 301
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..299
 <221> sig_peptide
 <222> 15..65
 <223> score 3.7
 seq ACLAGWLAWLAWL/AV

<400> 327
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 Met Ala Trp Leu Ala Cys Leu Ala Gly Trp Leu Ala
 -15 -10
 tgg ctg gct tgg ctg gct gtc tgg ctg gat tgg cag gct tgg ctg gat 98
 Trp Leu Ala Trp Leu Ala Val Trp Leu Asp Trp Gln Ala Trp Leu Asp
 -5 1 5 10
 ggc tgg ctt ggc tgg ctt ggc tgg ctc tgg agg tgg ttg cat caa gtg 146
 Gly Trp Leu Gly Trp Leu Gly Trp Leu Trp Arg Trp Leu His Gln Val
 15 20 25
 tgc cgt gta caa tgc cct gtt gcg gtg aga cct ggt gga gca gct gtt 194
 Cys Arg Val Gln Cys Pro Val Ala Val Arg Pro Gly Gly Ala Ala Val
 30 35 40

atg cct ggt gtt cag tgg cag gac agc agt acc ttc ccc cag gct agt	242
Met Pro Gly Val Gln Trp Gln Asp Ser Ser Thr Phe Pro Gln Ala Ser	
45 50 55	
tct gta gca tgg ctt cag ttt ggt ctg gct gct gct gct tct cct ctc	290
Ser Val Ala Trp Leu Gln Phe Gly Leu Ala Ala Ala Ala Ser Pro Leu	
60 65 70 75	
ttc ctc ctc ct	301
Phe Leu Leu	

<210> 328
 <211> 217
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..217

<221> sig_peptide
 <222> 35..76
 <223> score 3.8
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<400> 328	
cttggggtcag ctctgcaaag ggggtgttta ctga atg ctt ctg gta tct gca gcc	55
Met Leu Leu Val Ser Ala Ala	
-10	

ccg ctg ggg ttc gga cag ggg gtc tgg aat agg gct tca caa cta cag	103
Pro Leu Gly Phe Gly Gln Gly Val Trp Asn Arg Ala Ser Gln Leu Gln	
-5 1 5	

cag ggc tas gac cct ctt ggg ctg gaa gga gct gga gag gcc tct gca	151
Gln Gly Xaa Asp Pro Leu Gly Leu Glu Gly Ala Gly Glu Ala Ser Ala	
10 15 20 25	

agc tgt cac agg ctc ttg gtg ctg gca ctg gct cag gct ttc aca cac	199
Ser Cys His Arg Leu Leu Val Leu Ala Leu Ala Gln Ala Phe Thr His	
30 35 40	

aca cac gcg cac aca cac	217
Thr His Ala His Thr His	
45	

<210> 329
 <211> 184
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 32..184

<221> sig_peptide
 <222> 32..139
 <223> score 4.4
 seq WLLFCTNQSLSL/PP

<400> 329
tagtggtttt aattcatcaa tggtctagtt a atg tct acc tca gca cct cct 52
Met Ser Thr Ser Ala Pro Pro
-35 -30
ctt agc cta att tta gga ggt tgc cca att ttg ttt ctt caa ttt tac 100
Leu Ser Leu Ile Leu Gly Gly Cys Pro Ile Leu Phe Leu Gln Phe Tyr
-25 -20 -15
tgg tta ctt ttt tgt aca aat caa tct ctt tct ctc tct cct ccc cac 148
Trp Leu Leu Phe Cys Thr Asn Gln Ser Leu Ser Leu Ser Pro Pro His
-10 -5 1
ctc tca ccc ttg ccc tct cca tct ccc tct ccc gcc 184
Leu Ser Pro Leu Pro Ser Pro Ser Pro Ser Pro Ala
5 10 15

<210> 330
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..281
<221> sig_peptide
<222> 84..161
<223> score 12
seq LLLALLLPTQIYS/SE

<400> 330
accttgccctg cgcccgcccg gagccagcgg ttctccaagc acccagcatc ctgctagacg 60
cgccgcgcac cgacggaggg gac atg ggc aga gca atg gtg gcc agg ctc ggg 113
Met Gly Arg Ala Met Val Ala Arg Leu Gly
-25 -20
ctg ggg ctg ctg ctg ctg gca ctg ctc cta ccc acg cag att tat tcc 161
Leu Gly Leu Leu Leu Leu Ala Leu Leu Leu Pro Thr Gln Ile Tyr Ser
-15 -10 -5
agt gaa aca aca act gga act tca agt aac tcc tcc cag agt act tcc 209
Ser Glu Thr Thr Thr Gly Thr Ser Ser Asn Ser Ser Gln Ser Thr Ser
1 5 10 15
aac tct ggg ttg gcc cca aat cca act aat gcc acc acc aag gcg gct 257
Asn Ser Gly Leu Ala Pro Asn Pro Thr Asn Ala Thr Thr Lys Ala Ala
20 25 30
ggg ggt gcc ctg cag tca aca gcc 281
Gly Gly Ala Leu Gln Ser Thr Ala
35 40

<210> 331
<211> 269
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 1..267

<221> sig_peptide
 <222> 1..120
 <223> score 6.4
 seq RGSLLLAAGATS/LV

<400> 331
 atg aaa gcc ccc tgc tct ggc tct ggt tca gtc tca atg ggg gca ctg 48
 Met Lys Ala Pro Cys Ser Gly Ser Gly Ser Val Ser Met Gly Ala Leu
 -40 -35 -30 -25
 ggg ctg gag ggc agg ggt ggg agg ctc cag ggg agg ggt tcc ctc ctg 96
 Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg Gly Ser Leu Leu
 -20 -15 -10
 cta gct gtg gca gga gcc act tct ctg gtg acc ttg ttg ctg gcg gtg 144
 Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu Leu Leu Ala Val
 -5 1 5
 cct atc act gtc ctg gct gtg ctg gcc tta gtg ccc cag gat cag gga 192
 Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro Gln Asp Gln Gly
 10 15 20
 gga ctg gta acg gag acg gcc gac ccc ggg gca cag gcc cag caa gga 240
 Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln Ala Gln Gln Gly
 25 30 35 40
 ctg ggg ttt cag aag ctg cca gag gag ga 269
 Leu Gly Phe Gln Lys Leu Pro Glu Glu
 45

<210> 332
 <211> 308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 114..308

<221> sig_peptide
 <222> 114..215
 <223> score 7.5
 seq FVFFVFFLRQSLA/LL

<400> 332
 ggctctcggg cctttggcct cagactgagg gctgcactgt tggttccct agttttgagg 60
 ctttcagact tggactgagc cacactaccg gcttctcttt cccagctgg cag atg 116
 Met
 gcc cat tst gcg act ttg cct tgt gat cat gtg agc caa ttc tcc cta 164
 Ala His Xaa Ala Thr Leu Pro Cys Asp His Val Ser Gln Phe Ser Leu
 -30 -25 -20
 ata aac ttt ttt ttt gtt ttt ttt gtt ttt ttt ttg agg cag agt cta 212
 Ile Asn Phe Phe Phe Val Phe Phe Val Phe Phe Leu Arg Gln Ser Leu

-15	-10	-5	
gct ctg ttg ccc agg ctg gag tgc aga ggc acg atc tcg gct cac tgc	260		
Ala Leu Leu Pro Arg Leu Glu Cys Arg Gly Thr Ile Ser Ala His Cys			
1 5 10 15			
aac ctc cac ctc ccg ggt tca cgc cat tct cct gcc tca gcc ccc gcc	308		
Asn Leu His Leu Pro Gly Ser Arg His Ser Pro Ala Ser Ala Pro Ala			
20 25 30			

<210> 333
 <211> 428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 114..428

<221> sig_peptide
 <222> 114..239
 <223> score 8.1
 seq LFCFLLLCLSAAS/LL

<400> 333	
aggcgtctgt gtgcgcgcgcc aagtcggtgg ggcgggggacg cgaggtgtgg atgggggggtc	60
gccttgacct ctgcctcagc cagtagcgca gtctcggcct cgccgttacg gag atg	116
	Met
gtg ccc tgg gtg cgg acg atg ggg cag aag ctg aag cag cgg ctg cga	164
Val Pro Trp Val Arg Thr Met Gly Gln Lys Leu Lys Gln Arg Leu Arg	
-40 -35 -30	
ctg gac gtg gga cgc gag atc tgc cgc cag tac ccg ctg ttc tgc ttc	212
Leu Asp Val Gly Arg Glu Ile Cys Arg Gln Tyr Pro Leu Phe Cys Phe	
-25 -20 -15 -10	
ctg ctg ctc tgt ctc agc gcc gcc tcc ctg ctt ctt aac agg tat att	260
Leu Leu Leu Cys Leu Ser Ala Ala Ser Leu Leu Leu Asn Arg Tyr Ile	
-5 1 5	
cat att tta atg atc ttc tgg tca ttt gtt gct gga gtt gtc aca ttt	308
His Ile Leu Met Ile Phe Trp Ser Phe Val Ala Gly Val Val Thr Phe	
10 15 20	
tac tgc tca cta gga cct gat tct ctc tta cca aat ata ttc ttc aca	356
Tyr Cys Ser Leu Gly Pro Asp Ser Leu Leu Pro Asn Ile Phe Phe Thr	
25 30 35	
ata aaa tac aaa ccc aag cag tta gga ctt cag gaa tta ttt cct caa	404
Ile Lys Tyr Lys Pro Lys Gln Leu Gly Leu Gln Glu Leu Phe Pro Gln	
40 45 50 55	
ggt cat agc tgt gct gtt tgt ggt	428
Gly His Ser Cys Ala Val Cys Gly	
60	

<210> 334
 <211> 167
 <212> DNA
 <213> Homo sapiens

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SECRET

35 40 45 254
 ttc gcc
 Phe Ala
 50

<210> 336
 <211> 174
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 9..173

<221> sig_peptide
 <222> 9..68
 <223> score 7.9
 seq FLFFIYFLRWSLA/LS

<400> 336
 tataatctg atg gct tat tta gtg gtg tat ttt tta ttt ttt att tat ttt 50
 Met Ala Tyr Leu Val Val Tyr Phe Leu Phe Phe Ile Tyr Phe
 -20 -15 -10
 ttg agg tgg agt ctt gct ctg tca ccc agg ctg gag tgc agt ggt gca 98
 Leu Arg Trp Ser Leu Ala Leu Ser Pro Arg Leu Glu Cys Ser Gly Ala
 -5 1 5 10
 atc ttg tct cac tgc aac ctc tgc cac ctg ggt yca cgc aat tct cct 146
 Ile Leu Ser His Cys Asn Leu Cys His Leu Gly Xaa Arg Asn Ser Pro
 15 20 25
 gcc tca gcc tac cta gta gct ggc tgt a 174
 Ala Ser Ala Tyr Leu Val Ala Gly Cys
 30 35

<210> 337
 <211> 284
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 49..282

<221> sig_peptide
 <222> 49..156
 <223> score 7.2
 seq FCFFGFFLRQSFA/LV

<400> 337
 attatatttcc gcagcatgtc agctaagtag acccaatggg gagagaaa atg cct gct 57
 Met Pro Ala
 -35
 ttc ttt ccc tct ttt tct gca ctg cca tat tca ccc cct gcc ttg ccg 105

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Phe Phe Pro Ser Phe Ser Ala Leu Pro Tyr Ser Pro Pro Ala Leu Pro
-30 -25 -20
ggt ttt ttt gtt ttt tgt ttt ttt ggg ttt ttt ttg aga cag agt ttc 153
Gly Phe Phe Val Phe Cys Phe Phe Gly Phe Phe Leu Arg Gln Ser Phe
-15 -10 -5
gct ctt gtt gcc cag gct gga gtg cag tgg tat gat atc agc gga ctg 201
Ala Leu Val Ala Gln Ala Gly Val Gln Trp Tyr Asp Ile Ser Gly Leu
1 5 10 15
caa cct ccg cct ccc agg ttc aag cga cta tcc tac ctc agc ctc cca 249
Gln Pro Pro Pro Pro Arg Phe Lys Arg Leu Ser Tyr Leu Ser Leu Pro
20 25 30
agt agc tgg att aca ggc atg cat cac tat gca ct 284
Ser Ser Trp Ile Thr Gly Met His His Tyr Ala
35 40

<210> 338
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..346

<221> sig_peptide
<222> 152..286
<223> score 4.6
seq LIFCIFSRRGGVSQ/CW

<400> 338
caaaaaaatt agctgggcat tgtggcatgt gcctgtaatc ccagctactc aggaggctga 60
ggcagaagaa ttgcttgaac ctgggatgcg gaggttgcag tgagccgaga tcccactgct 120
gcactccagt ctgggcaaca gtggtgcaat c atg gct cac tgt agc ctt gac 172
Met Ala His Cys Ser Leu Asp
-45 -40
ttc cca ggt tca agc aat tct tgt gcc tca gcc acc caa gta gct gag 220
Phe Pro Gly Ser Ser Asn Ser Cys Ala Ser Ala Thr Gln Val Ala Glu
-35 -30 -25
att aca ggt gtg tgc cac cat gcc cag cta att ttt tgc att ttc agt 268
Ile Thr Gly Val Cys His His Ala Gln Leu Ile Phe Cys Ile Phe Ser
-20 -15 -10
aga ggt gga gtt tcg caa tgt tgg cta ggc aaa ctt gaa tcc tgt tgg 316
Arg Gly Gly Val Ser Gln Cys Trp Leu Gly Lys Leu Glu Ser Cys Trp
-5 1 5 10
cta gga tcc tgt tgg cct gag tcc ttg aac tc 348
Leu Gly Ser Cys Trp Pro Glu Ser Leu Asn
15 20

<210> 339
<211> 504
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 16..504

<221> sig_peptide
 <222> 16..99
 <223> score 4.2
 seq CLETLAVPSECSA/FS

<400> 339
 cctttgtcat cagat atg ctc att atg ccc aaa gct ttg aaa gaa gag agc 51
 Met Leu Ile Met Pro Lys Ala Leu Lys Glu Glu Ser
 -25 -20
 gag gat acc tgc cta gag acc ctg gct gtt ccc tct gaa tgc tct gct 99
 Glu Asp Thr Cys Leu Glu Thr Leu Ala Val Pro Ser Glu Cys Ser Ala
 -15 -10 -5
 ttc tca gag aat att gag gat cct gga gag ggt ccc tca aat cca tgc 147
 Phe Ser Glu Asn Ile Glu Asp Pro Gly Glu Gly Pro Ser Asn Pro Cys
 1 5 10 15
 tta gat acc agc cag aat caa cct tcc atg gaa tca gar atg ggg gct 195
 Leu Asp Thr Ser Gln Asn Gln Pro Ser Met Glu Ser Glu Met Gly Ala
 20 25 30
 gca gca tgc cct ggg agt tgt tca agg gaa tgc gag gtt tca ttt agt 243
 Ala Ala Cys Pro Gly Ser Cys Ser Arg Glu Cys Glu Val Ser Phe Ser
 35 40 45
 gcc tct aac cct gtc tgg gat tat tca cat ctt atg agt agt gaa aga 291
 Ala Ser Asn Pro Val Trp Asp Tyr Ser His Leu Met Ser Ser Glu Arg
 50 55 60
 aat ttt cag aga ctg gat ttt gaa gaa ctt gag gaa gaa ggt caa gcc 339
 Asn Phe Gln Arg Leu Asp Phe Glu Glu Leu Glu Glu Glu Gly Gln Ala
 65 70 75 80
 tct gac aag tca ttg ctt cca agt cgc att aat ctt tct cta tta gat 387
 Ser Asp Lys Ser Leu Leu Pro Ser Arg Ile Asn Leu Ser Leu Leu Asp
 85 90 95
 gat gat gag gaa gac gaa gaa ctt cca cgc ttc att tta cat tat gag 435
 Asp Asp Glu Glu Asp Glu Glu Leu Pro Arg Phe Ile Leu His Tyr Glu
 100 105 110
 aca cat ccg ttt gaa aca gga atg ata gtc tgg ttt aaa tat cag aaa 483
 Thr His Pro Phe Glu Thr Gly Met Ile Val Trp Phe Lys Tyr Gln Lys
 115 120 125
 tat cca ttt tgg cna gcg gaa 504
 Tyr Pro Phe Trp Xaa Ala Glu
 130 135

<210> 340
 <211> 308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 77..307

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<221> sig_peptide
 <222> 77..169
 <223> score 4.5
 seq VAFGLYNPSLCHA/CT

<400> 340
 ctgacgtgtc tttgctcctg ataccatttt tccccacacc acaccactgt cctctgtgcc 60
 tgtggaaacc actcaa atg cct ctc ccc aag cct tct ttc agt aac aac cat 112
 Met Pro Leu Pro Lys Pro Ser Phe Ser Asn Asn His
 -30 -25 -20
 ctc atc cgg ttg att act gta gct ttc ggc ctg tat aac ccc tcc tta 160
 Leu Ile Arg Leu Ile Thr Val Ala Phe Gly Leu Tyr Asn Pro Ser Leu
 -15 -10 -5
 tgt cat gcc tgt acc aga tgt tcc act gca tct gta tcc cac cag att 208
 Cys His Ala Cys Thr Arg Cys Ser Thr Ala Ser Val Ser His Gln Ile
 1 5 10
 gca cat tcc ccg aag cag aaa cct tct aat ctg ggg gcc att cag ggc 256
 Ala His Ser Pro Lys Gln Lys Pro Ser Asn Leu Gly Ala Ile Gln Gly
 15 20 25
 cta gca cag tgc cta gta gag cat atg tgt tgt aga ata aat ata gac 304
 Leu Ala Gln Cys Leu Val Glu His Met Cys Cys Arg Ile Asn Ile Asp
 30 35 40 45
 aca t 308
 Thr

<210> 341
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..261

<221> sig_peptide
 <222> 55..150
 <223> score 3.8
 seq IRTATLVISLARG/WQ

<400> 341
 acactcattt tagccagtgt ccaggctatc agcagagaaa gacaggtggg cagc atg 57
 Met
 gct ccg ggc gaa aag gaa agc ggg gag ggc cca gcc aag agc gcc ctc 105
 Ala Pro Gly Glu Lys Glu Ser Gly Glu Gly Pro Ala Lys Ser Ala Leu
 -30 -25 -20
 cgg aag ata cgc aca gcc acc ctg gtc atc agc ttg gcc cga ggt tgg 153
 Arg Lys Ile Arg Thr Ala Thr Leu Val Ile Ser Leu Ala Arg Gly Trp
 -15 -10 -5 1
 cag cag tgg gcg aat gag aac agc atc agg cag gcc cag gag cct aca 201
 Gln Gln Trp Ala Asn Glu Asn Ser Ile Arg Gln Ala Gln Glu Pro Thr
 5 10 15
 ggc tgg ctg ccg gga ggg acc cag gac tca cct caa gct cct aaa cca 249

004220"666T560

Gly Trp Leu Pro Gly Gly Thr Gln Asp Ser Pro Gln Ala Pro Lys Pro
20 25 30
atc aca ccc cgg
Ile Thr Pro Arg
35

261

<210> 342
<211> 306
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..306

<221> sig_peptide
<222> 91..198
<223> score 6.7
seq LELLSSGCLPASA/SQ

<400> 342
aaaagaaaga gagaaaagaa gatgacattg aatgcaacca cccactgcta aatttgattg 60
gctaaaaaat tattattatt attacttgag atg gag tct cac ctg tct att ttt 114
Met Glu Ser His Leu Ser Ile Phe
-35 -30
gta ttt tta gta gag aca agt ttt tgc cat gtt ggc cag gct ggt ctc 162
Val Phe Leu Val Glu Thr Ser Phe Cys His Val Gly Gln Ala Gly Leu
-25 -20 -15
gaa ctc ctg agc tgc ggt tgt ctg cct gcc tca gcc tcc cag agt gct 210
Glu Leu Leu Ser Ser Gly Cys Leu Pro Ala Ser Ala Ser Gln Ser Ala
-10 -5 1
ggg att aca ggt gtg agc cac cgc acc cag cct gac tgg cta aaa aaa 258
Gly Ile Thr Gly Val Ser His Arg Thr Gln Pro Asp Trp Leu Lys Lys
5 10 15 20
att ttt tta ata aaa aaa aga aaa gaa aat tat att gag aag ggg aga 306
Ile Phe Leu Ile Lys Lys Arg Lys Glu Asn Tyr Ile Glu Lys Gly Arg
25 30 35

<210> 343
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 135..407

<221> sig_peptide
<222> 135..194
<223> score 7.9
seq TVTLALVLAWA/ME

<400> 343
gcagctggcg caagtagcct agctggagag gctcacccca ggaaggaggg aggccaccga 60
cctactgggc cgacggactc ccacacagtt cctgagctgg tgccaggcag gtgacacctc 120
ctgcagcccc cagc atg cgg gca ggc cca ggc ccc acc gtt aca ttg gcc 170
Met Arg Ala Gly Pro Gly Pro Thr Val Thr Leu Ala
-20 -15 -10
ctg gtg ctg gcg gtg gca tgg gcc atg gag ctc aag ccc aca gca cca 218
Leu Val Leu Ala Val Ala Trp Ala Met Glu Leu Lys Pro Thr Ala Pro
-5 1 5
ccc atc ttc act ggc cgg ccc ttt gtg gta gcg tgg gac gtg ccc aca 266
Pro Ile Phe Thr Gly Arg Pro Phe Val Val Ala Trp Asp Val Pro Thr
10 15 20
cag gac tgt ggc cca cgc ctc aag gtg cca ctg gac ctg aat gcc ttt 314
Gln Asp Cys Gly Pro Arg Leu Lys Val Pro Leu Asp Leu Asn Ala Phe
25 30 35 40
gat gtg cag gcc tca cct aat gag ggt ttt gtg aac cag aat att acc 362
Asp Val Gln Ala Ser Pro Asn Glu Gly Phe Val Asn Gln Asn Ile Thr
45 50 55
atc ttc tac cgc gac cgt cta ggc ctg tat cca cgc ttc gat tct 407
Ile Phe Tyr Arg Asp Arg Leu Gly Leu Tyr Pro Arg Phe Asp Ser
60 65 70

<210> 344
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..301
<221> sig_peptide
<222> 26..103
<223> score 6.5
seq LALGSAGLLWCLA/GF

<400> 344
gcagaccggc cgccgcttca ccggc atg gtc ttc gcc acc atc ggt ttc tcg 52
Met Val Phe Ala Thr Ile Gly Phe Ser
-25 -20
ctg aag tcg ggc ctg gcc ctt ggc tcg gcg ggc ctg ctg tgg tgc ctg 100
Leu Lys Ser Gly Leu Ala Leu Gly Ser Ala Gly Leu Leu Trp Cys Leu
-15 -10 -5
gcc ggt ttc ttc ggc tac gac aca cag cag ccc acg gca ccc aac gcc 148
Ala Gly Phe Phe Gly Tyr Asp Thr Gln Gln Pro Thr Ala Pro Asn Ala
1 5 10 15
atc gag ggc tac cgc gtc atg tcc agc ttc ggc gtc ggc gcg ctg ttc 196
Ile Glu Gly Tyr Arg Val Met Ser Ser Phe Gly Val Gly Ala Leu Phe
20 25 30
gcc gcc tgc acg atc tgc ctg ctg gcs rac aag ctg aac aag cag acg 244
Ala Ala Cys Thr Ile Cys Leu Leu Ala Xaa Lys Leu Asn Lys Gln Thr
35 40 45
acg ctg aag atg gcc gac gac ctc gcc caa cgg cgc cag cag gcc gac 292

Thr Leu Lys Met Ala Asp Asp Leu Ala Gln Arg Arg Gln Gln Ala Asp
 50 55 60
 ctt gcg ccg gc
 Leu Ala Pro
 65

303

<210> 345
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 197..367

<221> sig_peptide
 <222> 197..256
 <223> score 4.3
 seq FNFLFLVQLCILA/CD

<400> 345
 agataaattg gggaattcta gggaaaccct tgaataccaa gatagaaaac taaagttttt 60
 acttcatttg gtcattggaa acttgactg agcatgggag tcaataatta gaagcaagtk 120
 aaattcaaaa agtcgaaccc cattcataaa accagctgat agtctgaaaa tacgctttga 180
 gctaagcaaa gaatac atg ttg aca aat cgt aac tac ttt aac ttc ctt ttt 232
 Met Leu Thr Asn Arg Asn Tyr Phe Asn Phe Leu Phe
 -20 -15 -10
 ctt gta caa ttg tgc atc ctg gct tgt gac aat gca tac ctt cag tcg 280
 Leu Val Gln Leu Cys Ile Leu Ala Cys Asp Asn Ala Tyr Leu Gln Ser
 -5 1 5
 tgt ccc ctc acc tca aag act cct ctg tta caa acc cac tct gct ctt 328
 Cys Pro Leu Thr Ser Lys Thr Pro Leu Leu Gln Thr His Ser Ala Leu
 10 15 20
 ttc tat aat agt aca tat ggg att ttc cta ctc cta gga gt 369
 Phe Tyr Asn Ser Thr Tyr Gly Ile Phe Leu Leu Leu Gly
 25 30 35

<210> 346
 <211> 393
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..392

<221> sig_peptide
 <222> 60..143
 <223> score 9.8
 seq LLPLSLLVTSIQG/HL

<400> 346

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ctttttctag ccargctctc aactgtctcc tgcgttgctg ggaagttctg gaaggaagc      59
atg tgc tcc aga ggt tgg gat tgc tgt ctg gct ctg gaa ttg cta ctg      107
Met Cys Ser Arg Gly Trp Asp Ser Cys Leu Ala Leu Glu Leu Leu Leu
      -25                      -20                      -15

ctg cct ctg tca ctc ctg gtg acc agc att caa ggt cac ttg gta cat      155
Leu Pro Leu Ser Leu Leu Val Thr Ser Ile Gln Gly His Leu Val His
      -10                      -5                      1

atg acc gtg gtc tcc ggc agc aac gtg act ctg aac atc tct gag agc      203
Met Thr Val Val Ser Gly Ser Asn Val Thr Leu Asn Ile Ser Glu Ser
5                      10                      15                      20

ctg cct gag aac tac aaa caa cta acc tgg ttt tat act ttc gac cag      251
Leu Pro Glu Asn Tyr Lys Gln Leu Thr Trp Phe Tyr Thr Phe Asp Gln
      25                      30                      35

aag att gta gaa tgg gat tcc aga rra tct aag tac ttt gaa tcc aaa      299
Lys Ile Val Glu Trp Asp Ser Arg Xaa Ser Lys Tyr Phe Glu Ser Lys
      40                      45                      50

ttt aaa ggc agg gtc aga ctt gat cct cag agt ggt gca ctg tac atc      347
Phe Lys Gly Arg Val Arg Leu Asp Pro Gln Ser Gly Ala Leu Tyr Ile
      55                      60                      65

tct aag gtc cag aaa gag gac aac agc asc tac atc atg agg gtg t      393
Ser Lys Val Gln Lys Glu Asp Asn Ser Xaa Tyr Ile Met Arg Val
      70                      75                      80

<210> 347
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 229..396

<221> sig_peptide
<222> 229..285
<223> score 4.8
      seq ATYLVQSSACCPA/IV

<400> 347
ccacgggggac aaggactgck cccacgatgg tgctcctgcc avgccccagc tgbacgggga      60
gtcctgtggg gccaggcct tgaacagcca catgcctgct gagaccgagg agctgggacg      120
gtggggacca cagagagcaa cctgattacc tccctgcttg ggctgtgcca gagcaagaag      180
agtcgggtgg ccttgaaggc ccaggagaac ctgctgctcc tgggtgagc atg gcc tcc      237
      Met Ala Ser

cca gca gct gcc acc tac ctg gta cag agc agc gcc tgc tgc cct gcg      285
Pro Ala Ala Ala Thr Tyr Leu Val Gln Ser Ser Ala Cys Cys Pro Ala
      -15                      -10                      -5

atc gtc cgg cac ctt tgc cag tbg tac cgg tcc atg cct gtc ttc ctg      333
Ile Val Arg His Leu Cys Gln Xaa Tyr Arg Ser Met Pro Val Phe Leu
1                      5                      10                      15

gac ccc gca gas att gcc acc tta gag ggc atc agc tgg agg tta ccc      381
Asp Pro Ala Xaa Ile Ala Thr Leu Glu Gly Ile Ser Trp Arg Leu Pro
      20                      25                      30

agt gcc ccg tct gat ga      398

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Ser Ala Pro Ser Asp
35

<210> 348
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 130..321

<221> sig_peptide
<222> 130..171
<223> score 4.4
seq HIFFLSFFIETDS/HS

<400> 348
aacacaaaac cagcagccga cgccccagac acagaggcgt tgagggcggtg gggccaacac 60
gcttgcccc ctaacgggtt gctgaataat cactaacaat gaactagata gattactaag 120
aaacaagac atg cat att ttc ttt ctt tct ttt ttt att gag acg gac tct 171
Met His Ile Phe Phe Leu Ser Phe Phe Ile Glu Thr Asp Ser
-10 -5
cac tct gtc gcc cag gct gga gts cag trg cgc gat ctc ggc tca ctg 219
His Ser Val Ala Gln Ala Gly Val Gln Xaa Arg Asp Leu Gly Ser Leu
1 5 10 15
caa gct ccg ctt ccc ggg ttc acg cca ttc tcc tgc stc agc ctc ccg 267
Gln Ala Pro Leu Pro Gly Phe Thr Pro Phe Ser Cys Xaa Ser Leu Pro
20 25 30
agt agc tgg gac tac agg tgc cca yca cca tgc ccg gct aat ttt ttt 315
Ser Ser Trp Asp Tyr Arg Cys Pro Xaa Pro Cys Pro Ala Asn Phe Phe
35 40 45
tgc att 321
Cys Ile
50

<210> 349
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..360

<221> sig_peptide
<222> 16..84
<223> score 3.7
seq FLPLXRAFACRG/CQ

<400> 349
agggggcggtg gggcc atg gtg gtc ttg cgg gcg ggg aag aag acc ttt ctc 51

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Met Val Val Leu Arg Ala Gly Lys Lys Thr Phe Leu
-20 -15
ccc cct ctm wgc cgc gcc ttc gcc tgc cgc ggc tgt caa ctc gct ccg 99
Pro Pro Leu Xaa Arg Ala Phe Ala Cys Arg Gly Cys Gln Leu Ala Pro
-10 -5 1 5
gag cgc ggc gcc gag cgc agg gat aca gcg ccc agc ggg gtc tca aga 147
Glu Arg Gly Ala Glu Arg Arg Asp Thr Ala Pro Ser Gly Val Ser Arg
10 15 20
ttc tgc cct cca aga aag tct tgc cat gat tgg ata gga ccc cca gat 195
Phe Cys Pro Pro Arg Lys Ser Cys His Asp Trp Ile Gly Pro Pro Asp
25 30 35
aaa tat tca aac ctt cga cct gtt cac ttt tac ata cct gaa aat gaa 243
Lys Tyr Ser Asn Leu Arg Pro Val His Phe Tyr Ile Pro Glu Asn Glu
40 45 50
tct cca ttg gaa caa aag ctt aga aaa tta aga caa gaa aca caa gaa 291
Ser Pro Leu Glu Gln Lys Leu Arg Lys Leu Arg Gln Glu Thr Gln Glu
55 60 65
tgg aat caa cag ttc tgg gca aac cag aat ttg act ttt agt aag gaa 339
Trp Asn Gln Gln Phe Trp Ala Asn Gln Asn Leu Thr Phe Ser Lys Glu
70 75 80 85
aaa gaa gaa ttt att cac tca 360
Lys Glu Glu Phe Ile His Ser
90

<210> 350
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 139..303

<221> sig_peptide
<222> 139..240
<223> score 3.8
seq RWASSCLHPSARS/SN

<400> 350
agcccaaggt gctgccgttg cccgtacaac tcggacttgc tgttgctcga gccgcgtctg 60
cacgggtctc ggaccgagcg gagtccmagc ctccggtccc gagccacct tcgctcgcc 120
cttgcccagc ctgcggtg atg gag gcg gcc acc aca ctg cac cca ggc ccg 171
Met Glu Ala Ala Thr Thr Leu His Pro Gly Pro
-30 -25
cgc ccg gcg ctg ccc ctc ggg gcc cgg gcc cgc tgg gcg agt tcc tgc 219
Arg Pro Ala Leu Pro Leu Gly Ala Arg Ala Arg Trp Ala Ser Ser Cys
-20 -15 -10
ctc cac ccg agt gcc cgg tct tcg aac cca gct ggg aag agt tcg cgg 267
Leu His Pro Ser Ala Arg Ser Ser Asn Pro Ala Gly Lys Ser Ser Arg
-5 1 5
acc cct tsg ctt tca tcc aca aga tcc ggc ccg ggg 303
Thr Pro Xaa Leu Ser Ser Thr Arg Ser Gly Pro Gly
10 15 20

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<210> 351
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 70..375

<221> sig_peptide
 <222> 70..180
 <223> score 8.5
 seq LLVLLLYAPVGFC/LL

<400> 351
 aagagcscct gcggccgggc gcgaaaatgg cggcggcggc gacggccngg cgctcctgaa 60
 gcagcagtt atg gag ctt ccc tca ggg ccg ggg ccg gag cgg ctc ttt gac 111
 Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp
 -35 -30 -25
 tcg cac cgg ctt ccg ggt gac tgc ttc cta ctg ctc gtg ctg ctg ctc 159
 Ser His Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu
 -20 -15 -10
 tac gcg cca gtc ggg ttc tgc ctc ctc gtc ctg sgc ctc ttt ctc ggg 207
 Tyr Ala Pro Val Gly Phe Cys Leu Leu Val Leu Xaa Leu Phe Leu Gly
 -5 1 5
 atc cac gtc ttc ctg gtc agc tgc gcg ctg cca gac agc gtc ctt cgc 255
 Ile His Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg
 10 15 20 25
 aga ttc gta gtg cgg acc atg tgt gcg gtg cta ggg ctc gtg gcc cgg 303
 Arg Phe Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg
 30 35 40
 cag gag gac tcc gga ctc cgg gat cac agt gtc agg gtc ctc att tcc 351
 Gln Glu Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser
 45 50 55
 aac cat gtg aca cct ttc gac cac ca 377
 Asn His Val Thr Pro Phe Asp His
 60 65

<210> 352
 <211> 202
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 19..201

<221> sig_peptide
 <222> 19..78
 <223> score 10.5
 seq PLALCLLAAPASA/LV

<400> 352
gacccggccg cgcgcgcc atg cag ccc tcc agc ctt ctg ccg ctc gcc ctc 51
Met Gln Pro Ser Ser Leu Leu Pro Leu Ala Leu
-20 -15 -10
tgc ctg ctg gct gca ccc gcc tcc gcg ctc gtc agg atc ccg ctg cac 99
Cys Leu Leu Ala Ala Pro Ala Ser Ala Leu Val Arg Ile Pro Leu His
-5 1 5
aag ttc acg tcc atc cgc cgg acc atg tcg gag gtt ggg ggc tct gtg 147
Lys Phe Thr Ser Ile Arg Arg Thr Met Ser Glu Val Gly Gly Ser Val
10 15 20
gag gac ctg att gcc aaa ggc ccc tcc cac aca cac cca cac act cgc 195
Glu Asp Leu Ile Ala Lys Gly Pro Ser His Thr His Pro His Thr Arg
25 30 35
cca cca t 202
Pro Pro
40

<210> 353
<211> 377
<212> DNA
<213> Homo sapiens

<220>
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<222> 222..377
<221> sig_peptide
<222> 222..296
<223> score 6.5
seq LGSLSXVWPAWP/CR

<400> 353
tgataagaaa gttcaaagtt tctcttcctt gctttgttgt gtgkdctaatt tcttttctgc 60
ccatccccca gtaaagaaaa ggctcagtat gatttcttga atagattgtt taagctattt 120
tcaaaacagg acttggtcag gggccgaagt gtgccctttg ctgcctctcc ctctgccctt 180
tgggatcacc ccagccacaa gcccttcgag grmcctatac c atg gcc cac ctt gga 236
Met Ala His Leu Gly
-25
gca gag agc caa gca tct tcc ctg gga agt ctt tct gky ywa gtc tgg 284
Ala Glu Ser Gln Ala Ser Ser Leu Gly Ser Leu Ser Xaa Xaa Val Trp
-20 -15 -10 -5
cca gcc tgg ccc tgc agg tct ccc atg aag gcc acc cca tgg tct gat 332
Pro Ala Trp Pro Cys Arg Ser Pro Met Lys Ala Thr Pro Trp Ser Asp
1 5 10
ggg cat gaa gca tct mag amt cct tgg caa aaa acg gag tcc gca 377
Gly His Glu Ala Ser Xaa Xaa Pro Trp Gln Lys Thr Glu Ser Ala
15 20 25

<210> 354
<211> 199
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> 40..198

<221> sig_peptide

<222> 40..81

<223> score 3.8

seq YCFFAKFVSLSHS/LP

<400> 354

ggctgggatt acagggcgtga gccaccgcac acagccgac atg tac tgt ttc ttt 54
Met Tyr Cys Phe Phe

-10
gct aaa ttt gtt tcc ctt tct cac tcc cta cct gat gaa aag cac cca 102
Ala Lys Phe Val Ser Leu Ser His Ser Leu Pro Asp Glu Lys His Pro

-5 1 5
ttg ttt acc cga aag tcc aaa cct agg gtt tca ccc cag aca ttt ccc 150
Leu Phe Thr Arg Lys Ser Lys Pro Arg Val Ser Pro Gln Thr Phe Pro

10 15 20
act tat aca tcc atg tcc ttc ctg cct tcc cca cca gtt cag ccc caa a 199
Thr Tyr Thr Ser Met Ser Phe Leu Pro Ser Pro Pro Val Gln Pro Gln

25 30 35
<210> 355
<211> 390
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> 91..390

<221> sig_peptide

<222> 91..138

<223> score 10.9

seq RVLLLTALTLCCHG/FN

<400> 355

ccttcttttgc tttggtggt tccttgtggt tcctcagtgg tgccctgcaac ccttggttca 60
cctccttcca ggttctggt ccttcagcc atg gct ctc aga gtc ctt ctg tta 114
Met Ala Leu Arg Val Leu Leu Leu

-15 -10
aca gcc ttg acc tta tgt cat ggg ttc aac ttg gac act gaa aac gca 162
Thr Ala Leu Thr Leu Cys His Gly Phe Asn Leu Asp Thr Glu Asn Ala

-5 1 5
atg acc ttc caa gag aac gca agg ggc ttc ggg cag agc gtg gtc cag 210
Met Thr Phe Gln Glu Asn Ala Arg Gly Phe Gly Gln Ser Val Val Gln

10 15 20
ctt cag gga tcc agg gtg gtg gtt gga gcc ccc cag gag ata gtg gct 258
Leu Gln Gly Ser Arg Val Val Val Gly Ala Pro Gln Glu Ile Val Ala

25 30 35 40

004220" 666ET560

<213> Homo sapiens

<220>

<221> CDS

<222> 31..198

<221> sig_peptide

<222> 31..90

<223> score 8.4

seq FSLTVLFLRQSFA/HV

<400> 357

aatgatgttt	tatttaggaa	agtaaataca	atg	agt	agg	act	cag	ctc	cag	ttt	54
			Met	Ser	Arg	Thr	Gln	Leu	Gln	Phe	
			-20				-15				
tct	ctt	act	ggt	ttg	ttt	ttg	aga	cag	agt	ttc	102
Ser	Leu	Thr	Val	Leu	Phe	Leu	Arg	Gln	Ser	Phe	
			-10			-5				1	
gct	gga	gtk	cag	kkg	gcw	tgg	tct	tgg	atc	act	150
Ala	Gly	Val	Gln	Xaa	Ala	Trp	Ser	Trp	Ile	Thr	
5				10				15		20	
cag	ggt	caa	gct	att	gtc	ctg	cct	cag	ccc	cca	198
Gln	Val	Gln	Ala	Ile	Val	Leu	Pro	Gln	Pro	Pro	
			25					30		35	

<210> 358

<211> 295

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 34..294

<221> sig_peptide

<222> 34..102

<223> score 4.6

seq LELLTSGGSPASA/SQ

<400> 358

ccatgcccg	ctaattgtgt	atTTTTtagta	gag	atg	ggg	ttt	ctc	cat	ggt	ggt	54
			Met	Gly	Phe	Leu	His	Val	Gly		
			-20								
cag	gct	ggt	ctc	gaa	ctc	ctg	acc	tca	ggt	gga	102
Gln	Ala	Gly	Leu	Glu	Leu	Leu	Thr	Ser	Gly	Gly	
			-15			-10				-5	
tcc	caa	aat	gct	gga	att	aca	ggc	atg	agc	cac	150
Ser	Gln	Asn	Ala	Gly	Ile	Thr	Gly	Met	Ser	His	
1			5					10		15	
ttt	ctt	ttt	tta	ata	cag	aat	ctc	act	ctg	tca	198
Phe	Leu	Phe	Leu	Ile	Gln	Asn	Leu	Thr	Leu	Ser	
			20					25		30	

004220"666E"560

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agt ggt gca gtc tca gct cac tgc aac ttc tgc ctt tgg aac tca tcc      246
Ser Gly Ala Val Ser Ala His Cys Asn Phe Cys Leu Trp Asn Ser Ser
      35              40              45
tcc cac ctt agt ctc ctg agt agc tgg gac tac agg tat gta cca cca c      295
Ser His Leu Ser Leu Leu Ser Ser Trp Asp Tyr Arg Tyr Val Pro Pro
      50              55              60
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<210> 359
<211> 293
<212> DNA
<213> Homo sapiens

<220>
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<222> 106..291

<221> sig_peptide
<222> 106..180
<223> score 4
seq LLQELGLCMCLLS/AE

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<400> 359
tatttttagt agaatgggg tttcaccatg ttggccagga tgatctcgat ctcttgatct      60
tgtgatccgc ccaactcggc ctcccaaagt cctgggatta caggc atg agc cac tgc      117
                                   Met Ser His Cys
                                   -25
gcc cag ccc aaa gcc tgc cct gag ctt ctg cag gag ctt ggc ctc tgc      165
Ala Gln Pro Lys Ala Cys Pro Glu Leu Leu Gln Glu Leu Gly Leu Cys
      -20              -15              -10
atg tgc ctt ctc agc gca gag ccc agc ctg cat ccc tgg cgt tgg ctg      213
Met Cys Leu Leu Ser Ala Glu Pro Ser Leu His Pro Trp Arg Trp Leu
      -5              1              5              10
cgc ccc ttg cac aca cac aac ctc ctg ggc cct cca ggg gaa gtg ttc      261
Arg Pro Leu His Thr His Asn Leu Leu Gly Pro Pro Gly Glu Val Phe
              15              20              25
ttc cca ttc ctg agt gcc aag ccc ccg ctc ta      293
Phe Pro Phe Leu Ser Ala Lys Pro Pro Leu
      30              35
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<210> 360
<211> 189
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..189

<221> sig_peptide
<222> 16..102
<223> score 5.9
seq FSYISXFLSPVCG/CS

<400> 360
tcaaaattct ctttg atg aaa tgt tta aaa gtg aac cct ttt tta ttt ctg 51
Met Lys Cys Leu Lys Val Asn Pro Phe Leu Phe Leu
-25 -20
gtw ttt aat ttc ttt tcc tac atc agt kgc ttt ttg tca cca gta tgt 99
Val Phe Asn Phe Phe Ser Tyr Ile Ser Xaa Phe Leu Ser Pro Val Cys
-15 -10 -5
gga tgt tct gtc tgt aat tta aaa cac tgg gag aat gag ctt cta ttt 147
Gly Cys Ser Val Cys Asn Leu Lys His Trp Glu Asn Glu Leu Leu Phe
1 5 10 15
cct tct ccc cac ttt ttg cca tat aaa ttt ttn ttt ctt ttt 189
Pro Ser Pro His Phe Leu Pro Tyr Lys Phe Xaa Phe Leu Phe
20 25

<210> 361
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 55..303
<221> sig_peptide
<222> 55..162
<223> score 7.4
seq LCLLGSSDSPASA/SR

<400> 361
tatttgaggg tttgtttctg gcttctctat tcttgctttt tttttcattt ttgc atg 57
Met
ggg gga tgg att ctc gct ctg tca tcc aag ctg gag tgc agc agt kag 105
Gly Gly Trp Ile Leu Ala Leu Ser Ser Lys Leu Glu Cys Ser Ser Xaa
-35 -30 -25 -20
atc ttg gct cac tgc aac ctc tgc ctc ctg ggt tca agt gat tct cct 153
Ile Leu Ala His Cys Asn Leu Cys Leu Leu Gly Ser Ser Asp Ser Pro
-15 -10 -5
gcc tca gcc tcc cga gta gct ggg att aca ggc atg tgc cac cat gcc 201
Ala Ser Ala Ser Arg Val Ala Gly Ile Thr Gly Met Cys His His Ala
1 5 10
tgg cta att ttt gta ttt tta gta gag atg ggg ttt cac cac gtt agt 249
Trp Leu Ile Phe Val Phe Leu Val Glu Met Gly Phe His His Val Ser
15 20 25
cag tct ggt ctc aaa ctc ctg acc tca agc aat ctg ccc gcc tcg gcc 297
Gln Ser Gly Leu Lys Leu Leu Thr Ser Ser Asn Leu Pro Ala Ser Ala
30 35 40 45
tcc cat 303
Ser His

<210> 362
<211> 202
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 24..200

<221> sig_peptide

<222> 24..80

<223> score 8.2

seq QVLALVLVAALWG/GT

<400> 362

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aagtagaaga cagcggcggtt gcc atg gcg gcg tct ctg ggg cag gtg ttg gct      53
                        Met Ala Ala Ser Leu Gly Gln Val Leu Ala
                        -15                               -10

ctg gtg ctg gtg gcc gct ctg tgg ggt ggc acg cag ccg ctg ctg aag      101
Leu Val Leu Val Ala Ala Leu Trp Gly Gly Thr Gln Pro Leu Leu Lys
                        -5                               1               5

cgg gcc tcc gcc ggc ctg cag cgg gtt cat gag ccg acc tgg gcc cag      149
Arg Ala Ser Ala Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala Gln
                        10                               15               20

cag ttg cta cag gag atg aag acc ctc ttc ttg aat act gag tac ctg      197
Gln Leu Leu Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu
                        25                               30               35

atg cc
Met
40
202

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<210> 363

<211> 243

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 79..243

<221> sig_peptide

<222> 79..150

<223> score 3.8

seq XVFXFXFLRXRX/XX

<400> 363

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tttttgacat cytattaata gccattctgg ctggtgtcag gtggtatctc attgtggttt      60
cgattttgga tttctcta atg att agt aat ggt aag ttt ttt tgt ttt ttt      111
                        Met Ile Ser Asn Gly Lys Phe Phe Cys Phe Phe
                        -20                               -15

ttk gtt ttt kgt ttt tkg ttt ttg ara cgg asy ttg cyc tkg ycg ccc      159
Xaa Val Phe Xaa Phe Xaa Phe Leu Xaa Arg Xaa Leu Xaa Xaa Xaa Pro
                        -10                               -5               1

agg ctg gag tgc aat ggm aar ayc tcg gcy cac tgm aac ctc cgc ctc      207
Arg Leu Glu Cys Asn Gly Lys Xaa Ser Ala His Xaa Asn Leu Arg Leu

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5 10 15 243
 ctg agt yca agc aat tcy ctk gcc tca gcc ccc cga
 Leu Ser Xaa Ser Asn Ser Leu Ala Ser Ala Pro Arg
 20 25 30

<210> 364
 <211> 202
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..201

<221> sig_peptide
 <222> 46..156
 <223> score 4.3
 seq LELMASSDLPASA/SQ

<400> 364 57
 agcgattctt ctgcctcagc ctccctgagta gctgagatta caagc atg cgc cac cat
 Met Arg His His
 -35

acc cag cta att ttt gta ttt tta gtt gag atg ggg ttt cac tat att 105
 Thr Gln Leu Ile Phe Val Phe Leu Val Glu Met Gly Phe His Tyr Ile
 -30 -25 -20

ggc cag gct gat ctc gaa ctc atg gcc tcg agt gat ctg cct gcc tca 153
 Gly Gln Ala Asp Leu Glu Leu Met Ala Ser Ser Asp Leu Pro Ala Ser
 -15 -10 -5

gcc tcc caa agt gct ggg att aca ggc gtg acs acc atg ccc cgc cga c 202
 Ala Ser Gln Ser Ala Gly Ile Thr Gly Val Thr Thr Met Pro Arg Arg
 1 5 10 15

<210> 365
 <211> 244
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..244

<221> sig_peptide
 <222> 89..154
 <223> score 4.4
 seq LVIPALWEAEVGG/SP

<400> 365 60
 caaacagaaa attttataag aaaattgttt ttctaaattt tattttgata gtaacacata 112
 ggttttgtct gtgctagtta aaacatgg atg ttc ggc cgg gcg tgg tgg ctc
 Met Phe Gly Arg Ala Trp Trp Leu
 -20 -15

atg ctt gta atc cca gca ctt tgg gag gcc gag gtg ggc gga tca cct	160
Met Leu Val Ile Pro Ala Leu Trp Glu Ala Glu Val Gly Gly Ser Pro	
-10 -5 1	
gag ctc acg agt tca agc aat cct tct gtc tgc gcc tcv vaa agt gct	208
Glu Leu Thr Ser Ser Ser Asn Pro Ser Val Ser Ala Ser Xaa Ser Ala	
5 10 15	
ggg att gca ggc atg tcc cac cat gcc cag act tta	244
Gly Ile Ala Gly Met Ser His His Ala Gln Thr Leu	
20 25 30	

<210> 366
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 98..259

<221> sig_peptide
 <222> 98..199
 <223> score 9.2
 seq VVVVCLFLRQSLA/LS

<400> 366	
tgtttaggtt attgattgga ttttttttta agtatcagag catactactc tacattttcc	60
tataagcact gtttctgctg catcccatgt ttttgga atg gta ctt tat ctt ttt	115
Met Val Leu Tyr Leu Phe	
-30	
gtt ttc att ttc att cat ctc aac ttg ttt ttt tgc ggg tct ttt gtt	163
Val Phe Ile Phe Ile His Leu Asn Leu Phe Phe Ser Gly Ser Phe Val	
-25 -20 -15	
gtt gtw gtt tgt ttg ttt ttg aga cag agt ctc gct ctg tca cac agg	211
Val Val Val Cys Leu Phe Leu Arg Gln Ser Leu Ala Leu Ser His Arg	
-10 -5 1	
ctg aag tgc agt ggc atg atc tca gct cac tgc aac ctc tgc ctc ccg	259
Leu Lys Cys Ser Gly Met Ile Ser Ala His Cys Asn Leu Cys Leu Pro	
5 10 15 20	
gg	261

<210> 367
 <211> 202
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..201

<221> sig_peptide
 <222> 46..156
 <223> score 4.3
 seq LELMASSDLPASA/SQ

<400> 367
agcsattctt ctgcctcagc ctcttgagta gctgagatta caagc atg cgc cac cat 57
Met Arg His His

acc cag cta att ttt gta ttt tta gtt gag atg ggg ttt cac tat att 105
Thr Gln Leu Ile Phe Val Phe Leu Val Glu Met Gly Phe His Tyr Ile
-30 -25 -20

ggc cag gct gat ctc gaa ctc atg gcc tcg agt gat ctg cct gcc tca 153
Gly Gln Ala Asp Leu Glu Leu Met Ala Ser Ser Asp Leu Pro Ala Ser
-15 -10 -5

gcc tcc caa agt gct ggg att aca ggc gtg asc acc atg ccc cgc cga c 202
Ala Ser Gln Ser Ala Gly Ile Thr Gly Val Xaa Thr Met Pro Arg Arg
1 5 10 15

<210> 368
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..231

<221> sig_peptide
<222> 1..117
<223> score 4.2
seq SLALASLRLGITG/TR

<400> 368
atg ctc ttg tcg ccc agg ctg gag tgc agt gac gcg atc tcg gct cac 48
Met Leu Leu Ser Pro Arg Leu Glu Cys Ser Asp Ala Ile Ser Ala His
-35 -30 -25

tgc aac ctc cgc ctc ctg ggt tca aac gat tct ctt gcc tta gcc tcc 96
Cys Asn Leu Arg Leu Leu Gly Ser Asn Asp Ser Leu Ala Leu Ala Ser
-20 -15 -10

ctg agg cta gga att aca ggc acc cgc cgc cac ccc tgg cta att ttt 144
Leu Arg Leu Gly Ile Thr Gly Thr Arg Arg His Pro Trp Leu Ile Phe
-5 1 5

gta ttt tta gta gag aca grg ttt cgc cat gtt agc cag gct ggt ctc 192
Val Phe Leu Val Glu Thr Xaa Phe Arg His Val Ser Gln Ala Gly Leu
10 15 20 25

gaa ctc ctg acc tca ggt gat cca ccc acc tcg gcc tcc 231
Glu Leu Leu Thr Ser Gly Asp Pro Pro Thr Ser Ala Ser
30 35

<210> 369
<211> 203
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> 43..201

<221> sig_peptide
<222> 43..138
<223> score 4.7
seq FVCLFVFKTESHS/VT

<400> 369
tctggactta ayaaaaattg aacatgtacc attattcttt tc atg aca ttt aaa 54
Met Thr Phe Lys
-30
act cct caa aat caa gag cgc aca gct ctg cct cag ttt tgt ttt ttt 102
Thr Pro Gln Asn Gln Glu Arg Thr Ala Leu Pro Gln Phe Cys Phe Phe
-25 -20 -15
gtt tgt ttg ttt gtt ttt aag aca gag tct cac tct gtc acc cag gct 150
Val Cys Leu Phe Val Phe Lys Thr Glu Ser His Ser Val Thr Gln Ala
-10 -5 1
gga gtg cag tgg tgt gat ctt ggc tca ctg caa cct ctg cct ccc ggg 198
Gly Val Gln Trp Cys Asp Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly
5 10 15 20
ttc tt 203
Phe

<210> 370
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 145..315
<221> sig_peptide
<222> 145..273
<223> score 4.5
seq LELLTSGDPPALA/SQ

<400> 370
tgggtcaattt tgttttaaga ctgagtttca ctcttggtgc ccaggctgga gtgcaatggc 60
acgatctcgg ctactgcaa cctccacctc ctgagttcaa gtgattctcc tgcctcagta 120
tctcgagtag ctgagattac aggc atg cac cac cac gcc tgg cta ttt att 171
Met His His His Ala Trp Leu Phe Ile
-40 -35
tat tta ttt tta ttt tta ttt ttt ttt agt aga gac aga ttt ttc cat 219
Tyr Leu Phe Leu Phe Leu Phe Phe Phe Ser Arg Asp Arg Phe Phe His
-30 -25 -20
gtt ggt cag gct ggt ctc gaa ctc ctg acc tca gga gat cca ccc gcc 267
Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Pro Pro Ala
-15 -10 -5
ttg gcc tcc caa act gct ggg att ata ggc atg agc cac cgt gcc cgg c 316
Leu Ala Ser Gln Thr Ala Gly Ile Ile Gly Met Ser His Arg Ala Arg

1 5 10

<210> 371
 <211> 185
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 33..185

<221> sig_peptide
 <222> 33..131
 <223> score 5.5
 seq SLCLLTVAVLVLT/FK

<400> 371
 aatgaagggt actagaacac ctgcccattcc at atg gga aaa aaa atc tgg 53
 Met Gly Lys Lys Lys Ile Trp
 -30
 acc cct agc tca tat ccc atg ccc agt cat aaa cat gta tcc cta tgt 101
 Thr Pro Ser Ser Tyr Pro Met Pro Ser His Lys His Val Ser Leu Cys
 -25 -20 -15
 ctt cta acg gtt gca gtt tta gtt ctt aca ttt aag tct tta att cat 149
 Leu Leu Thr Val Ala Val Leu Val Leu Thr Phe Lys Ser Leu Ile His
 -10 -5 1 5
 ttt gag tda att ttt gca tat gag ata ggg gtc cag 185
 Phe Glu Xaa Ile Phe Ala Tyr Glu Ile Gly Val Gln
 10 15

<210> 372
 <211> 322
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 111..320

<221> sig_peptide
 <222> 111..215
 <223> score 6.3
 seq LFFLDGVSLRAQA/GV

<400> 372
 tttgtatctt tgtagagac garkttctcc atgttggtca gactgggtctt gaactcctga 60
 gctcaagtta tctacctgtc ttggcctccc atagtgtctgg gattacaggc atg agc 116
 Met Ser
 -35
 cac cat gcc cgg ccc gtt atg ccc ttt tgc ttt ata ttt ttc gtt ttt 164
 His His Ala Arg Pro Val Met Pro Phe Cys Phe Ile Phe Phe Val Phe
 -30 -25 -20

caa att ttc ttt ctt ttt ttt tta gac gga gtc tcg ctc cgt gcc cag	212
Gln Ile Phe Phe Leu Phe Phe Leu Asp Gly Val Ser Leu Arg Ala Gln	
-15 -10 -5	
gct gga gtg cag tgg cac gat atc ggc tca ctg cdd yct cca cct ccc	260
Ala Gly Val Gln Trp His Asp Ile Gly Ser Leu Xaa Xaa Pro Pro Pro	
1 5 10 15	
tgg ttc aag caa ttc gcc tgc ctc agc ctc cca agt agc tgg gat tac	308
Trp Phe Lys Gln Phe Ala Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr	
20 25 30	
agn cgm acg cca at	322
Xaa Arg Thr Pro	
35	

<210> 373
 <211> 175
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..173
 <221> sig_peptide
 <222> 15..53
 <223> score 4.9
 seq MVVCACSSSCLRG/LR

<400> 373	
tggccgggct gggc atg gtg gtg tgc gcc tgt agt tcc agc tgc ttg agg	50
Met Val Val Cys Ala Cys Ser Ser Ser Cys Leu Arg	
-10 -5	
ggg ctg agg cgg gag aat cac ttg aac ctg gga agt gga agt cac agt	98
Gly Leu Arg Arg Glu Asn His Leu Asn Leu Gly Ser Gly Ser His Ser	
1 5 10 15	
gag cca aga tcg tgc cay tac act tcc arg gyt ggg cam cag aat gag	146
Glu Pro Arg Ser Cys His Tyr Thr Ser Xaa Xaa Gly Xaa Gln Asn Glu	
20 25 30	
act ccg tct caa aaa aaa aaa aaa aa	175
Thr Pro Ser Gln Lys Lys Lys Lys Lys	
35 40	

<210> 374
 <211> 263
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 102..263
 <221> sig_peptide
 <222> 102..230
 <223> score 3.7

seq VWCLXLKLVPAIC/IS

<400> 374
 tcccagcaga aggggyagcg cctggctgtc agcagcgtgt gcctcaggag ggatctgcgg 60
 tgacgggggtt gttacttcag taggatgagg aagagtcaca a atg cgg ggt tgg mmg 116
 Met Arg Gly Trp Xaa
 -40
 gct cct gct tgg aga sgh ytg arc acy agg aga cta cca atg ggg agc 164
 Ala Pro Ala Trp Arg Xaa Leu Xaa Thr Arg Arg Leu Pro Met Gly Ser
 -35 -30 -25
 agg cac ggt gcc agc ccg gcc tct gcc gtc tgg tgt ctg tmc ctc aag 212
 Arg His Gly Ala Ser Pro Ala Ser Ala Val Trp Cys Leu Xaa Leu Lys
 -20 -15 -10
 tta gtc cca gct ttg tgc att agc ggg ctc acc ctc gga atc cag gga 260
 Leu Val Pro Ala Leu Cys Ile Ser Gly Leu Thr Leu Gly Ile Gln Gly
 -5 1 5 10
 ttc 263
 Phe

<210> 375
 <211> 304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 141..302
 <221> sig_peptide
 <222> 141..245
 <223> score 8.7
 seq LLLSVAFNQLVFA/LY

<400> 375
 tttctcatca atttcttgct tctctggcaa cctcaacctc tgattcctga ggccaataaa 60
 actgaaactt tctgcttgag ctcttggttt gccaggctga tggggctgag gtgcaccctc 120
 tgaggaaaag ctgtaaatac atg gat ttt acc caa tgc cat tcc ctt ctt tta 173
 Met Asp Phe Thr Gln Cys His Ser Leu Leu Leu
 -35 -30 -25
 agg gtt gaa tat tct cca gtg tct gtc tgc ttt tta tta ctt tcc gtt 221
 Arg Val Glu Tyr Ser Pro Val Ser Val Cys Phe Leu Leu Leu Ser Val
 -20 -15 -10
 gcc ttc aat cag ttg gtt ttt gct ttg tat cca ata caa gct acw btc 269
 Ala Phe Asn Gln Leu Val Phe Ala Leu Tyr Pro Ile Gln Ala Thr Xaa
 -5 1 5
 tgt ttc tct dda gtt tct ctc cct ttc ccc gct ca 304
 Cys Phe Ser Xaa Val Ser Leu Pro Phe Pro Ala
 10 15

<210> 376
 <211> 237
 <212> DNA

Cys Cys His Cys His Asn Ala Phe Phe Leu Thr Leu Ser Phe Leu Ala
 30 35 40 45
 tcc
 Ser

259

<210> 378
 <211> 291
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 104..289

<221> sig_peptide
 <222> 104..154
 <223> score 3.6
 seq VIFVSLXXYSIYS/RX

<400> 378
 ttaaaaacat cagcatgtgt ctagtgtata aaatacatat gcaccaagat ggtctgtatt 60
 catcttgtga tttttttttt tttaaataca gaatatatgc tgg atg att twa ttk 115
 Met Ile Xaa Xaa
 -15
 gth att ttt gtw agy ctc akg tkg tac tct att tac agt agg yct ttt 163
 Val Ile Phe Val Ser Leu Xaa Xaa Tyr Ser Ile Tyr Ser Arg Xaa Phe
 -10 -5 1
 tkt gtt tkg ttt tctg awa cag agc ttc gct ctt gtg acc agg ctg gag 211
 Xaa Val Xaa Phe Ser Xaa Gln Ser Phe Ala Leu Val Thr Arg Leu Glu
 5 10 15
 tds aat ggc aca atc tca gct cac tgc aac ctc cac ctt ckg ggt tca 259
 Xaa Asn Gly Thr Ile Ser Ala His Cys Asn Leu His Leu Xaa Gly Ser
 20 25 30 35
 agt gat tcy cck gcc tca gcc tcc caa gta gc 291
 Ser Asp Ser Pro Ala Ser Ala Ser Gln Val
 40 45

<210> 379
 <211> 158
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..156

<221> sig_peptide
 <222> 1..144
 <223> score 5
 seq VVVVVSSSPCVPG/EV

<400> 379

atg gat tca ata acg cca gag ctt aaa aaa cac cac aaa ttc tca ggc	48
Met Asp Ser Ile Thr Pro Glu Leu Lys Lys His His Lys Phe Ser Gly	
-45 -40 -35	
tcc acc ctg gat gga ctg gtt cag aaa cac tgg ggc aat gga ttt tgg	96
Ser Thr Leu Asp Gly Leu Val Gln Lys His Trp Gly Asn Gly Phe Trp	
-30 -25 -20	
gaa ttt gtt gtt gtt gtt gtt gtt tca agt tcc cca tgt gtt cct ggc	144
Glu Phe Val Val Val Val Val Val Val Ser Ser Ser Pro Cys Val Pro Gly	
-15 -10 -5	
gaa gtt gca gtg at	158
Glu Val Ala Val	
1	

<210> 380
 <211> 267
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..265
 <221> sig_peptide
 <222> 14..82
 <223> score 4.5
 seq LELLTSGDPPALA/SQ

<400> 380	
atttttagta gaa atg ggg ttt cac cat gtt agc cag gct ggt ctc gaa	49
Met Gly Phe His His Val Ser Gln Ala Gly Leu Glu	
-20 -15	
ctc ctg acc tca ggt gat cct ccc gct ttg gcc tct caa agt gct ggg	97
Leu Leu Thr Ser Gly Asp Pro Pro Ala Leu Ala Ser Gln Ser Ala Gly	
-10 -5 1 5	
att aca gat gtg agc cac cgt gcc cgc cct caa aat aaa aat gta gaa	145
Ile Thr Asp Val Ser His Arg Ala Arg Pro Gln Asn Lys Asn Val Glu	
10 15 20	
aac att gat ttt ggt gga tct atc ttg aca acc ata ttt ctc cgt gag	193
Asn Ile Asp Phe Gly Gly Ser Ile Leu Thr Thr Ile Phe Leu Arg Glu	
25 30 35	
aag ctt cag ctg ttc ctc ctt ctt cgt gtc cat ctt ctg aaa tgc cct	241
Lys Leu Gln Leu Phe Leu Leu Leu Arg Val His Leu Leu Lys Cys Pro	
40 45 50	
gtt ggc att ata gta caa aac cac ca	267
Val Gly Ile Ile Val Gln Asn His	
55 60	

<210> 381
 <211> 296
 <212> DNA
 <213> Homo sapiens

<220>

004220 "666E7560

<221> CDS
 <222> 108..296

<221> sig_peptide
 <222> 108..176
 <223> score 5.4
 seq LELLTSTDPPASA/SQ

<400> 381
 acctccacct tccaggttca agtgatcctc ctgcctcagc ctcccaagta gctgggatta 60
 caggcgagag ccaccatgcc cagctaattt ttgtattttc agtaaag atg ggg ttt 116
 Met Gly Phe
 cac cat gtt ggc cag gct ggt ctc gaa ctc ctg acc tca act gat cca 164
 His His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Thr Asp Pro
 -20 -15 -10 -5
 ccc gcc tcg gcc tca caa agt gct ggg att aca tgc gtg ags cac tgc 212
 Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Cys Val Xaa His Cys
 1 5 10
 gcc cca cca ttc tgc ttt gtc tat gaa ttt gac tgc tct ggg tat ctt 260
 Ala Pro Pro Phe Cys Phe Val Tyr Glu Phe Asp Cys Ser Gly Tyr Leu
 15 20 25
 acg aaa gcg gaa ttg gtg ggg cgc agt ggc tca cgc 296
 Thr Lys Ala Glu Leu Val Gly Arg Ser Gly Ser Arg
 30 35 40

<210> 382
 <211> 266
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..264

<221> sig_peptide
 <222> 43..135
 <223> score 4
 seq FLSFLKILRQGLA/LS

<400> 382
 tatttggcaa ttagtgcttg tattttaatt ttcatttcac at atg tgt tcc att 54
 Met Cys Ser Ile
 -30
 ttc cta acy aag att gaa ata agc cat ctc cta tta ggt att ttt ctt 102
 Phe Leu Thr Lys Ile Glu Ile Ser His Leu Leu Leu Gly Ile Phe Leu
 -25 -20 -15
 tct ttt tta aaa att ttg aga cag ggt ctt gct ctg tca ctc agg ctg 150
 Ser Phe Leu Lys Ile Leu Arg Gln Gly Leu Ala Leu Ser Leu Arg Leu
 -10 -5 1 5
 gag tgc aga ggt gca atc atg gct cag tgc aac atc cac ctc cca ggc 198
 Glu Cys Arg Gly Ala Ile Met Ala Gln Cys Asn Ile His Leu Pro Gly
 10 15 20

004220"6664550

tca agc gat cct gcc ccc tca ccc tct ggc gta stg gga cca cag gtg	246
Ser Ser Asp Pro Ala Pro Ser Pro Ser Gly Val Xaa Gly Pro Gln Val	
25 30 35	
cgc acc acc atg ccc ggc ag	266
Arg Thr Thr Met Pro Gly	
40	

<210> 383
 <211> 282
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 64..282

<221> sig_peptide
 <222> 64..162
 <223> score 8.1
 seq LFCFVLFCFVLFC/FV

<400> 383	
acactat ttt cttacaagag tcctaataac tgattagggc tcttgtaaga gccactaaat	60
cca atg gct aca gtc aca aga ata ccc tgt gaa tgc cag ctt cta gtt	108
Met Ala Thr Val Thr Arg Ile Pro Cys Glu Cys Gln Leu Leu Val	
-30 -25 -20	
ctc cat tgg tgt gtt ttg ttt tgt ttt gtt ttg ttt tgt ttt gtt ttg	156
Leu His Trp Cys Val Leu Phe Cys Phe Val Leu Phe Cys Phe Val Leu	
-15 -10 -5	
ttt tgt ttt gtt ttg ttt gag aca ggg tct cag tct gtt gcc cag gct	204
Phe Cys Phe Val Leu Phe Glu Thr Gly Ser Gln Ser Val Ala Gln Ala	
1 5 10	
gga gta cag tca tgt gat ctc tgc tca ctg caa cct cca cct cct ggg	252
Gly Val Gln Ser Cys Asp Leu Cys Ser Leu Gln Pro Pro Pro Pro Gly	
15 20 25 30	
ctc aag cga ttc tcc cag ctc agc ctc ccc	282
Leu Lys Arg Phe Ser Gln Leu Ser Leu Pro	
35 40	

<210> 384
 <211> 332
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 89..331

<221> sig_peptide
 <222> 89..208
 <223> score 4.4
 seq LNLGVLMCIECSG/IH

0044220 66667550

004220"666E7550

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<400> 384
ccaagccatc cagagccaga tcttgccag cctgcagtc tgcgagagca gtaaaagcaa 60
gtcccagctg accagccaga gtgaggcc atg gcc ctg cag tgc atc caa aac 112
Met Ala Leu Gln Ser Ile Gln Asn
-40 -35
atg cgt ggg aac tcc cac tgc gtg gac tgt gag acc cag aat cct aag 160
Met Arg Gly Asn Ser His Cys Val Asp Cys Glu Thr Gln Asn Pro Lys
-30 -25 -20
tgg gcc agt ttg aac ttg gga gtc ctc atg tgt att gaa tgt tca gga 208
Trp Ala Ser Leu Asn Leu Gly Val Leu Met Cys Ile Glu Cys Ser Gly
-15 -10 -5
atc cac cgc agt ctt ggc acc cgc ctt tcc cgt gtg cga tct ctg gag 256
Ile His Arg Ser Leu Gly Thr Arg Leu Ser Arg Val Arg Ser Leu Glu
1 5 10 15
ctg gat gac tgg cca gtt gag ctc agg aag gtt atg tca tct att ggc 304
Leu Asp Asp Trp Pro Val Glu Leu Arg Lys Val Met Ser Ser Ile Gly
20 25 30
aat gac cta gcc aac agc atc cgg gaa g 332
Asn Asp Leu Ala Asn Ser Ile Arg Glu
35 40

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<210> 385
<211> 286
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 119..286

<221> sig_peptide
<222> 119..202
<223> score 7.6
seq LLFLLTXPHSCXP/PS

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<400> 385
attctcagct gtgaaaggaa tattctggtg gggacaagggt tacagagttg ctgagagggt 60
ctcatgacat gaaggtactg gccttgccac agtgccctggg ggggcgggga ctccgcac 118
atg cct gtg atg tca cag tta ctg tca gtt cac agt gaa cct tcc ctc 166
Met Pro Val Met Ser Gln Leu Leu Ser Val His Ser Glu Pro Ser Leu
-25 -20 -15
ctt ttc ctg ttg act ttc cca cac tcc tgt rrc cct ccc tcc ctc cct 214
Leu Phe Leu Leu Thr Xaa Pro His Ser Cys Xaa Pro Pro Ser Leu Pro
-10 -5 1
tct tcc tct ctc tct stc tca ctc acg cac acg cac aca cac aca cac 262
Ser Ser Ser Leu Ser Xaa Ser Leu Thr His Thr His Thr His Thr His
5 10 15 20
aca cac aca cac aca cac aca cac 286
Thr His Thr His Thr His Thr His
25

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<210> 386

<211> 263
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..262

<221> sig_peptide
 <222> 59..127
 <223> score 3.6
 seq VLFVAVCFLVLFX/IY

<400> 386
 tatttactta gaactgtgat cagtgtctaca gaggagaata tgacctatca gatacaga 58
 atg att aac agt ggt tct aca cct ccc agg gtt ctt ttt gtt gct gtt 106
 Met Ile Asn Ser Gly Ser Thr Pro Pro Arg Val Leu Phe Val Ala Val
 -20 -15 -10
 tgt ttt ttg gtt tta ttt tkt att tat kka ttt att tat ttt ttt gag 154
 Cys Phe Leu Val Leu Phe Xaa Ile Tyr Xaa Phe Ile Tyr Phe Phe Glu
 -5 1 5
 acg aak ytc act ctt gtc cct cag gct gga gtg caa tgg tgc aat ctc 202
 Thr Xaa Xaa Thr Leu Val Pro Gln Ala Gly Val Gln Trp Cys Asn Leu
 10 15 20 25
 agc tca ctg caa cct ccg cct ccc ggg ttc agg caa ttc tcc tgc ctc 250
 Ser Ser Leu Gln Pro Pro Pro Pro Gly Phe Arg Gln Phe Ser Cys Leu
 30 35 40
 aag ccg ccc gag g 263
 Lys Pro Pro Glu
 45

<210> 387
 <211> 377
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 4..375

<221> sig_peptide
 <222> 4..93
 <223> score 5.2
 seq SLCFIFWDGVSLC/RS

<400> 387
 tta atg gaa tgc tct gta tat gga atg cca ggg gat ggg aag aga aga 48
 Met Glu Cys Ser Val Tyr Gly Met Pro Gly Asp Gly Lys Arg Arg
 -30 -25 -20
 gaa aaa tcg ctt tgt ttt att ttt tgg gat gga gtc tcg cta tgt cgc 96
 Glu Lys Ser Leu Cys Phe Ile Phe Trp Asp Gly Val Ser Leu Cys Arg
 -15 -10 -5 1

tcg gga tgg agt ctc gct atg tgc ctc agg ctg gag tgc agt agc acc	144
Ser Gly Trp Ser Leu Ala Met Ser Leu Arg Leu Glu Cys Ser Ser Thr	
5 10 15	
gta ctg gct cac tgc aac ctc cac ctc ctg agt tca ggc gaa ttt cct	192
Val Leu Ala His Cys Asn Leu His Leu Leu Ser Ser Gly Glu Phe Pro	
20 25 30	
gct tca gcc tcc gaa gta gct gag att acc ggc gca tgt cac cac acc	240
Ala Ser Ala Ser Glu Val Ala Glu Ile Thr Gly Ala Cys His His Thr	
35 40 45	
cag caa att ttt gtg tkt tta ttg gag atg ggg ttt cat cat gtt ggc	288
Gln Gln Ile Phe Val Xaa Leu Leu Glu Met Gly Phe His His Val Gly	
50 55 60 65	
cag gct gtt ctc aaa ctc ctg atg aca agt gat ctg ctg tct tgg cct	336
Gln Ala Val Leu Lys Leu Leu Met Thr Ser Asp Leu Leu Ser Trp Pro	
70 75 80	
ccc aaa gtt ctg gaa tta cca gca ggt gtg agc cac cgc rh	377
Pro Lys Val Leu Glu Leu Pro Ala Gly Val Ser His Arg	
85 90	

<210> 388
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 51..458

<221> sig_peptide
 <222> 51..122
 <223> score 7.8
 seq VALLLAAAGTAVG/DR

<400> 388	
acagcaggctc gtgatccggg tcgggacact gcctggcaga ggctgcgagc atg ggg	56
Met Gly	
ccc tgg ggc tgg aaa ttg cgc tgg acc gtc gcc ttg ctc ctc gcc gcg	104
Pro Trp Gly Trp Lys Leu Arg Trp Thr Val Ala Leu Leu Ala Ala	
-20 -15 -10	
gcg ggg act gca gtg ggc gac aga tgc gaa aga aac gag ttc cag tgc	152
Ala Gly Thr Ala Val Gly Asp Arg Cys Glu Arg Asn Glu Phe Gln Cys	
-5 1 5 10	
caa gac ggg aaa tgc atc tcc tac aag tgg gtc tgc gat ggc agc gct	200
Gln Asp Gly Lys Cys Ile Ser Tyr Lys Trp Val Cys Asp Gly Ser Ala	
15 20 25	
gag tgc cag gat ggc tct gat gag tcc cag gag acg tgc ttg tct gtc	248
Glu Cys Gln Asp Gly Ser Asp Glu Ser Gln Glu Thr Cys Leu Ser Val	
30 35 40	
acc tgc aaa tcc ggg gac hhc agc tgt ggg ggc cgt gtc aac cgc tgc	296
Thr Cys Lys Ser Gly Asp Xaa Ser Cys Gly Gly Arg Val Asn Arg Cys	
45 50 55	
att cct cag ttc tgg agg tgc gat ggc caa gtg gac tgc gac aac ggc	344
Ile Pro Gln Phe Trp Arg Cys Asp Gly Gln Val Asp Cys Asp Asn Gly	

60	65	70	
tca gac gag caa ggc tgt ccc ccc aag acg tgc tcc cag gac gag ttt			392
Ser Asp Glu Gln Gly Cys Pro Pro Lys Thr Cys Ser Gln Asp Glu Phe			
75	80	85	90
cgc tgc cac gat ggg aag tgc atc tct cgg cag ttc gtc tgt gac tca			440
Arg Cys His Asp Gly Lys Cys Ile Ser Arg Gln Phe Val Cys Asp Ser			
	95	100	105
gac cgg gac tgc ttg gac			458
Asp Arg Asp Cys Leu Asp			
110			

<210> 389
 <211> 349
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 119..349

<221> sig_peptide
 <222> 119..190
 <223> score 11
 seq LVLLFTLVQRSNG/EC

<400> 389	
agatgcgggd sgacastgac ttgctgagac cdrggcgggg aggcgcggac vccrgtgtgg	60
tccttgccgc getgacttct ccactgggttc ctgggcaccg aaagataaac ctctcaka	118
atg aag gcc ccc gct gtg ctt gca cct ggc atc ctc gtg ctc ctg ttt	166
Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe	
-20 -15 -10	
acc ttg gtg cag agg agc aat ggg gag tgt aaa gag gca cta gca aag	214
Thr Leu Val Gln Arg Ser Asn Gly Glu Cys Lys Glu Ala Leu Ala Lys	
-5 1 5	
tcc gag atg aat gtg aat atg aag tat cag ctt ccc aac ttc acc gca	262
Ser Glu Met Asn Val Asn Met Lys Tyr Gln Leu Pro Asn Phe Thr Ala	
10 15 20	
gaa aca ccc atc cag aat gtc att cta cat gag cat cac att ttc ctt	310
Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu	
25 30 35 40	
ggg gcc act aac tac att tak gtt tta aat gag gaa gac	349
Gly Ala Thr Asn Tyr Ile Xaa Val Leu Asn Glu Glu Asp	
45 50	

<210> 390
 <211> 433
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 268..432

<221> sig_peptide
 <222> 268..411
 <223> score 4.1
 seq FTTLSNLSLPSQT/KD

<400> 390
 cgtccatcag atcctgaccc taaggctggg gactttgtag ctatgaaagc aggaaatgaa 60
 ggcatagtag aatttcctaa agatgaaaaa caatatcttg ttcccctctg tttttggtat 120
 tacaagaaat aatctatcta ctactcgtca gcacctgtct ttgtgtctga agccaagaat 180
 aaattcatca acttggttagc cactgctgca actgaagcca accgcagtca atgttggtga 240
 tatgttgagt tgccggaggc gcctgga atg tgc tac ctt gca gaa ttg tcc ctg 294
 Met Cys Tyr Leu Ala Glu Leu Ser Leu
 -45 -40

aca aca ttt ckv mat ggc tat att gtt acc agt agg gcc aca aca aca 342
 Thr Thr Phe Xaa Xaa Gly Tyr Ile Val Thr Ser Arg Ala Thr Thr Thr
 -35 -30 -25
 aca aca ctt gca atc caa cct ggg ctt cct ttc acc aca cta agc aat 390
 Thr Thr Leu Ala Ile Gln Pro Gly Leu Pro Phe Thr Thr Leu Ser Asn
 -20 -15 -10
 cta tct ttg cca agt cag aca aaa gat gaa ctc cac cct ccc t 433
 Leu Ser Leu Pro Ser Gln Thr Lys Asp Glu Leu His Pro Pro
 -5 1 5

<210> 391
 <211> 210
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 47..208

<221> sig_peptide
 <222> 47..118
 <223> score 4.6
 seq SLLLYSLPLNIIG/LN

<400> 391
 tagcaataga aagagccaga atatgtgctt tagtttgttt taatga atg tat cct 55
 Met Tyr Pro
 tca ctt tta gtt gac tat ttc cct agt ctt ttg cta tac agt tta ccc 103
 Ser Leu Leu Val Asp Tyr Phe Pro Ser Leu Leu Leu Tyr Ser Leu Pro
 -20 -15 -10
 ttg aac atc ata ggt ttg aac tgt gca tat cca ctt ata aat aat ttt 151
 Leu Asn Ile Ile Gly Leu Asn Cys Ala Tyr Pro Leu Ile Asn Asn Phe
 -5 1 5 10
 tta aaa aat aat agt tac act tgt gtg cvt gtc cct ctt gct ttc cct 199
 Leu Lys Asn Asn Ser Tyr Thr Cys Val Xaa Val Pro Leu Ala Phe Pro
 15 20 25
 tcc atg ccg tc 210
 Ser Met Pro
 30

<210> 392
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..259

<221> sig_peptide
 <222> 80..199
 <223> score 6.1
 seq ICIGILVLPFIRC/CC

<400> 392
 agaataggat nattcactgg taataataga gtcattaaga aatattaagc attgcagcta 60
 aaaattgaac aaccctgta atg ata cat tta aga att att caa agg tgc tac 112
 Met Ile His Leu Arg Ile Ile Gln Arg Cys Tyr
 -40 -35 -30
 atg gca ggg tta gag aat aaa aag aac gtg gtg ttt gaa gca aaa cag 160
 Met Ala Gly Leu Glu Asn Lys Lys Asn Val Val Phe Glu Ala Lys Gln
 -25 -20 -15
 atc tgt att ggc atc ttg gtt ctc cct ttt atc aga tgt tgt tgc ctt 208
 Ile Cys Ile Gly Ile Leu Val Leu Pro Phe Ile Arg Cys Cys Cys Leu
 -10 -5 1
 gtg caa atc aca ttt tct ctg agt ctc cat ttt ctc att tat aac atg 256
 Val Gln Ile Thr Phe Ser Leu Ser Leu His Phe Leu Ile Tyr Asn Met
 5 10 15
 cgg cg 261
 Arg
 20

<210> 393
 <211> 340
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 71..340

<221> sig_peptide
 <222> 71..148
 <223> score 5.5
 seq AMFLLSYAXPSCG/RS

<400> 393
 gttctcaggg tgtgtggaat caactttccg gaagcaacca gcccaccaga ggaggtcccg 60
 agcgcgasgh atg acg atg cag cgg aga ctg gtt cag cag tgg agc gtc 109
 Met Thr Met Gln Arg Arg Leu Val Gln Gln Trp Ser Val
 -25 -20 -15

gcg atg ttc ctg ctg agc tac gcg ntg ccc tcc tgc ggg cgc tcg gtg	157
Ala Met Phe Leu Leu Ser Tyr Ala Xaa Pro Ser Cys Gly Arg Ser Val	
-10 -5 1	
gag ggt ctc agc cgc cgc ctc aaa aga gct gtg tct gaa cat cag ctc	205
Glu Gly Leu Ser Arg Arg Leu Lys Arg Ala Val Ser Glu His Gln Leu	
5 10 15	
ctc cat gac aag ggg aag tcc atc caa gat tta cgg cga cga ttc ttc	253
Leu His Asp Lys Gly Lys Ser Ile Gln Asp Leu Arg Arg Arg Phe Phe	
20 25 30 35	
ctt cac cat ctg atc gca gaa atc cac aca gct gaa atc aga gct acc	301
Leu His His Leu Ile Ala Glu Ile His Thr Ala Glu Ile Arg Ala Thr	
40 45 50	
tcg gag gtg tcc cct aac tcc aag ccc tct ccc aac aac	340
Ser Glu Val Ser Pro Asn Ser Lys Pro Ser Pro Asn Asn	
55 60	

<210> 394
 <211> 417
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 233..415

<221> sig_peptide
 <222> 233..364
 <223> score 3.8
 seq AIASLTLNEEILA/RV

<400> 394	
agactctgat ggctctgtag ctaactggcc catcctcaga gactaacgca aaggaacgaa	60
tttccaggat gttcgactat gtggagaaaa caaaaaaaaaa gcaaagaaaa aaatattttt	120
aaagawagaa rgaaggccag gtgcagtggc tcacgcctgt aatcccaaca ctttgggagg	180
ccgaggcaga cagatcacct gaggtcagga gttcaagacc agcctggcca ac atg gag	238
Met Glu	
atc tgc gct gac ccc cag ttt atc att gga gga gcc acc cgc aca gac	286
Ile Cys Ala Asp Pro Gln Phe Ile Ile Gly Gly Ala Thr Arg Thr Asp	
-40 -35 -30	
atc tgc caa gga gcc cta ggt gac trc tgg ctg ctg gca gcc att gcc	334
Ile Cys Gln Gly Ala Leu Gly Asp Xaa Trp Leu Leu Ala Ala Ile Ala	
-25 -20 -15	
tcc ctc acc ttg aat gaa gaa atc ctg gct cga gtc gtc ccc cta aac	382
Ser Leu Thr Leu Asn Glu Glu Ile Leu Ala Arg Val Val Pro Leu Asn	
-10 -5 1 5	
cag agc ttc cag gaa aac tat gca ggg atc ttt ca	417
Gln Ser Phe Gln Glu Asn Tyr Ala Gly Ile Phe	
10 15	

<210> 395
 <211> 344
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> 54..344

<221> sig_peptide

<222> 54..119

<223> score 5.9

seq LIYILWQLTGSAA/SG

<400> 395

aatacctaag agggaagtgg cttcatttca gtggctgact tccagagagc aat atg 56
Met
gct ggt tcc cca aca tgc ctc acc ctc atc tat atc ctt tgg cag ctc 104
Ala Gly Ser Pro Thr Cys Leu Thr Leu Ile Tyr Ile Leu Trp Gln Leu
-20 -15 -10
aca ggg tca gca gcc tct gga ccc gtg aaa gag ctg gtc ggt tcc gtt 152
Thr Gly Ser Ala Ala Ser Gly Pro Val Lys Glu Leu Val Gly Ser Val
-5 1 5 10
ggg ggg gcc gtg act ttc ccc ctg aag tcc aaa gta aag caa gtk gac 200
Gly Gly Ala Val Thr Phe Pro Leu Lys Ser Lys Val Lys Gln Val Asp
15 20 25
tct att gtc tgg acc ttc aac aca acc cct ctt gtc acc ata cag cca 248
Ser Ile Val Trp Thr Phe Asn Thr Thr Pro Leu Val Thr Ile Gln Pro
30 35 40
gaa ggg ggc act atc ata gtg acc caa aat cgt aat agg gag aga gta 296
Glu Gly Gly Thr Ile Ile Val Thr Gln Asn Arg Asn Arg Glu Arg Val
45 50 55
gac ttc cca gat gga ggc tac tcc ctg aag ctc agc aaa ctg aag aag 344
Asp Phe Pro Asp Gly Gly Tyr Ser Leu Lys Leu Ser Lys Leu Lys Lys
60 65 70 75

<210> 396

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 216..479

<221> sig_peptide

<222> 216..326

<223> score 6.5

seq LLVFFLIVRTLSC/RS

<400> 396

gcatccccck ktagctcaga gaagtttggt rdgaccgata ttctgaagcc tacttctgtc 60
aactcatcaa agtcattctc catccagctt tgttccatta tgggtgagga gctacgatcc 120
tttggaggag aagaggcaact ctgattttta gaattttcag cttttctgct ctgggttcgc 180
cccattcttg tggttttatc taccttcggg ctttg atg atg gtg acc tac aga 233
Met Met Val Thr Tyr Arg

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                                -35
tgg ggt ttt ggt gtg gat gtc mtt ttt gtt gct gtt gat gct att cct      281
Trp Gly Phe Gly Val Asp Val Xaa Phe Val Ala Val Asp Ala Ile Pro
      -30                      -25                      -20
ttc tgt ttg tta gtt ttc ttt cta ata gtc agg acc ctc agc tgc agg      329
Phe Cys Leu Leu Val Phe Phe Leu Ile Val Arg Thr Leu Ser Cys Arg
      -15                      -10                      -5                      1
tct gtt gga gta tgc tgg agg tcc act cca gac cct gtt tgc cta ggt      377
Ser Val Gly Val Cys Trp Arg Ser Thr Pro Asp Pro Val Cys Leu Gly
              5                      10                      15
atc acc agc aga ggc tgc aga aca gaa ata ttg cag aac agc aaa tgt      425
Ile Thr Ser Arg Gly Cys Arg Thr Glu Ile Leu Gln Asn Ser Lys Cys
              20                      25                      30
tgc tcc ctg atc ctt cct ctg gaa gct tcg tct caa agg ggc act gaa      473
Cys Ser Leu Ile Leu Pro Leu Glu Ala Ser Ser Gln Arg Gly Thr Glu
              35                      40                      45
tgt atg a
Cys Met
50
480

<210> 397
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..426

<221> sig_peptide
<222> 31..111
<223> score 4.4
      seq TSLLSPAAGPSFC/IV

<400> 397
tgtgtgtttg atatcagagg agaggaatga atg tgt cat tgc cac gga ggt ata      54
Met Cys His Cys His Gly Gly Ile
                                -25                      -20
agg cag gag cct acc tgg aca tcc ctg ctc agc ccc gcg gct gga cct      102
Arg Gln Glu Pro Thr Trp Thr Ser Leu Leu Ser Pro Ala Ala Gly Pro
              -15                      -10                      -5
tcc ttc tgc att gtt tac att gca tcc tgg atg gga cgt ttt tca tat      150
Ser Phe Cys Ile Val Tyr Ile Ala Ser Trp Met Gly Arg Phe Ser Tyr
              1                      5                      10
gca acg tgc tgc tct cag gag gag gag gga atg gca gga acc gga cag      198
Ala Thr Cys Cys Ser Gln Glu Glu Glu Gly Met Ala Gly Thr Gly Gln
              15                      20                      25
act gtg aac ttg cca aga gat gca ata ccc ttc cac acc ttt ggg tgt      246
Thr Val Asn Leu Pro Arg Asp Ala Ile Pro Phe His Thr Phe Gly Cys
              30                      35                      40                      45
ctg tct ggc atc aga ttg gca gct gca cca acc aga gga aca gaa gag      294
Leu Ser Gly Ile Arg Leu Ala Ala Ala Pro Thr Arg Gly Thr Glu Glu
              50                      55                      60

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aag aga gat gcc act ggg cac tgc cct gcc agt agt ggc ctt cag ggg      342
Lys Arg Asp Ala Thr Gly His Cys Pro Ala Ser Ser Gly Leu Gln Gly
      65                                70                                75
gct cct tcc ggg gct ccg gcc tgt ttt cca gag aga gtd gca gta gcc      390
Ala Pro Ser Gly Ala Pro Ala Cys Phe Pro Glu Arg Val Ala Val Ala
      80                                85                                90
cca tgg ggc ccg gag ctg ctg tgg cct cca ctg gca t      427
Pro Trp Gly Pro Glu Leu Leu Trp Pro Pro Leu Ala
      95                                100                                105

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<210> 398
 <211> 252
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 59..250

<221> sig_peptide
 <222> 59..115
 <223> score 5.2
 seq LLVAFRVFLGLFS/LP

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<400> 398
ctgtagccaa attaaaatct gagtctggcg tttccvtttg ggaaggtgct cagtagct      58
atg tac atg tgg tcc aaa ctc ttg gtg gca ttc agg gtc ttt ctt ggc      106
Met Tyr Met Trp Ser Lys Leu Leu Val Ala Phe Arg Val Phe Leu Gly
      -15                                -10                                -5
ctt ttc agc ctc ccc tct aac cac aac aca tac tgt ccc ttc cag cct      154
Leu Phe Ser Leu Pro Ser Asn His Asn Thr Tyr Cys Pro Phe Gln Pro
      1                                5                                10
tgg gga att cct tgc agc ctc aga ata gga ggc ctc ctc cat ctg cag      202
Trp Gly Ile Pro Cys Ser Leu Arg Ile Gly Gly Leu Leu His Leu Gln
      15                                20                                25
tgc cct ttg ccc ccc tct cta cat cct ctk cct agt cta ctc acc agc      250
Cys Pro Leu Pro Pro Ser Leu His Pro Leu Pro Ser Leu Leu Thr Ser
      30                                35                                40                                45
cg      252

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<210> 399
 <211> 181
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..180

<221> sig_peptide
 <222> 28..105
 <223> score 4.7
 seq TALSLVSSAFSFC/DM

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<400> 399
caagttgcta tctactcagc cttatga atg ccc ctc gct ttt cta agg cca tgt 54
Met Pro Leu Ala Phe Leu Arg Pro Cys
-25 -20
gaa aat cac ggc act gcc ctt agc ctt gtg tca tct gct ttt tcg ttc 102
Glu Asn His Gly Thr Ala Leu Ser Leu Val Ser Ser Ala Phe Ser Phe
-15 -10 -5
tgc gat atg ccc agt tcc caa atc aat tat agg tac ctg ttt agg aga 150
Cys Asp Met Pro Ser Ser Gln Ile Asn Tyr Arg Tyr Leu Phe Arg Arg
1 5 10 15
gag gaa gat ttt acc tct caa agg gtg aga a 181
Glu Glu Asp Phe Thr Ser Gln Arg Val Arg
20 25

<210> 400
<211> 280
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 85..279

<221> sig_peptide
<222> 85..180
<223> score 5.9
seq WTAMLISLAIVIA/LP

<400> 400
cgaatttact atactacaga gagagacgaa caaggcagca aaatcaatga tttctttctg 60
cggtctgaag acctcttcaa tgaa atg aat tgg cag aag aaa ctg aga ggg 111
Met Asn Trp Gln Lys Lys Leu Arg Gly
-30 -25
acc ctg gag ccc cac tgg tcg gga ctc ctg tgg aca gcc atg ctc atc 159
Thr Leu Glu Pro His Trp Ser Gly Leu Leu Trp Thr Ala Met Leu Ile
-20 -15 -10
tct ctg gcc atc gtc att gcc ctc ccc aag ccc cat ggc atc cgg gcc 207
Ser Leu Ala Ile Val Ile Ala Leu Pro Lys Pro His Gly Ile Arg Ala
-5 1 5
tta att gcc tcc aca att cta cga ctg ata ttt tca gtc ggg tta caa 255
Leu Ile Ala Ser Thr Ile Leu Arg Leu Ile Phe Ser Val Gly Leu Gln
10 15 20 25
ccc acg ttg ttt ctt ctg ggc gcc t 280
Pro Thr Leu Phe Leu Leu Gly Ala
30

<210> 401
<211> 270
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 49..270

<221> sig_peptide
 <222> 49..159
 <223> score 4.4
 seq LELLTSGDPPASA/SQ

<400> 401
 gtctcccagg ttcaagtgat tctcctgcct aagtctggga ttacaggc atg cac cac 57
 Met His His
 -35
 cac acc cgg cta att ttt gta ttt tta gta gag atg ggg ttt cac cat 105
 His Thr Arg Leu Ile Phe Val Phe Leu Val Glu Met Gly Phe His His
 -30 -25 -20
 att ggc cag gct agt ctt gaa ctt ctg act tca ggt gat cca cct gcc 153
 Ile Gly Gln Ala Ser Leu Glu Leu Leu Thr Ser Gly Asp Pro Pro Ala
 -15 -10 -5
 tcg gcc tcc caa agt gct ggg att aca ggc gtg aag cac cac gcc cag 201
 Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly Val Lys His His Ala Gln
 1 5 10
 cct gaa ata ata ttt tac ctt tta ctt tgt gct ttt tgt gtt tta ctc 249
 Pro Glu Ile Ile Phe Tyr Leu Leu Leu Cys Ala Phe Cys Val Leu Leu
 15 20 25 30
 agg aag tcc tcc cct acc cta 270
 Arg Lys Ser Ser Pro Thr Leu
 35

<210> 402
 <211> 396
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 192..395

<221> sig_peptide
 <222> 192..236
 <223> score 8
 seq FISFLCLIALAGT/SS

<400> 402
 gattctcagc ttagttgctg ttggtgtata ggagagctac tgatttgtgt acattaattt 60
 tgtatccgga aactttgttg aattatatta tcagttctag gagctttttg gaggagtctt 120
 tagggttctc taggtataca atcatatcat cagcaaacag tgacaattcg acttcctctt 180
 tatggatttg t atg ccc ttt att tct ttc ctt tgt ctg att gct ctg gct 230
 Met Pro Phe Ile Ser Phe Leu Cys Leu Ile Ala Leu Ala
 -15 -10 -5
 ggg act tcc agt act atg ttg aga agt gct ctg gct ggg act tcc agt 278
 Gly Thr Ser Ser Thr Met Leu Arg Ser Ala Leu Ala Gly Thr Ser Ser

1	5	10	
act atg tkg arg aga agt ggt gam agt ggg wat cct kgh ctk gty cma			326
Thr Met Xaa Xaa Arg Ser Gly Xaa Ser Gly Xaa Pro Xaa Leu Val Xaa			
15	20	25	30
gtc ctm aga ggg aat gct ttc agc ttt ttc cca ttc agt ctg atg twg			374
Val Leu Arg Gly Asn Ala Phe Ser Phe Phe Pro Phe Ser Leu Met Xaa			
	35	40	45
gct atg ggt tgt cat aga tgg c			396
Ala Met Gly Cys His Arg Trp			
50			

<210> 403
 <211> 197
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 15..197

<221> sig_peptide
 <222> 15..92
 <223> score 7.9
 seq RVCLLSLSLFLWA/NR

<400> 403	
aatacgccag gaac atg cta agg acc tgg agc tct cta ccc tgg acc cgt	50
Met Leu Arg Thr Trp Ser Ser Leu Pro Trp Thr Arg	
-25 -20 -15	
ttt cgg gtt tgc ttg ctc tct ctc tct ctc ttt ctc tgg gct aat cgt	98
Phe Arg Val Cys Leu Leu Ser Leu Ser Leu Phe Leu Trp Ala Asn Arg	
-10 -5 1	
tta gag gac agt cgc tcc tgc caa cct aat ccc atg agc ctg act acc	146
Leu Glu Asp Ser Arg Ser Cys Gln Pro Asn Pro Met Ser Leu Thr Thr	
5 10 15	
ttg ccg ggc cac agg ctc aaa gaa gca gtg tgg ctg cca gca ccc tca	194
Leu Pro Gly His Arg Leu Lys Glu Ala Val Trp Leu Pro Ala Pro Ser	
20 25 30	
ctt	197
Leu	
35	

<210> 404
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 147..299

<221> sig_peptide
 <222> 147..272

<223> score 7
seq LFLYSLFTENVLA/HP

<400> 404
tgtattgttt mmmttattta ctagtatgca gatctggttt tcattctttt catattgaat 60
ttcgttatgg gtagaatcat ttgcaaacat ttctagacat ttttaaagat ctatttaatt 120
tgtttaagaa tggaaaacat aaaata atg cat gat tct tca ggc aag aat aat 173
Met His Asp Ser Ser Gly Lys Asn Asn
-40 -35
ttc aga aag ata cct gtt gta aat tta att tat ctc tat gta gac ata 221
Phe Arg Lys Ile Pro Val Val Asn Leu Ile Tyr Leu Tyr Val Asp Ile
-30 -25 -20
cat ata cat aaa tta ttt tta tat agt ctc ttt aca gaa aat gta ttg 269
His Ile His Lys Leu Phe Leu Tyr Ser Leu Phe Thr Glu Asn Val Leu
-15 -10 -5
gca cat cct tgc att gtt cta cgc cgc cta t 300
Ala His Pro Cys Ile Val Leu Arg Arg Leu
1 5

<210> 405
<211> 371
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 187..369

<221> sig_peptide
<222> 187..270
<223> score 8.3
seq ILFLINILPGTTG/QG

<400> 405
aagctagcga gcaaaccaga gagacagacc gagagagggga ccaggagaga gacccagaga 60
gagaagaagc agccagaagc cgagctctgt cagggctcaa cctccaactt gtttcagttc 120
attcatcctt ctctcctttc cgctcagact gtagagctcg gtctctccaa gtttgcct 180
aagaag atg ata atc aca caa aca agt cac tgt tac atg acc agc ctt 228
Met Ile Ile Thr Gln Thr Ser His Cys Tyr Met Thr Ser Leu
-25 -20 -15
ggg att ctt ttc ctg att aat att ctc cct gga acc act ggt caa ggg 276
Gly Ile Leu Phe Leu Ile Asn Ile Leu Pro Gly Thr Thr Gly Gln Gly
-10 -5 1
gaa tca aga cga caa gaa ccc ggg gac ttt gtg aag cag gac att ggc 324
Glu Ser Arg Arg Gln Glu Pro Gly Asp Phe Val Lys Gln Asp Ile Gly
5 10 15
ggg ctg tct cct aag cat gcc cca gat att cct gat gac agc act ga 371
Gly Leu Ser Pro Lys His Ala Pro Asp Ile Pro Asp Asp Ser Thr
20 25 30

<210> 406
<211> 268

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 41..268

<221> sig_peptide
<222> 41..100
<223> score 5.4
seq WFFVHSSALGLVLA/PP

<400> 406
acgatacaaaa tggtaggcct tcatgtgagc cagtdactac atg aat ctt cat ttc 55
Met Asn Leu His Phe
-20
cca cag tgg ttt gtt cat tca tca gcg tta ggc ttg gtc ctg gct cca 103
Pro Gln Trp Phe Val His Ser Ser Ala Leu Gly Leu Val Leu Ala Pro
-15 -10 -5 1
cct ttc tcc tct ccg ggc act gac ccc acc ttt ccg tgt att tac tgt 151
Pro Phe Ser Ser Pro Gly Thr Asp Pro Thr Phe Pro Cys Ile Tyr Cys
5 10 15
agg cta tta aat atg atc atg acc cgc ctt gca ttt tca ttc atc acc 199
Arg Leu Leu Asn Met Ile Met Thr Arg Leu Ala Phe Ser Phe Ile Thr
20 25 30
tgt tta tgc cca aat tta aag gaa gtt tgt ctc att ttg cca gaa aaa 247
Cys Leu Cys Pro Asn Leu Lys Glu Val Cys Leu Ile Leu Pro Glu Lys
35 40 45
aat tgt aat agt cga cac gct 268
Asn Cys Asn Ser Arg His Ala
50 55

<210> 407
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..307

<221> sig_peptide
<222> 89..190
<223> score 4.4
seq SLHLLWSRTVTTG/ET

<400> 407
tctcattggt gcaggttgct ttcccagaca ctactggaa ggaagaacgg gaattgtag 60
tttaagctca tactaaagt cgcacaa atg cac gga cct tct ccc agg aag 112
Met His Gly Pro Ser Pro Arg Lys
-30
gcg gcc ttt tgc att atg aac ccc act gga aga gct cca agt ctt cac 160

Ala Ala Phe Cys Ile Met Asn Pro Thr Gly Arg Ala Pro Ser Leu His
 -25 -20 -15
 ttg ctg tgg tca aga act gta acc aca gga gag acg gga ttt cac tat 208
 Leu Leu Trp Ser Arg Thr Val Thr Thr Gly Glu Thr Gly Phe His Tyr
 -10 -5 1 5
 gtt ggc cgg gct ggt ctt gaa ctc cta acc tcr dga tct gcc tgc ctc 256
 Val Gly Arg Ala Gly Leu Glu Leu Leu Thr Ser Xaa Ser Ala Cys Leu
 10 15 20
 ggc ctc cca aac tgc tgg gat tac agg cgt gag cca ccc cac ccg gac 304
 Gly Leu Pro Asn Cys Trp Asp Tyr Arg Arg Glu Pro Pro His Pro Asp
 25 30 35
 atc 307
 Ile
 <210> 408
 <211> 434
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 146..433
 <221> sig_peptide
 <222> 146..232
 <223> score 11.2
 seq GLLVLLVGGCAA/EE
 <400> 408
 acgatgtgaa gcggggcaga gccgggggag cccagcccag ccagcctcca gacgttgccc 60
 catctgacgc tcggctcgag gcctctctgt gagggaccgg ggggccatcc ccctccaggg 120
 cggagatcgg aggtcgcgtgc caagc atg gcg ccc acc tgg ggc cct ggc atg 172
 Met Ala Pro Thr Trp Gly Pro Gly Met
 -25
 gtg tct gtg gtt ggt ccc atg ggc ctc ctt gtg gtc ctg ctc gtt gga 220
 Val Ser Val Val Gly Pro Met Gly Leu Leu Val Val Leu Leu Val Gly
 -20 -15 -10 -5
 ggc tgt gca gca gaa gag ccc ccc agg ttt atc aaa gaa ccc aag gac 268
 Gly Cys Ala Ala Glu Glu Pro Pro Arg Phe Ile Lys Glu Pro Lys Asp
 1 5 10
 cag atc ggc gtg tgc ggg ggt gtg gcc tct ttc gtg tgt cag gcc acg 316
 Gln Ile Gly Val Ser Gly Gly Val Ala Ser Phe Val Cys Gln Ala Thr
 15 20 25
 ggt gac ccc aag cca cga gtg acc tgg aac aag aag ggc aag aag gtc 364
 Gly Asp Pro Lys Pro Arg Val Thr Trp Asn Lys Lys Gly Lys Lys Val
 30 35 40
 aac tct cag cgc ttt gag acg att gag tkt gat gag agt gcc ggg gca 412
 Asn Ser Gln Arg Phe Glu Thr Ile Glu Xaa Asp Glu Ser Ala Gly Ala
 45 50 55 60
 gtg ctg agg atc cag ccg ctg a 434
 Val Leu Arg Ile Gln Pro Leu
 65

<210> 409
 <211> 340
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 17..340

<221> sig_peptide
 <222> 17..94
 <223> score 3.6
 seq TQAFGALLSGAGS/QV

<400> 409
 tcttcatttc acccag atg tac ttg act tgc ctg cag ccc tgt ctc aag agc 52
 Met Tyr Leu Thr Cys Leu Gln Pro Cys Leu Lys Ser
 -25 -20 -15
 ctc aca cag gct ttt ggg gcc ctc ctc tca ggt gct ggc tct cag gtc 100
 Leu Thr Gln Ala Phe Gly Ala Leu Leu Ser Gly Ala Gly Ser Gln Val
 -10 -5 1
 cta gcc ccc acc agc tct aca cta aac tgg ccc ctt tct tcc cag atg 148
 Leu Ala Pro Thr Ser Ser Thr Leu Asn Trp Pro Leu Ser Ser Gln Met
 5 10 15
 ggc cgt ctc cca cag gca gcg cct gct gga act caa cag ctc cct gga 196
 Gly Arg Leu Pro Gln Ala Ala Pro Ala Gly Thr Gln Gln Leu Pro Gly
 20 25 30
 gtt caa gct gca ccg act gca ctt cat ccg cct ctt ggc agg agg css 244
 Val Gln Ala Ala Pro Thr Ala Leu His Pro Pro Leu Gly Arg Arg Xaa
 35 40 45 50
 cgc gaa gag ctg gag gcc ctc agc tat gct cgg cac ttc cag ccc ttt 292
 Arg Glu Glu Leu Glu Ala Leu Ser Tyr Ala Arg His Phe Gln Pro Phe
 55 60 65
 gct cgg mtg cac cag cgg ggt gag tgc cca gcc agc tgg ggt tgt gct 340
 Ala Arg Xaa His Gln Arg Gly Glu Cys Pro Gly Ser Trp Gly Cys Ala
 70 75 80

<210> 410
 <211> 198
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..197

<221> sig_peptide
 <222> 45..191
 <223> score 4.4
 seq CLFSILFPLFIIS/AK

<400> 410

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cactgtactg ctttgaatat cgttggttca ataaaggaat tgaw atg cac cag cgg      56
                                   Met His Gln Arg
ttg tct aac ata gaa agg aat tgg cct tac tac ttt agg ttt ggt ttg      104
Leu Ser Asn Ile Glu Arg Asn Trp Pro Tyr Tyr Phe Arg Phe Gly Leu
-45                               -40                               -35                               -30
ccc ttg gct ttt ctc aca gca atg cag tcc tca tat att atc agt ggc      152
Pro Leu Ala Phe Leu Thr Ala Met Gln Ser Ser Tyr Ile Ile Ser Gly
                               -25                               -20                               -15
tgc ctt ttc tct atc ctc ttt cct tta ttc att atc agc gcc aag a      198
Cys Leu Phe Ser Ile Leu Phe Pro Leu Phe Ile Ile Ser Ala Lys
                               -10                               -5                               1
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<210> 411
<211> 204
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..204

<221> sig_peptide
<222> 46..162
<223> score 4.4
seq LELLTSGDPPASA/SQ

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<400> 411
agttcaagca attctctctcc ctcagcctcc ctagtacgtg ggact atg ggc atg tgc      57
                                   Met Gly Met Cys
cac cat gcc cag cta att ttt gta ttt tta gta gag acg ggg ttt cac      105
His His Ala Gln Leu Ile Phe Val Phe Leu Val Glu Thr Gly Phe His
-35                               -30                               -25                               -20
cat gtt ggc cag gct ggt ctc gaa ctc ctg acc tca ggt gat cct ccc      153
His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Pro Pro
                               -15                               -10                               -5
gcc tcg gcc tcc caa agt gct ggg att aca ggc ctg agc cac cac gcc      201
Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly Leu Ser His His Ala
                               1                               5                               10
acg      204
Thr
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<210> 412
<211> 341
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 79..339

<221> sig_peptide
<222> 79..135
<223> score 10.8

[illegible]

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<210> 413
<211> 430
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 58..429
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<400> 413																
agagctccag gcgcacatcc gcagtcagcc acctcgcgcg ckystccagg agcaagg																57
atg gag agg ctg gtg atc agg atg ccc ttc tgt cat ctg tct acc tac																105
Met	Glu	Arg	Leu	Val	Ile	Arg	Met	Pro	Phe	Cys	His	Leu	Ser	Thr	Tyr	
-30				-25				-20				-15				
agc ctg gtt tgg gtc atg gca gca gtg gtg ctg tgc aca gca caa gtg																153
Ser	Leu	Val	Trp	Val	Met	Ala	Ala	Val	Leu	Cys	Thr	Ala	Gln	Val		
				-10				-5				1				
caa gtg gtg acc cag gat gaa aga gag cag ctg tac aca cct gct tcc																201
Gln	Val	Val	Thr	Gln	Asp	Glu	Arg	Glu	Gln	Leu	Tyr	Thr	Pro	Ala	Ser	
5				10				15								
tta aaa tgc tct ctg caa aat gcc cag gaa gcc ctc att gtg aca tgg																249
Leu	Lys	Cys	Ser	Leu	Gln	Asn	Ala	Gln	Glu	Ala	Leu	Ile	Val	Thr	Trp	
20				25				30								
cag aaa aag aaa gct gta agc cca gaa aac atg gtc acc ttc agc gag																297

Gln	Lys	Lys	Lys	Ala	Val	Ser	Pro	Glu	Asn	Met	Val	Thr	Phe	Ser	Glu	
35					40				45						50	
aac	cat	ggg	gtg	gtg	atc	cag	cct	gcc	tat	aag	gac	aag	ata	aac	att	345
Asn	His	Gly	Val	Val	Ile	Gln	Pro	Ala	Tyr	Lys	Asp	Lys	Ile	Asn	Ile	
			55					60					65			
acc	cag	ctg	gga	ctc	caa	aac	tca	acc	atc	acc	ttc	tgg	aat	atc	acc	393
Thr	Gln	Leu	Gly	Leu	Gln	Asn	Ser	Thr	Ile	Thr	Phe	Trp	Asn	Ile	Thr	
		70					75					80				
ctg	gag	gat	gaa	ggg	tgt	tac	atg	tgt	ctc	ttc	aat	a				430
Leu	Glu	Asp	Glu	Gly	Cys	Tyr	Met	Cys	Leu	Phe	Asn					
	85						90									

<210> 414
 <211> 223
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..222
 <221> sig_peptide
 <222> 10..150
 <223> score 4.5
 seq PIFGLLVPSQIFS/SL

<400> 414																	
caaccatac	atg	tgc	aca	ctc	aca	gac	aca	cac	act	cac	gtc	caa	gtg	cac		51	
	Met	Cys	Thr	Leu	Thr	Asp	Thr	His	Thr	His	Val	Gln	Val	His			
			-45				-40					-35					
aag	tca	aaa	cct	tgc	cag	ctc	ctc	tcc	cct	cca	cca	rsc	cat	ggt		99	
Lys	Ser	Lys	Pro	Cys	Gln	Leu	Leu	Ser	Pro	Pro	Pro	Xaa	His	Gly			
		-30				-25					-20						
cct	ctt	ctt	ctc	cct	atc	ttt	ggc	ctt	ctt	gtg	ccc	tct	cag	att	ttc	147	
Pro	Leu	Leu	Leu	Pro	Ile	Phe	Gly	Leu	Leu	Val	Pro	Ser	Gln	Ile	Phe		
		-15				-10				-5							
agc	tct	ctt	ctc	aat	tct	cta	cat	ctg	ggc	ctg	cct	tcc	ttc	cca	aag	195	
Ser	Ser	Leu	Leu	Asn	Ser	Leu	His	Leu	Gly	Leu	Pro	Ser	Phe	Pro	Lys		
	1			5				10					15				
atg	cca	ctc	atg	att	ttc	ctc	ccc	cgc	t							223	
Met	Pro	Leu	Met	Ile	Phe	Leu	Pro	Arg									
			20														

<210> 415
 <211> 428
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 203..427
 <221> sig_peptide

<222> 203..259

<223> score 8

seq LLLLATAWHGQG/IP

<400> 415

aactctgtgg ttgccttgcc tagctaaaag gggaagaaga ggatcagccc aaggaggagg 60
aagaggaaaa caagacaaac agccagtgc gagagagga acgtgtgtcc agtgtcccga 120
tccctgcgga stagtagctg agagctctgt gccctgggca ccttgcagcc ctgcacctgc 180
ctgccacttc cccaccgagg cc atg ggc cca gga gtt ctg ctg ctc ctg ctg 232

Met Gly Pro Gly Val Leu Leu Leu Leu Leu
-15 -10

gtg gcc aca gct tgg cat ggt cag gga atc cca gtg ata gag ccc agt 280
Val Ala Thr Ala Trp His Gly Gln Gly Ile Pro Val Ile Glu Pro Ser

-5 1 5

gtc cct gag ctg gtc gtg aag cca gga gca acg gtg acc ttg cga tgt 328
Val Pro Glu Leu Val Val Lys Pro Gly Ala Thr Val Thr Leu Arg Cys
10 15 20

gtg ggc aat ggc agc gtg gaa tgg gat ggc ccc cca tca cct cac tgg 376
Val Gly Asn Gly Ser Val Glu Trp Asp Gly Pro Pro Ser Pro His Trp
25 30 35

acc ctg tac tct gat ggc tcc agc agc atc ctc agc acc aac aac gct 424
Thr Leu Tyr Ser Asp Gly Ser Ser Ser Ile Leu Ser Thr Asn Asn Ala
40 45 50 55

acc g 428
Thr

<210> 416

<211> 273

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 83..271

<221> sig_peptide

<222> 83..136

<223> score 4.7

seq LFFCFCFVLRQ/SL

<400> 416

cttgcccttg catttattta ttcattttta agttattttg ccagcatctt tttaatgata 60
aataataatt gtatatattt at atg gta cag ggt gat ttg ttt ttt tgt ttt 112
Met Val Gln Gly Asp Leu Phe Phe Cys Phe

-15 -10

tgt ttt tgt ttt gtt ttg aga cag agt ctc cct ctg tca ccc agg ctg 160
Cys Phe Cys Phe Val Leu Arg Gln Ser Leu Pro Leu Ser Pro Arg Leu
-5 1 5

gag tgc agt ggc gcg atc tca gct cac tgc aac ctc tac ctc ctg gat 208
Glu Cys Ser Gly Ala Ile Ser Ala His Cys Asn Leu Tyr Leu Leu Asp
10 15 20

tca gac gat tct tat gcc tta gtc tcc cta gta gca ggg act aca ggc 256

004220"66667550

Ser Asp Asp Ser Tyr Ala Leu Val Ser Leu Val Ala Gly Thr Thr Gly
 25 30 35 40
 atc tgc cac cat acc cc
 Ile Cys His His Thr
 45

273

<210> 417
 <211> 200
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..200

<221> sig_peptide
 <222> 12..83
 <223> score 5.1
 seq IFIYLLFSRQGLA/LS

<400> 417
 acagtammag t atg tat gtt tgt gat atg caa gta gtt ggg gaa att ttt 50
 Met Tyr Val Cys Asp Met Gln Val Val Gly Glu Ile Phe
 -20 -15
 att tat ctc ctt ttt tcg aga cag ggt ctt gct ctg tca ccc agg ctg 98
 Ile Tyr Leu Leu Phe Ser Arg Gln Gly Leu Ala Leu Ser Pro Arg Leu
 -10 -5 1 5
 gag tgc agt tgt gtg aat ata gct cac tac agc ctt caa mtt ctg ggc 146
 Glu Cys Ser Cys Val Asn Ile Ala His Tyr Ser Leu Gln Xaa Leu Gly
 10 15 20
 tca aac aat cct ccc ata tca gct tcc caa gta tct tct ggg acc aca 194
 Ser Asn Asn Pro Pro Ile Ser Ala Ser Gln Val Ser Ser Gly Thr Thr
 25 30 35
 ggc atg 200
 Gly Met

<210> 418
 <211> 248
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..246

<221> sig_peptide
 <222> 46..147
 <223> score 4
 seq VIFLSIFVIIIVTC/LM

<400> 418
 aatccagggg gctgatgttg tgggagggga cttaaaacag aaaaa atg ttt tac aag 57

<213> Homo sapiens

<220>

<221> CDS

<222> 229..387

<221> sig_peptide

<222> 229..282

<223> score 6.3

seq LFLLLFFFHFSFL/NW

<400> 420

catttgagca cggagcctct gcggccgtct tccttggatt ctctcatatc cctgaaaaac 60
acaaattgta cctggatttt ccttctgttt ccaaagtcca ccaacttggt cttcaatgta 120
attgatttta acttgttttc tttcttttac ttttcttatt tttttctttc ttttcatttt 180
tttcttattt cttttccttc tatttatttt acttttctta tttgttat atg tta ttt 237
Met Leu Phe
ctt ttt ctt ttc tta ctt ttc ttc ttt ttt cat ttt tct ttt tta aat 285
Leu Phe Leu Phe Leu Leu Phe Phe Phe Phe His Phe Ser Phe Leu Asn
-15 -10 -5 1
tgg agt ctc act ctg ttg ccc agg ctg gag tgc agt ggt gca atc ttg 333
Trp Ser Leu Thr Leu Leu Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu
5 10 15
gct cac tgc agc ctc cac ctc ctg ggt tca agc gat tct cct gcc tca 381
Ala His Cys Ser Leu His Leu Leu Gly Ser Ser Asp Ser Pro Ala Ser
20 25 30
gcc ccc cc 389
Ala Pro
35

<210> 421

<211> 461

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 75..461

<221> sig_peptide

<222> 75..125

<223> score 9.2

seq PALLLAFLPLASQ/KS

<400> 421

gacctgagtt ttganagcgt cttctgctcc tcttcatctg gtccctttcc ttccaagacc 60
ccagagagga aggc atg cgg tgg gcc cca gcc ctg ctt cta gct ttc ctg 110
Met Arg Trp Ala Pro Ala Leu Leu Leu Ala Phe Leu
-15 -10
cct ctt gcc agt cag aaa tct tcc aac ttg caa ggg aga agg aag tca 158
Pro Leu Ala Ser Gln Lys Ser Ser Asn Leu Gln Gly Arg Arg Lys Ser
-5 1 5 10

gtc acc agg cca gct ggg tca tct gct gta atc act tgt gat ctt act	206
Val Thr Arg Pro Ala Gly Ser Ser Ala Val Ile Thr Cys Asp Leu Thr	
15 20 25	
gta ata aat acc ttc tac atc cac tgg tac ctg cac cag gcg ggg aag	254
Val Ile Asn Thr Phe Tyr Ile His Trp Tyr Leu His Gln Ala Gly Lys	
30 35 40	
gcc cca cag cat ctt cca tac tat gac ccc tac tac tcc agg gtt gtg	302
Ala Pro Gln His Leu Pro Tyr Tyr Asp Pro Tyr Tyr Ser Arg Val Val	
45 50 55	
ttg gaa tca aga atc agt aga gga aag tat ttt act tat gca agc atg	350
Leu Glu Ser Arg Ile Ser Arg Gly Lys Tyr Phe Thr Tyr Ala Ser Met	
60 65 70 75	
agg agg agc tgg aaa ttg ata ctg caa aat cta att gaa aat gat tct	398
Arg Arg Ser Trp Lys Leu Ile Leu Gln Asn Leu Ile Glu Asn Asp Ser	
80 85 90	
gga tct att act gtg cca cct ggg aca ggc aca gtg att cac acc tgc	446
Gly Ser Ile Thr Val Pro Pro Gly Thr Gly Thr Val Ile His Thr Cys	
95 100 105	
cct aca cca cac tgg	461
Pro Thr Pro His Trp	
110	

<210> 422
 <211> 386
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 105..386
 <221> sig_peptide
 <222> 105..203
 <223> score 5
 seq LELLGLSGPPASG/SL

<400> 422	
aataatattt ctcagagtc taactgtctt gctttccctg tctctccag attttgcct	60
gaaagccttc cctgtaggaa gaatgtytgt ttttttttaa agmg atg ggg tct tta	116
Met Gly Ser Leu	
-30	
ctc tgt tgc cca agc tgg agt gca gtg gtg atc ata gtt cac tgt aac	164
Leu Cys Cys Pro Ser Trp Ser Ala Val Val Ile Ile Val His Cys Asn	
-25 -20 -15	
ctc gaa ctt ctg ggc tta agt ggt cct cct gcc tca ggt tcc cta gta	212
Leu Glu Leu Leu Gly Leu Ser Gly Pro Pro Ala Ser Gly Ser Leu Val	
-10 -5 1	
ggg agg act aca ggt gtg tgc cag cat gcc ccg cta att aaa aaa aat	260
Gly Arg Thr Thr Gly Val Cys Gln His Ala Pro Leu Ile Lys Lys Asn	
5 10 15	
ttt ttt ttc gta gag aca ggg gtc tca cta tgt ttg acc agg ctg gtc	308
Phe Phe Phe Val Glu Thr Gly Val Ser Leu Cys Leu Thr Arg Leu Val	
20 25 30 35	

004220"666E560

tgg aac tct ggg cct caa gca aag cat tgg gat tac agg tcc aag cca 356
 Trp Asn Ser Gly Pro Gln Ala Lys His Trp Asp Tyr Arg Ser Lys Pro
 40 45 50

ctg tgc cag gtc cag gaa gaa tgc gcc ccc 386
 Leu Cys Gln Val Gln Glu Glu Cys Ala Pro
 55 60

<210> 423
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..349

<221> sig_peptide
 <222> 23..151
 <223> score 11
 seq VFVLLLVLSLAIG/LY

<400> 423
 agatcacaga cacagtgagg at atg agt gta ggg gtg agc ayc bba gcc cct 52
 Met Ser Val Gly Val Ser Xaa Xaa Ala Pro
 -40 -35

ctt tcc cca acc tcg ggc aca agc gtc ggc atg tct acc ttc tcc atc 100
 Leu Ser Pro Thr Ser Gly Thr Ser Val Gly Met Ser Thr Phe Ser Ile
 -30 -25 -20

atg gac tat gtg gtg ttc gtc ctg ctg ctg gtt ctc tct ctt gcc att 148
 Met Asp Tyr Val Val Phe Val Leu Leu Leu Val Leu Ser Leu Ala Ile
 -15 -10 -5

ggg ctc tac cat gct tgt cgt ggc tgg ggc cgg cat act gtt ggt gas 196
 Gly Leu Tyr His Ala Cys Arg Gly Trp Gly Arg His Thr Val Gly Xaa
 1 5 10 15

ctg ctg atg gcg gac cgc aaa atg ggc tgc ctt ccg gtg gca ctg tcc 244
 Leu Leu Met Ala Asp Arg Lys Met Gly Cys Leu Pro Val Ala Leu Ser
 20 25 30

ctg ctg gcc acc ttc cag tca gcc gtg gcc atc ctg ggt gtg ccg tca 292
 Leu Leu Ala Thr Phe Gln Ser Ala Val Ala Ile Leu Gly Val Pro Ser
 35 40 45

gag mbc tac cga ttt ggg acc baa tat tgg ttc ctg ggc tgc tgc tac 340
 Glu Xaa Tyr Arg Phe Gly Thr Xaa Tyr Trp Phe Leu Gly Cys Cys Tyr
 50 55 60

ttt ctg ggg c 350
 Phe Leu Gly
 65

<210> 424
 <211> 449
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 185..448

<221> sig_peptide
<222> 185..325
<223> score 5.8
seq LMCFGALIGLCAC/IC

<400> 424
cattagtgat gaggcagatg aaaagactta taatgatgca ctttttcgat acaatggcac 60
agtgggattg tggagacggt gtatcaccat acccaaaaac atacattggt atagcccacc 120
agaaaggaca gagtcatttg atgtgggtcac aaaatgtgtg agtttcacac taactgagca 180
gttc atg gag aaa ttt gtt gat ccc gga aac cac aat agc ggg att gat 229
Met Glu Lys Phe Val Asp Pro Gly Asn His Asn Ser Gly Ile Asp
-45 -40 -35
ctc ctt agg acc tat ctt tgg cgt tgc cag ttc ctt tta cct ttt gtg 277
Leu Leu Arg Thr Tyr Leu Trp Arg Cys Gln Phe Leu Leu Pro Phe Val
-30 -25 -20
agt tta ggt ttg atg tgc ttt ggg gct ttg atc gga ctt tgt gct tgc 325
Ser Leu Gly Leu Met Cys Phe Gly Ala Leu Ile Gly Leu Cys Ala Cys
-15 -10 -5
att tgc cga agc tta tat ccc acc att gcc acg ggc att ctc cat ctc 373
Ile Cys Arg Ser Leu Tyr Pro Thr Ile Ala Thr Gly Ile Leu His Leu
1 5 10 15
ctt gca ggt ctg tgt aca ctg ggc tca gta agt tgt tat gtt gct gga 421
Leu Ala Gly Leu Cys Thr Leu Gly Ser Val Ser Cys Tyr Val Ala Gly
20 25 30
att gaa cta ctc cac cag aaa cta gag g 449
Ile Glu Leu Leu His Gln Lys Leu Glu
35 40

<210> 425
<211> 430
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 125..430

<221> sig_peptide
<222> 125..199
<223> score 7.1
seq LFVMAFLLSGAAP/LK

<400> 425
attgccgagg aaggcttgca cagggtgaaa gctttgcttc tctgctgctg taacagggac 60
tagcacagac acacggatga gtgggggtcat ttccagatat taggtcacag cagaarcagc 120
maaa atg gat ccc cag tgc act atg gga ctg agt aac att ctc ttt gtg 169
Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val
-25 -20 -15
atg gcc ttc ctg ctc tct ggt gct gct cct ctg aag att caa gct tat 217

Met	Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr		
-10					-5					1				5			
ttc	aat	gag	act	gca	gac	ctg	cca	tgc	caa	ttt	gca	aac	tct	caa	aac	265	
Phe	Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn		
			10					15					20				
caa	agc	ctg	agt	gag	cta	gta	gta	ttt	tgg	cag	gac	cag	gaa	aac	ttg	313	
Gln	Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu		
		25					30					35					
gtt	ctg	aat	gag	gta	tac	tta	ggc	aaa	gag	aaa	ttt	gac	agt	gtt	cat	361	
Val	Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His		
		40				45					50						
tcc	aag	tat	atg	ggc	cgc	aca	agt	ttt	gat	tcg	gac	agt	tgg	acc	ctg	409	
Ser	Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu		
55					60				65					70			
aga	ctt	cac	aat	ctt	cag	atc										430	
Arg	Leu	His	Asn	Leu	Gln	Ile											
				75													

<210> 426
 <211> 173
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 11..172

<221> sig_peptide
 <222> 11..118
 <223> score 4.4
 seq LWFFLPSLXCPEC/CP

<400>	426																
tct	ggt	ctg	ctg	atg	tgg	acc	ctc	ccc	agc	ctc	agt	gca	tcg	ttt	cag	cct	49
	Met	Trp	Thr	Leu	Pro	Ser	Leu	Ser	Ala	Ser	Phe	Gln	Pro				
			-35				-30					-25					
ttt	ctg	ggc	agc	ctt	cgc	cct	tct	cac	atc	ctg	tgg	ttc	ttc	ctg	ccc	97	
Phe	Leu	Gly	Ser	Leu	Arg	Pro	Ser	His	Ile	Leu	Trp	Phe	Phe	Leu	Pro		
			-20				-15					-10					
tcc	ctc	cmc	tgc	cca	gaa	tgc	tgc	cct	cct	gat	cca	gga	tct	cca	gcc	145	
Ser	Leu	Xaa	Cys	Pro	Glu	Cys	Cys	Pro	Pro	Asp	Pro	Gly	Ser	Pro	Ala		
		-5				1				5							
tcc	agg	gac	cct	aac	gtg	gcc	tgc	gaa	c							173	
Ser	Arg	Asp	Pro	Asn	Val	Ala	Cys	Glu									
10					15												

<210> 427
 <211> 183
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 6..182

<221> sig_peptide

<222> 6..62

<223> score 4.1

seq FLWLSSIPSYIYT/HT

<400> 427

tgcaa atg cca tta att cat tcc ttt tta tgg ctg agt agt att cca tca 50
Met Pro Leu Ile His Ser Phe Leu Trp Leu Ser Ser Ile Pro Ser

-15 -10 -5
tat ata tac aca cat aca cac atg tat gta tat aca tat ata tac aca 98
Tyr Ile Tyr Thr His Thr His Met Tyr Val Tyr Thr Tyr Ile Tyr Thr

1 5 10
cgc aca tat atg tat gta tat aca tac aca cac aca aac acc ccc acc 146
Arg Thr Tyr Met Tyr Val Tyr Thr Tyr Thr His Thr Asn Thr Pro Thr

15 20 25
cac cac agt ttc ttt atc ctt tca ttg att gct ggg c 183
His His Ser Phe Phe Ile Leu Ser Leu Ile Ala Gly

<210> 428

<211> 249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 43..249

<221> sig_peptide

<222> 43..96

<223> score 5.7

seq AFFSLAALAEVAA/ME

<400> 428

acacaacacc gaggtcgggg agmcgcggas agtactccag aa atg cct gcc gtg 54
Met Pro Ala Val

-15
tct gcg ttc ttt agc ctc gct gcg ctg gct gaa gtg gca gcc atg gaa 102
Ser Ala Phe Phe Ser Leu Ala Ala Leu Ala Glu Val Ala Ala Met Glu

-10 -5 1
aat gtg cac aga ggt cag agg tca act ccg ctc acc cat gat gga cag 150
Asn Val His Arg Gly Gln Arg Ser Thr Pro Leu Thr His Asp Gly Gln

5 10 15
cca aaa gaa atg ccg cag gtc ctg tac tta ttt cct gcg ctg acc agt 198
Pro Lys Glu Met Pro Gln Val Leu Tyr Leu Phe Pro Ala Leu Thr Ser

20 25 30
gaa gcg ccc ttt cat tgt aaa aca ttg tgc ttt acc tac tac cct agc 246
Glu Ala Pro Phe His Cys Lys Thr Leu Cys Phe Thr Tyr Tyr Pro Ser

35 40 45 50
act 249

Thr

<210> 429
<211> 452
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 237..452

<221> sig_peptide
<222> 237..287
<223> score 4.2
seq LAFLLVSLYWSHM/HP

<400> 429
atagggctga accgaggact gaaaaaggga ggaggcagac cactcggaga ggagctggga 60
agcagtgcag agaggagagc ggassnagct gccgctgagc aaagtgcgac tgtatctggt 120
ttggcctgct cttcctcacc ttcctccttt ccctgagctg gctgtacatc gggctcgtcc 180
ttctcaatga cctgcacaac ttcaatgaat tcctcttccg ccgctgggga cactgg atg 239
Met
gac tgg tcc ctg gca ttc ctg ctg gta tct ctc tac tgg tca cat atg 287
Asp Trp Ser Leu Ala Phe Leu Leu Val Ser Leu Tyr Trp Ser His Met
-15 -10 -5
cat cct tgc tat tgg tcc tgg ccc tgc tcc tgc ggc ttt gta gac agc 335
His Pro Cys Tyr Trp Ser Trp Pro Cys Ser Cys Gly Phe Val Asp Ser
1 5 10 15
ccc tgc atc tgc aca gcc tcc aca agg tgc tgc tgc tcc tca tta tgc 383
Pro Cys Ile Cys Thr Ala Ser Thr Arg Cys Cys Cys Ser Ser Leu Cys
20 25 30
tgc ttg tgg cgg ctg gcc ttg tgg gac tgg aca tcc aat ggc agc agg 431
Cys Leu Trp Arg Leu Ala Leu Trp Asp Trp Thr Ser Asn Gly Ser Arg
35 40 45
agt ggc ata gct tgc gtg tgt 452
Ser Gly Ile Ala Cys Val Cys
50 55

<210> 430
<211> 222
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 24..221

<221> sig_peptide
<222> 24..65
<223> score 3.7
seq CSLLSGWGQLLRC/VQ

<220>
 <221> CDS
 <222> 11..211
 <221> sig_peptide
 <222> 11..76
 <223> score 7.2
 seq IIYALQFLFLVFA/PS

<400> 432
 attcaatcaa atg aac cga tct tgt aga aac act gga atc att tat gcg 49
 Met Asn Arg Ser Cys Arg Asn Thr Gly Ile Ile Tyr Ala
 -20 -15 -10
 ttg cag ttt ctc ttt ctt gtt ttc gct cct tct tcc ctg gga tat ttt 97
 Leu Gln Phe Leu Phe Leu Val Phe Ala Pro Ser Ser Leu Gly Tyr Phe
 -5 1 5
 gag tgg att gtg gct att aat caa gat ctc gtg cta ttc gtg ttt tgc 145
 Glu Trp Ile Val Ala Ile Asn Gln Asp Leu Val Leu Phe Val Phe Cys
 10 15 20
 ttg tgc ttt tgc ctc agg att agc atc att caa ggc aaa cgc aaa gct 193
 Leu Ser Phe Ser Leu Arg Ile Ser Ile Ile Gln Gly Lys Arg Lys Ala
 25 30 35
 gct ttt ccc acc ccc ccc cc 213
 Ala Phe Pro Thr Pro Pro
 40 45

<210> 433
 <211> 195
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 16..195
 <221> sig_peptide
 <222> 16..144
 <223> score 4
 seq AAWCSLVLSFCRL/HK

<400> 433
 tcctgggcta ctacg atg gcg atg agt ttc gag tgg ccg tgg cag tat cgc 51
 Met Ala Met Ser Phe Glu Trp Pro Trp Gln Tyr Arg
 -40 -35
 ttc cca ccc ttc ttt acg tta caa ccg aat gtg gac act cgg cag aag 99
 Phe Pro Pro Phe Phe Thr Leu Gln Pro Asn Val Asp Thr Arg Gln Lys
 -30 -25 -20
 cag ctg gcc gcc tgg tgc tgc ctg gtc ctg tcc ttc tgc cgc ctg cac 147
 Gln Leu Ala Ala Trp Cys Ser Leu Val Leu Ser Phe Cys Arg Leu His
 -15 -10 -5 1
 aaa cag tcc agc atg acg gtg atg gaa gct cag gag agc ccg ctc cga 195
 Lys Gln Ser Ser Met Thr Val Met Glu Ala Gln Glu Ser Pro Leu Arg

5

10

15

<210> 434
 <211> 155
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..154

<221> sig_peptide
 <222> 2..100
 <223> score 6
 seq LAHFLIGLTVCFG/EG

<400> 434
 c atg tac ctg tac ctg ttg tcc att tgt atg tct tct ttg aag aaa tgt 49
 Met Tyr Leu Tyr Leu Leu Ser Ile Cys Met Ser Ser Leu Lys Lys Cys
 -30 -25 -20
 cta ttc aag ttc tta gcc cac ttt tta atc ggg tta aca gtt tgt ttt 97
 Leu Phe Lys Phe Leu Ala His Phe Leu Ile Gly Leu Thr Val Cys Phe
 -15 -10 -5
 ggt gag ggr wgg cta atg agt tat agg agt tct tat tta tta ctt aaa 145
 Gly Glu Gly Xaa Leu Met Ser Tyr Arg Ser Ser Tyr Leu Leu Leu Lys
 1 5 10 15
 gga cca ccg g 155
 Gly Pro Pro

<210> 435
 <211> 190
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..190

<221> sig_peptide
 <222> 29..109
 <223> score 5
 seq CVLTASSWAVLWS/AR

<400> 435
 aagaaaagct ttgggtcaac tcagcatc atg ttt gca gat gct gac aga cgg 52
 Met Phe Ala Asp Ala Asp Arg Arg
 -25 -20
 gat cct aat gag agt caa tgt gtg ctc act gcc agc tcc tgg gct gtg 100
 Asp Pro Asn Glu Ser Gln Cys Val Leu Thr Ala Ser Ser Trp Ala Val
 -15 -10 -5
 ctc tgg tca gcc agg tgt gag ggc ctg gcc tgg ggt cac aca gct gac 148
 Leu Trp Ser Ala Arg Cys Glu Gly Leu Ala Trp Gly His Thr Ala Asp

	1		5		10	
tca	r	b	t	a	g	a
gga	a	t	g	c	c	c
atg	a	t	g	t	t	c
ctc	a	g	c	a	t	t
gga	a	g	g	a	a	c
agg	a	c	t			
act						
Ser	Xaa	Arg	Gly	Met	Pro	Met
Val	Leu	Ser	Ile	Gly	Arg	Thr
15				20		25

190

<210> 436
 <211> 210
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 58..210

<221> sig_peptide
 <222> 58..108
 <223> score 3.6
 seq WIYAFISLGYILG/SG

<400> 436	
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atg agh ntt tgc tgg ata tat gct ttc att tct ctt ggg tat ata ctt	105
Met Xaa Xaa Cys Trp Ile Tyr Ala Phe Ile Ser Leu Gly Tyr Ile Leu	
-15 -10 -5	
ggg agt gga att gtt ggg tta ttt ggt aat ttt atg ttt aaa ctt ttg	153
Gly Ser Gly Ile Val Gly Leu Phe Gly Asn Phe Met Phe Lys Leu Leu	
1 5 10 15	
agg aac tgc cag acc gtt ttc cag gat ggc tat gct ata tta ccc ttc	201
Arg Asn Cys Gln Thr Val Phe Gln Asp Gly Tyr Ala Ile Leu Pro Phe	
20 25 30	
cca cca acg	210
Pro Pro Thr	

<210> 437
 <211> 166
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..166

<221> sig_peptide
 <222> 5..88
 <223> score 4.5
 seq FLPFLSLPLDQT/LP

<400> 437	
agat atg tkc scb aaa gcc tgc aga acc ctc gct tgg ttg cct gas ccg	49
Met Xaa Xaa Lys Ala Cys Arg Thr Leu Ala Trp Leu Pro Xaa Pro	
-25 -20 -15	
ttc tta ccc ttt ctc ctc agt ctt ccc ttg gac cag acg ctt cct cgc	97

004220" 556E550

Phe Leu Pro Phe Leu Leu Ser Leu Pro Leu Asp Gln Thr Leu Pro Arg
 -10 -5 1
 cag ggt cct ggc caa tcc ctg tcc ttc cca gaa aac tac cag act ctt 145
 Gln Gly Pro Gly Gln Ser Leu Ser Phe Pro Glu Asn Tyr Gln Thr Leu
 5 10 15
 ccc aag agc acc cga cac cct 166
 Pro Lys Ser Thr Arg His Pro
 20 25

<210> 438
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 151..378

<221> sig_peptide
 <222> 151..189
 <223> score 4.9
 seq MLTASLAFQLVDG/VS

<400> 438
 gaatctgctc gctcttctgg agctgagaca ctcatcttct cctgccctgg cacatcaaaa 60
 ctccagggttc tctgatcttt gaacactggg acttaatcca gcatccctt actgcctgaa 120
 gttctcagga ctttggaactt ggactgaacg atg cta aca gct tcc ctg gct ttc 174
 Met Leu Thr Ala Ser Leu Ala Phe
 -10
 cag ctt gta gat ggc gta tca tgg aat ttc tca gtc tcc aaa atg ctg 222
 Gln Leu Val Asp Gly Val Ser Trp Asn Phe Ser Val Ser Lys Met Leu
 -5 1 5 10
 gca tca cca tct aca tca ggt cag ctg tct cag ttt ggg gca agt tta 270
 Ala Ser Pro Ser Thr Ser Gly Gln Leu Ser Gln Phe Gly Ala Ser Leu
 15 20 25
 tac ggg caa caa agt gca cta ggc ctt cca atg agg ggg atg agc aac 318
 Tyr Gly Gln Gln Ser Ala Leu Gly Leu Pro Met Arg Gly Met Ser Asn
 30 35 40
 aat acc cct cag tta aat cgc agc tta tca caa gsa ctc agt tac cga 366
 Asn Thr Pro Gln Leu Asn Arg Ser Leu Ser Gln Xaa Leu Ser Tyr Arg
 45 50 55
 gcc acg tca cgc ca 380
 Ala Thr Ser Arg
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<210> 439
 <211> 226
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 23..226

<221> sig_peptide
 <222> 23..166
 <223> score 5.2
 seq EVVTLPLTSHCLA/QV

<400> 439
 tgaatttcta aaactctttt tt atg gga ctt cac att tct ctg att aaa ttt 52
 Met Gly Leu His Ile Ser Leu Ile Lys Phe
 -45 -40
 ctt ctt gct aat gga ccc cat att cct agt cac caa aga cct ttt gaa 100
 Leu Leu Ala Asn Gly Pro His Ile Pro Ser His Gln Arg Pro Phe Glu
 -35 -30 -25
 cct aaa ggg gaa aaa agc tgc aga att gaa gtg gtg act ctg cca ctt 148
 Pro Lys Gly Glu Lys Ser Cys Arg Ile Glu Val Val Thr Leu Pro Leu
 -20 -15 -10
 act agc cat tgt ctt gcc caa gtt gca agt tct gac ctc atc cat agg 196
 Thr Ser His Cys Leu Ala Gln Val Ala Ser Ser Asp Leu Ile His Arg
 -5 1 5 10
 atg aga acc ata aca ggt acc tcg tca cac 226
 Met Arg Thr Ile Thr Gly Thr Ser Ser His
 15 20

<210> 440
 <211> 339
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..338
 <221> sig_peptide
 <222> 42..179
 <223> score 6.9
 seq VTMLMGFLGCIGA/VN

<400> 440
 cttctgtgaa atggccatgc tagtgctgc caggcagggt g atg tca gag ttg gag 56
 Met Ser Glu Leu Glu
 -45
 acg gcg tgt gga aag ccc atg agg cac aaa acc tcc tcc agc tcg ctt 104
 Thr Ala Cys Gly Lys Pro Met Arg His Lys Thr Ser Ser Ser Ser Leu
 -40 -35 -30
 agg atg ggg gcc tat gtc ttc atc ggc gtg ggg gca gtc act atg ctc 152
 Arg Met Gly Ala Tyr Val Phe Ile Gly Val Gly Ala Val Thr Met Leu
 -25 -20 -15 -10
 atg ggc ttc ctg ggc tgc atc ggc gcc gtc aac gag gtc cgc tgc ctg 200
 Met Gly Phe Leu Gly Cys Ile Gly Ala Val Asn Glu Val Arg Cys Leu
 -5 1 5
 ctg ggg ctg tac ttt gct ttc ctg ctc ctg atc ctc att gcc cag gtg 248
 Leu Gly Leu Tyr Phe Ala Phe Leu Leu Leu Ile Leu Ile Ala Gln Val

10	15	20	
acg gcc ggg gcc ctc ttc tac ttc aac atg ggc aag ctg aag cag gag			296
Thr Ala Gly Ala Leu Phe Tyr Phe Asn Met Gly Lys Leu Lys Gln Glu			
25	30	35	
atg ggt ggc atc gtg act gag ctc att cga gac tac aac agc c			339
Met Gly Gly Ile Val Thr Glu Leu Ile Arg Asp Tyr Asn Ser			
40	45	50	

<210> 441
 <211> 239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..239

<221> sig_peptide
 <222> 42..116
 <223> score 4.6
 seq GFFCLFVLRQSFT/LS

<400> 441	
aatttttaggg tgacggtgat actcaaaaat ctcacactgc c atg ttt cca ttc cca	56
Met Phe Pro Phe Pro	
-25	
cat act cag tgt ctt cac tta ggt ttc ttt tgt ttg ttt gtt ttg aga	104
His Thr Gln Cys Leu His Leu Gly Phe Phe Cys Leu Phe Val Leu Arg	
-20 -15 -10 -5	
cag agt ttc act ctg tca ccc agg ctg gag tgc agt ggc gca atc ttg	152
Gln Ser Phe Thr Leu Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu	
1 5 10	
gct cac tgc aac ctc tgc ctc cca cgt tca agc agt act cct gcm tca	200
Ala His Cys Asn Leu Cys Leu Pro Arg Ser Ser Ser Thr Pro Ala Ser	
15 20 25	
gcc tcc caa gag cta gga ttg cag atg cgc acc acc gta	239
Ala Ser Gln Glu Leu Gly Leu Gln Met Arg Thr Thr Val	
30 35 40	

<210> 442
 <211> 207
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 9..206

<221> sig_peptide
 <222> 9..116
 <223> score 5.5
 seq LHFVYCFLCCA EA/FL

<400> 442
 ctccttat atg ttt cag tta ctg atc ctt tgt cag atg aat agt ttg aaa 50
 Met Phe Gln Leu Leu Ile Leu Cys Gln Met Asn Ser Leu Lys
 -35 -30 -25
 ata ttt tct ccc att ctt gga tgg tct ctt cat ttt gtt tat tgt ttc 98
 Ile Phe Ser Pro Ile Leu Gly Trp Ser Leu His Phe Val Tyr Cys Phe
 -20 -15 -10
 ctt tgc tgt gca gaa gcc ttt tta ctt gat atg atc cca ttt atg caa 146
 Leu Cys Cys Ala Glu Ala Phe Leu Leu Asp Met Ile Pro Phe Met Gln
 -5 1 5 10
 ttt tac ttt ggt tac ctg tgc ttg tgg ggt att act tta aaa atc ttt 194
 Phe Tyr Phe Gly Tyr Leu Cys Leu Trp Gly Ile Thr Leu Lys Ile Phe
 15 20 25
 gcc cag tcc aat t 207
 Ala Gln Ser Asn
 30

<210> 443
 <211> 175
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 7..174

 <221> sig_peptide
 <222> 7..102
 <223> score 10.6
 seq VVFLLLLVSTLSS/VV

<400> 443
 cgtata atg act tac ttt cct ctg ggt aga tac cca gta atg gga ttg 48
 Met Thr Tyr Phe Pro Leu Gly Arg Tyr Pro Val Met Gly Leu
 -30 -25 -20
 ctg gat caa atg gta gtt gtg ttt tta ctt ctt tta gtc tcc aca ctt 96
 Leu Asp Gln Met Val Val Val Phe Leu Leu Leu Leu Val Ser Thr Leu
 -15 -10 -5
 tct tcc gta gtg gtt tta cta gtt tgc att ccc acc agc agt gta aaa 144
 Ser Ser Val Val Val Leu Leu Val Cys Ile Pro Thr Ser Ser Val Lys
 1 5 10
 ttg ttc cct ttt cac cat atc cac acc aac t 175
 Leu Phe Pro Phe His His Ile His Thr Asn
 15 20

<210> 444
 <211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 28..231

<221> sig_peptide

<222> 28..120

<223> score 6.4

seq GFMVLLMIPWGSA/AK

<400> 444

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agagcaggac ctggaaagct ggtttgt atg ggc tgc agc ctg ccg ctg agc tgc      54
                               Met Gly Cys Ser Leu Pro Leu Ser Cys
                               -30      -25
atc atg gtg cgg tct gtg gcc tgg gca ggt ttc atg gtc ctg ctg atg      102
Ile Met Val Arg Ser Val Ala Trp Ala Gly Phe Met Val Leu Leu Met
      -20      -15      -10
atc cca tgg ggc tct gct gca aaa ctg gtc tgc tac ttc acc aac tgg      150
Ile Pro Trp Gly Ser Ala Ala Lys Leu Val Cys Tyr Phe Thr Asn Trp
      -5      1      5      10
gcc cag tac agr cag ggg gar gct cgc ttc cwr gcc caa rga stt gga      198
Ala Gln Tyr Arg Gln Gly Glu Ala Arg Phe Xaa Ala Gln Xaa Xaa Gly
      15      20      25
ccc cag cct ttg mam cca cct cat cta cgc ctt c      232
Pro Gln Pro Leu Xaa Pro Pro His Leu Arg Leu
      30      35

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<210> 445

<211> 336

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 177..335

<221> sig_peptide

<222> 177..320

<223> score 3.5

seq LIIHLMGTTGLCA/SL

<400> 445

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catattaact cttcakgtaa aaaccatctt gtagctgggc aagggtggcac atgcctgtag      60
tcccagctac ttggggggact gaggcaggtg gatcgcttga gcctaggagt tcaaggctgt      120
agtagcctat kgatcacgtc tatcaatagc cactggactc cagcctggac aatgta atg      179
                               Met
aga gtc tgt ctc rra aaa aag gaa caa tct tgt gtt tgc gtg tgt gct      227
Arg Val Cys Leu Xaa Lys Lys Glu Gln Ser Cys Val Cys Val Cys Ala
      -45      -40      -35
cat gtc ttt gtt gga ata ata ctg aca cag tca ctc aaa tta act ctc      275
His Val Phe Val Gly Ile Ile Leu Thr Gln Ser Leu Lys Leu Thr Leu
      -30      -25      -20
aaa tct ttg att att cat ttg atg gga aca aca ggt tta tgt gcc agc      323
Lys Ser Leu Ile Ile His Leu Met Gly Thr Thr Gly Leu Cys Ala Ser
      -15      -10      -5      1

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tta tca gga ctt a
Leu Ser Gly Leu
5

336

<210> 446
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 68..241

<221> sig_peptide
<222> 68..133
<223> score 4.3
seq LFFETGSPSVAQS/GV

<400> 446
cttacagagt taataagcat caaagaactt actgaaggac tttataaatt aaataaccatt 60
atgtaga atg gtg gtt agt gcc ttt att tat tta ttt ttt gag aca 109
Met Val Val Val Ser Ala Phe Ile Tyr Leu Phe Phe Glu Thr
-20 -15 -10
ggg tct ccc tct gtc gcc cag tct gga gtg cag tgg tgt gat ctc ggc 157
Gly Ser Pro Ser Val Ala Gln Ser Gly Val Gln Trp Cys Asp Leu Gly
-5 1 5
tta ctg cag cct ccg cct cct gga ttc aag cga ttc tct tgc ctc agc 205
Leu Leu Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser
10 15 20
ctc cta ggt agb drg gat tgc aga cgt gcg cca ccc 241
Leu Leu Gly Xaa Xaa Asp Cys Arg Arg Ala Pro Pro
25 30 35

<210> 447
<211> 179
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..177

<221> sig_peptide
<222> 10..117
<223> score 5.3
seq SLLIATSTSRVQA/TL

<400> 447
aaagatgct atg ctg gtt cgt tgt ttt ttt ttg aga tgg agt ctc act ctg 51
Met Leu Val Arg Cys Phe Phe Leu Arg Trp Ser Leu Thr Leu
-35 -30 -25
tca cct gac tgg agt aca gtg gcg caa tct ctg ctc att gca acc tcc 99

Ser	Pro	Asp	Trp	Ser	Thr	Val	Ala	Gln	Ser	Leu	Leu	Ile	Ala	Thr	Ser	
		-20					-15					-10				
acc	tcc	egg	gtt	caa	gcg	acc	ctc	ctg	cct	cag	cct	tgt	gag	tat	ctg	147
Thr	Ser	Arg	Val	Gln	Ala	Thr	Leu	Leu	Pro	Gln	Pro	Cys	Glu	Tyr	Leu	
	-5					1			5						10	
gaa	cta	cag	gca	tgt	gcc	acc	aca	cct	ggc	at						179
Glu	Leu	Gln	Ala	Cys	Ala	Thr	Thr	Pro	Gly							
			15					20								

<210> 448
 <211> 286
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 84..284

<221> sig_peptide
 <222> 84..203
 <223> score 4.9
 seq SLKICGLVFGILA/LT

<400>	448																
agccgactca	cttgcaactc	cacctcagca	gtgggtctctc	agtcctctca	aagcaaggaa												60
agagtactgt	gtgctgagag	acc atg	gca aag	aat cct	cca gag	aat tgt	gaa										113
		Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu						
		-40															
gac tgt	cac att	cta aat	gca gaa	gct ttt	aaa tcc	aag aaa	ata tgt										161
Asp Cys	His Ile	Leu Asn	Ala Glu	Ala Phe	Lys Ser	Lys Lys	Ile Cys										
-30		-25			-20		-15										
aaa tca	ctt aag	att tgt	gga ctg	gtg ttt	ggg atc	ctg gcc	cta act										209
Lys Ser	Leu Lys	Ile Cys	Gly Leu	Val Phe	Gly Ile	Leu Ala	Leu Thr										
		-10			-5		1										
cta att	gtc ctg	ttt tgg	ggg agc	aag cac	ttc tgg	ccg gag	gta ccc										257
Leu Ile	Val Leu	Phe Trp	Gly Ser	Lys His	Phe Trp	Pro Glu	Val Pro										
	5		10			15											
aaa aaa	gcc tat	gac atg	gag cac	act ac													286
Lys Lys	Ala Tyr	Asp Met	Glu His	Thr													
20			25														

<210> 449
 <211> 249
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..248

<221> sig_peptide
 <222> 12..146
 <223> score 14

seq LLLLLLLPSPLHP/HP

<400> 449
 ttttagtcctc c atg ggg cta gaa gag aga agg acg gag tcg agt ggc acc 50
 Met Gly Leu Glu Glu Arg Arg Thr Glu Ser Ser Gly Thr
 -45 -40 -35
 cta gaa gac gct ctg tgc ctt cgg agg tct ttc tgc ctg cct gtc ctc 98
 Leu Glu Asp Ala Leu Cys Leu Arg Arg Ser Phe Cys Leu Pro Val Leu
 -30 -25 -20
 atg cct ctc ctc ctc ttg ctg ctc ctg ctg cca agc ccc tta cac ccc 146
 Met Pro Leu Leu Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro
 -15 -10 -5
 cac ccc atc tgt gag gtc tcc aaa gtg gcc agc cac cta gaa gtg aac 194
 His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn
 1 5 10 15
 tgt gac aag agg aat ctg aca gcg ctg cct cca gac ctg ccg aaa gac 242
 Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp
 20 25 30
 aca aac c 249
 Thr Asn

<210> 450
 <211> 169
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..168

<221> sig_peptide
 <222> 1..90
 <223> score 7.4
 seq LFPLLTHSEPSQG/QS

<400> 450
 atg tgt aga att tcc tgt tca aac ctt agt aac acg ttg atg aga aat 48
 Met Cys Arg Ile Ser Cys Ser Asn Leu Ser Asn Thr Leu Met Arg Asn
 -30 -25 -20 -15
 cta ctt ttt cca ctc ttg act cac tct gag cct tca cag ggg cag tct 96
 Leu Leu Phe Pro Leu Leu Thr His Ser Glu Pro Ser Gln Gly Gln Ser
 -10 -5 1
 gcg aag att gca ggc att gtt tgt tct tgt ctt gga ttt atg cct tta 144
 Ala Lys Ile Ala Gly Ile Val Cys Ser Cys Leu Gly Phe Met Pro Leu
 5 10 15
 aat ttc acc ttt tat tac aca gcc a 169
 Asn Phe Thr Phe Tyr Tyr Thr Ala
 20 25

<210> 451
 <211> 407
 <212> DNA

004230" 666F560

<213> Homo sapiens

<220>

<221> CDS

<222> 228..407

<221> sig_peptide

<222> 228..341

<223> score 4

seq FKPXSCLSLLSNX/DY

<400> 451

tgagttttat gmttgattta tatcttttgg ttacaagtcc tttgtcagat atatgatttg	60
caaataatttt ctactctgg gtaggttgtc tttttacttt cttgataatg tcctcttttg	120
ttgcttggtg tatctccttt tttgtttttt attcttttta aagttatctc ttacaggaag	180
gattcctttt ttcttaaaaa agtttttcaa ttcttttttt ttttgag atg gag tct	236
	Met Glu Ser
cac tct gtc gcc cag gct agg atg cgg ysg caw aat ctc agc tca ctg	284
His Ser Val Ala Gln Ala Arg Met Arg Xaa Xaa Asn Leu Ser Ser Leu	
-35 -30 -25 -20	
caa cct ctg ccg cct ggg ttc aag cca tts tcc tgc ctm agc ctc ctg	332
Gln Pro Leu Pro Pro Gly Phe Lys Pro Xaa Ser Cys Leu Ser Leu Leu	
-15 -10 -5	
agt aay tsa gat tac agg cat gca cca cca ttc ctg gct aat ttt kgw	380
Ser Asn Xaa Asp Tyr Arg His Ala Pro Pro Phe Leu Ala Asn Phe Xaa	
1 5 10	
att ttt cat aga gat gga gtt tca cca	407
Ile Phe His Arg Asp Gly Val Ser Pro	
15 20	

<210> 452

<211> 331

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 78..329

<221> sig_peptide

<222> 78..137

<223> score 6.9

seq LYLLGMLVPGGLG/YD

<400> 452

cttgatgcat tcattctcaa ggacacttga tccactgcca gagaggccca gaattttcta	60
acttactgtg tggcaga atg aag cct ctg ctt gaa acc ctt tat ctt ttg	110
	Met Lys Pro Leu Leu Glu Thr Leu Tyr Leu Leu
-20 -15 -10	
ggg atg ctg gtt cct gga ggg ctg gga tat gat aga tcc tta gcc caa	158
Gly Met Leu Val Pro Gly Gly Leu Gly Tyr Asp Arg Ser Leu Ala Gln	
-5 1 5	

cac aga caa gag att gtg gac aag tca gtg agt cca tgg agc ctg gag 206
 His Arg Gln Glu Ile Val Asp Lys Ser Val Ser Pro Trp Ser Leu Glu
 10 15 20
 acg tat tcc tat aac ata tac cac ccc atg gga gag atc tat gag tgg 254
 Thr Tyr Ser Tyr Asn Ile Tyr His Pro Met Gly Glu Ile Tyr Glu Trp
 25 30 35
 atg aga gag atc agt gag aag tac aag gaa gtg gtg aca cag cat ttc 302
 Met Arg Glu Ile Ser Glu Lys Tyr Lys Glu Val Val Thr Gln His Phe
 40 45 50 55
 cta gga gtg acc tat gag acc caa ccc gc 331
 Leu Gly Val Thr Tyr Glu Thr Gln Pro
 60

<210> 453
 <211> 267
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..267
 <221> sig_peptide
 <222> 31..102
 <223> score 4.6
 seq FFIFCSLNTLLLG/GV

<400> 453
 acaactatcc tgccgtgtgc ttgtgtgcacc atg aag tct gcc aag ctg gga ttt 54
 Met Lys Ser Ala Lys Leu Gly Phe
 -20
 ctt cta aga ttc ttc atc ttc tgc tca ttg aat acc ctg tta ttg ggt 102
 Leu Leu Arg Phe Phe Ile Phe Cys Ser Leu Asn Thr Leu Leu Leu Gly
 -15 -10 -5
 ggt gtt aat aaa att gcg gag aag ata tgt gga gac ctc aaa gat ccc 150
 Gly Val Asn Lys Ile Ala Glu Lys Ile Cys Gly Asp Leu Lys Asp Pro
 1 5 10 15
 tgc aaa ttg gac atg aat ttt gga agc tgc tat gaa gtt cac ttt aga 198
 Cys Lys Leu Asp Met Asn Phe Gly Ser Cys Tyr Glu Val His Phe Arg
 20 25 30
 tat ttc tac aac aga acc tcc aaa aga tgt gaa act ttt gtc ttc tcc 246
 Tyr Phe Tyr Asn Arg Thr Ser Lys Arg Cys Glu Thr Phe Val Phe Ser
 35 40 45
 agc tgt aat ggc aac ctt aac 267
 Ser Cys Asn Gly Asn Leu Asn
 50 55

<210> 454
 <211> 392
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS
<222> 172..390

<221> sig_peptide
<222> 172..288
<223> score 5.9
seq SAWWCVLLEWSQG/AS

<400> 454
ctggggaaat tgagcctaag agaacagaaa gtacttgagg tcccacaatg aatctatgga 60
tgaatgagtg cttattcatt cactcatttt ttaaaaaaat ccattccaca agtatgtctt 120
aatcactgca gtgtaaggca catagggaca aaatagaaga ttctgtcct c atg gaa 177
Met Glu
ctc aca aac aag caa aca gga act gac aga cat gaa cag gta cta cgg 225
Leu Thr Asn Lys Gln Thr Gly Thr Asp Arg His Glu Gln Val Leu Arg
-35 -30 -25
agg gta aag caa gac aag agg ata agt gca tgg tgg tgc gtt tta ctg 273
Arg Val Lys Gln Asp Lys Arg Ile Ser Ala Trp Trp Cys Val Leu Leu
-20 -15 -10
gag tgg tca cag ggg gcc tct ctg agg agg caa cat cga ggg gag aca 321
Glu Trp Ser Gln Gly Ala Ser Leu Arg Arg Gln His Arg Gly Glu Thr
-5 1 5 10
agc ccc aaa tct ggg gaa aga ctt tcc agg cag aga gaa cag caa aaa 369
Ser Pro Lys Ser Gly Glu Arg Leu Ser Arg Gln Arg Glu Gln Gln Lys
15 20 25
ccg cag atg agt gac aag agc ct 392
Pro Gln Met Ser Asp Lys Ser
30

<210> 455
<211> 350
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 185..349

<221> sig_peptide
<222> 185..253
<223> score 9.4
seq SLLFICFFGESFC/IC

<400> 455
atattttgct gactggcaag gttatatgaa gtgcttttat tgaagcacca ttttaactaa 60
tagctcctgg tattttctgc ttcccttcgt agggaaattta gttattttat tttattattt 120
agctaattta gctattttta aatagctaaa ttttagctac ttttttttca attgacaaag 180
aagg atg tct aat caa aga cta ccg ctg att ttt tct ctg ttg ttt atc 229
Met Ser Asn Gln Arg Leu Pro Leu Ile Phe Ser Leu Leu Phe Ile
-20 -15 -10
tgc ttc ttc ggg gag agt ttc tgc att tgt gat gga act gtc tgg aca 277
Cys Phe Phe Gly Glu Ser Phe Cys Ile Cys Asp Gly Thr Val Trp Thr

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-5      1      5
wwg gtt kra tgg gag att ctt cca gaa gaa gta cat tat tgg aaa gtt 325
Xaa Val Xaa Trp Glu Ile Leu Pro Glu Glu Val His Tyr Trp Lys Val
10      15      20
aag ggt tct cca tct cac tgc ctg c 350
Lys Gly Ser Pro Ser His Cys Leu
25      30

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<210> 456
 <211> 466
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 268..465

<221> sig_peptide
 <222> 268..372
 <223> score 7.3
 seq LDLLGSSSPPTSA/SQ

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<400> 456
cttaaacttt attatgttgk kttcacaaag agcagccttt gttgactttg aaatcattgc 60
ttcagtattc tagaaaatct tgtttttggt aaacatgggc agtaacttac tatttttgta 120
tagttgttgt wcatckttacc cccaccctgt tttaaaaata aaaagtagtt gtcagattac 180
tttggtttaa gaagtacctt ttcacttgcc ttagaatctt cattactttg agcctacact 240
ccacctctta ttggaacttc atgaaga atg atg ttg gat ttc gct ctg tgc ccc 294
Met Met Leu Asp Phe Ala Leu Ser Pro
-35      -30
agg cta gag cgc agt ggt ctg atc atg gct tgc tgt acc ctt gac ctc 342
Arg Leu Glu Arg Ser Gly Leu Ile Met Ala Cys Cys Thr Leu Asp Leu
-25      -20      -15
ctg ggt tca agc agt cct ccc acc tca gcc tcc cag gtg gct ggg act 390
Leu Gly Ser Ser Ser Pro Pro Thr Ser Ala Ser Gln Val Ala Gly Thr
-10      -5      1      5
ggg cat gtg cca cca cac cca gct agt ttt ttt tac ttt ktt gta wga 438
Gly His Val Pro Pro His Pro Ala Ser Phe Phe Tyr Phe Xaa Val Xaa
10      15      20
cag gtc tac tat gtt tgc cag ctg atc t 466
Gln Val Tyr Tyr Val Ser Gln Leu Ile
25      30

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<210> 457
 <211> 188
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..188

<221> sig_peptide

[illegible]

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<210> 458
<211> 269
<212> DNA
<213> Homo sapiens
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<221> sig_peptide
<222> 4..138
<223> score 4.2
      seq FLIFYLFIFETES/HS
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331

<210> 459
 <211> 313
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 161..313

<221> sig_peptide
 <222> 161..289
 <223> score 6.8
 seq ALSAXTFVSFLHA/AP

<400> 459
 gtacggatct ctttaatat ctgtgtaaca aaatagaaat gctcataaag tacttctgcg 60
 gcaaaccaaa gtatagcacc tgactcaagg aaaagcaagg aaaagcacat gtgggatccc 120
 ttgaatggca agtgaaacta gccactagtt tcattttttac atg aaa caa tgg ctg 175
 Met Lys Gln Trp Leu
 -40
 tgt tgg gtg ctg agg ctg gaa ggt aga cag ggg ctt ggg gtt gga gag 223
 Cys Trp Val Leu Arg Leu Glu Gly Arg Gln Gly Leu Gly Val Gly Glu
 -35 -30 -25
 cct cgt ggg ctg cgt ttg tgc ttg ggg gcc ttg agc gca scc acc ttt 271
 Pro Arg Gly Leu Arg Leu Cys Leu Gly Ala Leu Ser Ala Xaa Thr Phe
 -20 -15 -10
 gtc agc ttt cta cac gct gct ccc cac tcc cat cca gcc ctt 313
 Val Ser Phe Leu His Ala Ala Pro His Ser His Pro Ala Leu
 -5 1 5

<210> 460
 <211> 293
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 48..293

<221> sig_peptide
 <222> 48..95
 <223> score 10.1
 seq LVLTLCTLPLAVA/SA

<400> 460
 aagatccctg cagccccggca ggagagaagg ctgagccttc tggcgctc atg gag agg 56
 Met Glu Arg
 -15
 ctc gtc cta acc ctg tgc acc ctc ccg ctg gct gtg gcg tct gct ggc 104
 Leu Val Leu Thr Leu Cys Thr Leu Pro Leu Ala Val Ala Ser Ala Gly
 -10 -5 1
 tgc gcc acg acg cca gct cgc aac ctg agc tgc tac cag tgc ttc aag 152

Cys	Ala	Thr	Thr	Pro	Ala	Arg	Asn	Leu	Ser	Cys	Tyr	Gln	Cys	Phe	Lys	
5						10					15					
gtc	agc	agc	tgg	acg	gag	tgc	ccg	ccc	acc	tgg	tgc	agc	ccg	ctg	gac	200
Val	Ser	Ser	Trp	Thr	Glu	Cys	Pro	Pro	Thr	Trp	Cys	Ser	Pro	Leu	Asp	
20					25					30					35	
caa	gtc	tgc	atc	tcc	aac	gag	gtg	gtc	gtc	tct	ttt	aaa	tgg	agt	gta	248
Gln	Val	Cys	Ile	Ser	Asn	Glu	Val	Val	Val	Ser	Phe	Lys	Trp	Ser	Val	
				40					45					50		
cgc	gtc	ctg	ctc	agc	aaa	cgc	tgt	gct	ccc	aga	tgt	ccc	aac	tca		293
Arg	Val	Leu	Leu	Ser	Lys	Arg	Cys	Ala	Pro	Arg	Cys	Pro	Asn	Ser		
				55				60					65			

<210> 461
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 226..378

 <221> sig_peptide
 <222> 226..315
 <223> score 4.8
 seq CLFLNARLAGTLC/QL

<400> 461																	
acagacatca	gctcgggtca	accgcggggcc	tcgagcccga	gtggctgagg	gctgttacct											60	
tcaaaccttt	gaatcccacg	ttttcccctt	gacttcctgt	caccgttaga	gaaaagtgga											120	
cagcgtctcg	gtcacagagt	tggagaaata	gtgcagggac	tcttcagggg	gagcgttttc											180	
ctcatcaaag	caaactgcaa	aatcgcttct	gccggcgtgg	acctg atg	aga gtc ggt											237	
					Met Arg Val Gly												
					-30												
cgt cgt gag gga cac cct ctg ttc cct aac gtc ccc cgc tgc tta ttt																285	
Arg Arg Glu Gly His Pro Leu Phe Pro Asn Val Pro Arg Cys Leu Phe																	
-25					-20					-15							
tta aac gct cgg ttg gcg gga acc ctg tgc cag ctg aaa ctc ctt cag																333	
Leu Asn Ala Arg Leu Ala Gly Thr Leu Cys Gln Leu Lys Leu Leu Gln																	
-10					-5				1				5				
ttt ggc cgc cta gga aac acc gag agt cac cta cat ggg ctg gct gg																380	
Phe Gly Arg Leu Gly Asn Thr Glu Ser His Leu His Gly Leu Ala																	
				10				15					20				

<210> 462
 <211> 198
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 7..198

 <221> sig_peptide

<222> 7..63
 <223> score 3.9
 seq SVCLCPCLNKGQS/EN

<400> 462
 agcaag atg ttc tcc tgc tgt atc tca gtt tgt cta tgt cct tgt ctc 48
 Met Phe Ser Cys Cys Ile Ser Val Cys Leu Cys Pro Cys Leu
 -15 -10
 aac aaa ggc caa agt gag aat ctt tcc aga gac tgc ggw cat tgg ctg 96
 Asn Lys Gly Gln Ser Glu Asn Leu Ser Arg Asp Cys Gly His Trp Leu
 -5 1 5 10
 aac cct cac cat cga cgc ctc tgg cca ttt ggc aga agg cac cca cag 144
 Asn Pro His His Arg Arg Leu Trp Pro Phe Gly Arg Arg His Pro Gln
 15 20 25
 gat tgt gga ctc ttc caa gat tca caa tgr tat ggt gaa tcc aaa gac 192
 Asp Cys Gly Leu Phe Gln Asp Ser Gln Xaa Tyr Gly Glu Ser Lys Asp
 30 35 40
 tgg aac 198
 Trp Asn
 45

<210> 463
 <211> 196
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 42..194
 <221> sig_peptide
 <222> 42..152
 <223> score 5.6
 seq LVASFLMSSVVRT/SS

<400> 463
 attccctact aatcctcagt ggacatgcac agtggtttgta a atg act aat aca gtt 56
 Met Thr Asn Thr Val
 -35
 aag aca ttt gta cat cat cat ctt ctc atg gaa gat cct aga ctt tcc 104
 Lys Thr Phe Val His His His Leu Leu Met Glu Asp Pro Arg Leu Ser
 -30 -25 -20
 tta cag aaa ctg gtg gct tct ttt ctt atg tcc tca gtg gta aga aca 152
 Leu Gln Lys Leu Val Ala Ser Phe Leu Met Ser Ser Val Val Arg Thr
 -15 -10 -5
 tca tct ctt gag gag aat gtc aag gtt cat cct atc cca aca ta 196
 Ser Ser Leu Glu Glu Asn Val Lys Val His Pro Ile Pro Thr
 1 5 10

<210> 464
 <211> 417
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 198..416

<221> sig_peptide

<222> 198..251

<223> score 3.7

seq VCGHLLPARVST/RS

<400> 464

gagaycaact ctatttgagc aasagtkagg aagatttccc tgtctcccag ctgagtaacc 60
actcagggtt atttaaatac agtttaaata tggtttcagt aatgattttc caatggtcta 120
cagcaaagaa tgggtgctcca agcctgaaca ttgagcacga cccagggtcat atgcacaaca 180
cgacagggttg agcgtcc atg tgt ggc tac tgg gtt tgc tgg gga cac ctc 230

Met Cys Gly Tyr Trp Val Cys Trp Gly His Leu
-15 -10

ttg cct gcc agg gtg agc aca cgc agc agt gag cag ccc cgt gtg acc 278
Leu Pro Ala Arg Val Ser Thr Arg Ser Ser Glu Gln Pro Arg Val Thr

-5 1 5
cca cgg gat gag gat gcc atg atg tca gca tcc ctt ctg act tgg agg 326
Pro Arg Asp Glu Asp Ala Met Met Ser Ala Ser Leu Leu Thr Trp Arg
10 15 20 25

tat gtg aca ttc atg gtg cca atg cca ctg tca cct tgc aga tca gtc 374
Tyr Val Thr Phe Met Val Pro Met Pro Leu Ser Pro Cys Arg Ser Val
30 35 40

tgg gtt tgc ttc aga cag aag atc ctg gaa tat gtt can gca t 417
Trp Val Cys Phe Arg Gln Lys Ile Leu Glu Tyr Val Xaa Ala
45 50 55

<210> 465

<211> 464

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 89..463

<221> sig_peptide

<222> 89..178

<223> score 13.2

seq LLLLSTLVIPSAA/AP

<400> 465

aaacagtacg tgggcgcccg gaatccggga gtccggtgac ccgggctgtg gtctagcata 60
aaggcggagc cagaagaagg ggccgggt atg gga gaa gcc tcc cca cct gcc 112
Met Gly Glu Ala Ser Pro Pro Ala

-30 -25

ccc gca agg cgg cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg 160
Pro Ala Arg Arg His Leu Leu Val Leu Leu Leu Leu Ser Thr Leu

	-20		-15		-10		
gtg atc ccc tcc gct gca gct cct atc cat gat gct gac gcc caa gag							208
Val Ile Pro Ser Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu							
-5		1		5		10	
agc tcc ttg ggt ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc							256
Ser Ser Leu Gly Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser							
	15		20		25		
cga ctt ttc ctg aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc							304
Arg Leu Phe Leu Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe							
	30		35		40		
tct gcc ccc atg gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag							352
Ser Ala Pro Met Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu							
	45		50		55		
gag aac cag gag cac cag ctg ggg aac aac acc ctc tcc agc mac ctc							400
Glu Asn Gln Glu His Gln Leu Gly Asn Asn Thr Leu Ser Ser Xaa Leu							
	60		65		70		
cag atc gac nng atg acc gac aac aag aca gga gag gtg ctg atc tcc							448
Gln Ile Asp Xaa Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser							
	75		80		85		90
gag aat gtg gtg gca t							464
Glu Asn Val Val Ala							
	95						

<210> 466
 <211> 248
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 13..246
 <221> sig_peptide
 <222> 13..81
 <223> score 11.8
 seq CLFVCLFLSQSFA/FV

<400> 466	
aaaagtattg gg atg cct agt tac aar gtg tgt ggg gtt ttt tgt ttg ttt	51
Met Pro Ser Tyr Lys Val Cys Gly Val Phe Cys Leu Phe	
-20	-15
gtt tgt ttg ttt ttg agc cag agt ttt gct ttt gtc ctc cag gct gga	99
Val Cys Leu Phe Leu Ser Gln Ser Phe Ala Phe Val Leu Gln Ala Gly	
-10	-5
gtg cag tgg cgc gat ctc tgc tca ctg caa cct cag ctt ccc agg ttc	147
Val Gln Trp Arg Asp Leu Cys Ser Leu Gln Pro Gln Leu Pro Arg Phe	
	10
ggg cca tcc tcc tgc ctc agc ctc cca agt ggc tgg gac tgc agg cgc	195
Gly Pro Ser Ser Cys Leu Ser Leu Pro Ser Gly Trp Asp Cys Arg Arg	
	25
cca cca cca cgc ctg gct aat tct tgt gtt ttc ggt gga gac ggg gtt	243
Pro Pro Pro Arg Leu Ala Asn Ser Cys Val Phe Gly Gly Asp Gly Val	
	40
	45
	50

tca cc
Ser
55

248

<210> 467
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..348

<221> sig_peptide
<222> 46..102
<223> score 11
seq SLVLLLCLTCSYA/FM

<400> 467
aagcaaaccc gtcattgagca actcccttcc ccatctctgt tcacc atg tgg acg ctg 57
Met Trp Thr Leu
aaa tcg tcc ctg gtc ctg ctt ctg tgc ctc acc tgc agc tat gcc ttt 105
Lys Ser Ser Leu Val Leu Leu Leu Cys Leu Thr Cys Ser Tyr Ala Phe
-15 -10 -5 1
atg ttc tct tct ctg aga cag aaa act agc gaa ccc cag ggg aag gtg 153
Met Phe Ser Ser Leu Arg Gln Lys Thr Ser Glu Pro Gln Gly Lys Val
5 10 15
caa tac gga gag cac ttt cgg att cgg cag aat cta cca gag cac acc 201
Gln Tyr Gly Glu His Phe Arg Ile Arg Gln Asn Leu Pro Glu His Thr
20 25 30
caa ggc tgg ctt ggg agc aaa tgg ctc tgg ctt ctt ktt gtt gtt gtg 249
Gln Gly Trp Leu Gly Ser Lys Trp Leu Trp Leu Leu Xaa Val Val Val
35 40 45
ccg ttt gtg ata ctg cag tgt caa aga gac agt gag aag aat aag gag 297
Pro Phe Val Ile Leu Gln Cys Gln Arg Asp Ser Glu Lys Asn Lys Glu
50 55 60 65
cag agt cct cct ggc ctt cga ggc ggc caa ctt cac tct cca tta aag 345
Gln Ser Pro Pro Gly Leu Arg Gly Gly Gln Leu His Ser Pro Leu Lys
70 75 80
aaa a 349
Lys

<210> 468
<211> 347
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..345

<221> sig_peptide
<222> 106..237

004220"666EF560

<223> score 3.7
seq RFLLCVHGDGHA/EN

<400> 468
tatgagagga acgggagata tgagggctca agtcgcaatg tatctgctga gcaaaaagat 60
gaaaacaaag aagcaaagcc tcgatcccta cgcttcacct ggagc atg aaa acc act 117
Met Lys Thr Thr
agt tca atg gat ccc ggg gac atg atg cgg gaa atc cgc aaa gtg ttg 165
Ser Ser Met Asp Pro Gly Asp Met Met Arg Glu Ile Arg Lys Val Leu
-40 -35 -30 -25
gac gcc aat aac tgc gac tat gag cag agg gag cgc ttc ttg ctc ttc 213
Asp Ala Asn Asn Cys Asp Tyr Glu Gln Arg Glu Arg Phe Leu Leu Phe
-20 -15 -10
tgc gtc cac gga gat ggg cac gcg gag aac ctc gtg cag tgg gaa atg 261
Cys Val His Gly Asp Gly His Ala Glu Asn Leu Val Gln Trp Glu Met
-5 1 5
gaa gtg tgc aag ctg cca aga ctg tct ctg aac ggg gtc cgg ttt aag 309
Glu Val Cys Lys Leu Pro Arg Leu Ser Leu Asn Gly Val Arg Phe Lys
10 15 20
cgn ata tcg ggg aca tcc ata gcc ttc asa aat att gc 347
Arg Ile Ser Gly Thr Ser Ile Ala Phe Xaa Asn Ile
25 30 35

<210> 469
<211> 269
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 105..269

<221> sig_peptide
<222> 105..194
<223> score 4.3
seq LLPTLPWLPSTRL/LS

<400> 469
gcacagcgct grratgccag gttcgggtag gagggccctt ggggggrmnra ttcttttagga 60
aattccttta gaagvaaaca acttgggact ggatagcgtg cgat atg cag aga aat 116
Met Gln Arg Asn
-30
gca act ttc att cat ttg cag tta gcg atc cgc cct tcc ctg ctc ccc 164
Ala Thr Phe Ile His Leu Gln Leu Ala Ile Arg Pro Ser Leu Leu Pro
-25 -20 -15
acc ctt ccg tgg ctc ccc agt acc cgc ctg ctg tcg ccc aca ccc tta 212
Thr Leu Pro Trp Leu Pro Ser Thr Arg Leu Leu Ser Pro Thr Pro Leu
-10 -5 1 5
gga cag ctt cgt ggc ccc ccg gga dcg cag agg gcc atg cct acc gct 260
Gly Gln Leu Arg Gly Pro Pro Gly Xaa Gln Arg Ala Met Pro Thr Ala
10 15 20
cat tta aga 269

His Leu Arg
25

<210> 470
<211> 230
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..228

<221> sig_peptide
<222> 16..96
<223> score 8.8
seq VLLLLLPFTTSLC/EL

<400> 470
ttatcagcat tttgg atg aag gta aag gaa gac ttt cca ttg tta agt aga 51
Met Lys Val Lys Glu Asp Phe Pro Leu Leu Ser Arg
-25 -20
aag agt gtc ctg cta ttg cta cca ttc aca aca act agt ttg tgt gaa 99
Lys Ser Val Leu Leu Leu Leu Pro Phe Thr Thr Thr Ser Leu Cys Glu
-15 -10 -5 1
cta ggg ttt tcc atc tta acg cag tta maa aca amg gam aga mat ggg 147
Leu Gly Phe Ser Ile Leu Thr Gln Leu Xaa Thr Xaa Xaa Arg Xaa Gly
5 10 15
ctg aat tgt gca gca gtt atg cgg gta gca tta tct tcc tgt gtt cca 195
Leu Asn Cys Ala Ala Val Met Arg Val Ala Leu Ser Ser Cys Val Pro
20 25 30
gac tgg aat gaa cnt atg aac agg caa gca cac aa 230
Asp Trp Asn Glu Xaa Met Asn Arg Gln Ala His
35 40

<210> 471
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 179..358

<221> sig_peptide
<222> 179..307
<223> score 4.7
seq GIFLVIFCSESFS/LL

<400> 471
atggamtctt ggggtgacar atgttttggt gtgttttggt tatwcctcat ctgttctcta 60
ttgtttctag tttgtagtca gcattcatag gtgtacttga ttcctcctat rwtattagnn 120
tctagctggt ttcaggratt tctctttkat ttttgagttc cagtagtttg actataat 178

atg ata aac cta ctt gtg ggt aac tgc att tat ctg ctt gga gct att	226
Met Ile Asn Leu Leu Val Gly Asn Cys Ile Tyr Leu Leu Gly Ala Ile	
-40 -35 -30	
aga gct tct tgc atg tgt aga tkb atg tct ttc gcc aaa ttt ggg att	274
Arg Ala Ser Cys Met Cys Arg Xaa Met Ser Phe Ala Lys Phe Gly Ile	
-25 -20 -15	
ttt ctt gta ata ttt tgt tct gaa tca ttt tct ctt ctc ctc tgg aac	322
Phe Leu Val Ile Phe Cys Ser Glu Ser Phe Ser Leu Leu Leu Trp Asn	
-10 -5 1 5	
ttc agt tca ata tat gtt aag acc ttt tgg cca gtg g	359
Phe Ser Ser Ile Tyr Val Lys Thr Phe Trp Pro Val	
10 15	

<210> 472
 <211> 246
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 55..246
 <221> sig_peptide
 <222> 55..126
 <223> score 7.8
 seq FLLCLCIAYWAST/AV

<400> 472	
attctcatcg cgattgcact catcaaagaa gccagcaggg ctgtgggata cgtc atg	57
Met	
tgc tcc ttg ctc tac cca ctg gtc acc ttc ttc ttg ctg tgc ctc tgc	105
Cys Ser Leu Leu Tyr Pro Leu Val Thr Phe Phe Leu Leu Cys Leu Cys	
-20 -15 -10	
atc gcc tac tgg gcc agc act gct gtc ttc ctg tcc act tcc aac gaa	153
Ile Ala Tyr Trp Ala Ser Thr Ala Val Phe Leu Ser Thr Ser Asn Glu	
-5 1 5	
gcg gtc tat aag atc ttt gat gac agc ccc tgc cca ttt act gcg aaa	201
Ala Val Tyr Lys Ile Phe Asp Asp Ser Pro Cys Pro Phe Thr Ala Lys	
10 15 20 25	
acc tgc aac cca gag acc ttc ccc tcc tcc aat gag ccc cgc cat	246
Thr Cys Asn Pro Glu Thr Phe Pro Ser Ser Asn Glu Pro Arg His	
30 35 40	

<210> 473
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 105..407
 <221> sig_peptide

<222> 105..242
 <223> score 7.8
 seq LVLLGTRVPLSGG/GP

<400> 473
 aaacagggcc attggcaaag ctgggggtacc agtcacccag ccacgctcta gggtaggtagc 60
 caagaagacg gaccccgagt gggaggcaga gagacaagag gtgg atg aag cag agc 116
 Met Lys Gln Ser
 -45
 aag cgt gas atg gtg aag aga aga cgg agc ccc gcg ctg gga gag gaa 164
 Lys Arg Xaa Met Val Lys Arg Arg Arg Ser Pro Ala Leu Gly Glu Glu
 -40 -35 -30
 cgc ttc agt ccg agt tcc att ctg cac cca agg ctc ccc ttg gtc ctc 212
 Arg Phe Ser Pro Ser Ser Ile Leu His Pro Arg Leu Pro Leu Val Leu
 -25 -20 -15
 ctg gga acc agg gtg ccc ctt agt ggt ggt ggc cca gga gaa ccc gac 260
 Leu Gly Thr Arg Val Pro Leu Ser Gly Gly Pro Gly Glu Pro Asp
 -10 -5 1 5
 caa ggc agg agc gcc ccc tcc tgg aag agc ctc gct tca acg cat mat 308
 Gln Gly Arg Ser Ala Pro Ser Trp Lys Ser Leu Ala Ser Thr His Xaa
 10 15 20
 cat tcc cgg ccg gca gca ggg gcg acg cca gca agg cct gcg act cag 356
 His Ser Arg Pro Ala Ala Gly Ala Thr Pro Ala Arg Pro Ala Thr Gln
 25 30 35
 agc cag ctt ggc ccg ttc gcc ccg ccc ctt ccc ggt gtc cgc ccc gcc 404
 Ser Gln Leu Gly Pro Phe Ala Pro Pro Leu Pro Gly Val Arg Pro Ala
 40 45 50
 cca t 408
 Pro
 55

<210> 474
 <211> 335
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 169..333

<221> sig_peptide
 <222> 169..267
 <223> score 5.4
 seq AACHTLSLSLTTA/HN

<400> 474
 ttaaaaatgc aackngtttt atcttccttg gttttttctca acaatttcca aagaaaattc 60
 tggcttcaaa tactggaata tgttcacccg actgaggtct gagaaagaag aaaattaaaa 120
 attgaamcaa yttgmttwtt kcttccttga tttttctgaa cagcttcc atg gaa act 177
 Met Glu Thr
 ttt gcc tca tac agt gga att ggg ttc atc caa ctg agg ggt ggt gga 225
 Phe Ala Ser Tyr Ser Gly Ile Gly Phe Ile Gln Leu Arg Gly Gly Gly

-30	-25	-20	-15	
aaa gct gca tgt cac acg ctg tca ctc agt ctg acc aca gca cat aat				273
Lys Ala Ala Cys His Thr Leu Ser Leu Ser Leu Thr Thr Ala His Asn				
	-10	-5	1	
ttc aag gat gga ggg cca cat tca gac aca tgg cct tgc aaa gag aaa				321
Phe Lys Asp Gly Gly Pro His Ser Asp Thr Trp Pro Cys Lys Glu Lys				
	5	10	15	
act ggg cct tgt ca				335
Thr Gly Pro Cys				
20				

<210> 475
 <211> 209
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 36..209

<221> sig_peptide
 <222> 36..86
 <223> score 7.5
 seq FLFLFLLXXLIVA/VT

<400> 475	
cttttttdtc ckgcacaagg gatttccggg tcagg atg aac aaa cac ttc ttg	53
Met Asn Lys His Phe Leu	
-15	
ttc ctc ttc ctc ctt dac kgc ctc att gtg gca gtg aca tca ctt cag	101
Phe Leu Phe Leu Leu Xaa Xaa Leu Ile Val Ala Val Thr Ser Leu Gln	
-10 -5 1 5	
tgc ata aca tgc cac ctt cgc aca cgg aca gac cgc tgt aga aga ggc	149
Cys Ile Thr Cys His Leu Arg Thr Arg Thr Asp Arg Cys Arg Arg Gly	
10 15 20	
ttt ggt gdc tgt act gct cag aag ggc gag gca tgc atg ctc tta agg	197
Phe Gly Xaa Cys Thr Ala Gln Lys Gly Glu Ala Cys Met Leu Leu Arg	
25 30 35	
att cac cag cgc	209
Ile His Gln Arg	
40	

<210> 476
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..327

<221> sig_peptide
 <222> 79..201

<223> score 3.6
seq LHTSVTLFLLSYC/DC

<400> 476
agatgattcc ctgattctcc agagagatta cacacttcgt ttgtggctaa gggtactgtg 60
acccaatgaa agaagaaa atg aaa gcc ata aag aaa agt ctt aca gaa gaa 111
Met Lys Ala Ile Lys Lys Ser Leu Thr Glu Glu
-40 -35
gaa tac ctg tac ctg gac ttt tct cac caa aca gaa gga tgc atc ttt 159
Glu Tyr Leu Tyr Leu Asp Phe Ser His Gln Thr Glu Gly Cys Ile Phe
-30 -25 -20 -15
cct ctt cat aca tct gta act tta ttt ctg tta tct tac tgt gac tgt 207
Pro Leu His Thr Ser Val Thr Leu Phe Leu Leu Ser Tyr Cys Asp Cys
-10 -5 1
aaa atc ttt aaa att tgc tta gtt gtc acc aaa gag gtg agt aga gat 255
Lys Ile Phe Lys Ile Cys Leu Val Val Thr Lys Glu Val Ser Arg Asp
5 10 15
avn tca cta cta aga gat gac ctg atc cag gat gtt gaa ata cag att 303
Xaa Ser Leu Leu Arg Asp Leu Ile Gln Asp Val Glu Ile Gln Ile
20 25 30
att tca agg cag gag ctc cca cca a 328
Ile Ser Arg Gln Glu Leu Pro Pro
35 40

<210> 477
<211> 470
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 268..468
<221> sig_peptide
<222> 268..375
<223> score 5.6
seq SFLLFXXVLKTES/CS

<400> 477
tgacactgtg gaatggatgg ggacatgggg gttcatcctg atattttcaa cactgtttta 60
tatgtttgaa aaaatttaag tacttgggaa gtgaaagtgc tcagagatac cagaatcaaa 120
gtgggatgag attaatcttg tttgagtgtt gctgggaaga ctgcatggag gaggtgggaa 180
ctggtataag atgggaagaa acggtattcc cctaggcahv gaggccactg cttcctgaga 240
gtcagcgcca tctgaagagg aagggag atg aag ctg ggt gcc gag gag gag gaa 294
Met Lys Leu Gly Ala Glu Glu Glu Glu
-35 -30
agg tta gaa agt ggc ctg agc agc tct ata aaa csm tnc act tca ttt 342
Arg Leu Glu Ser Gly Leu Ser Ser Ser Ile Lys Xaa Xaa Thr Ser Phe
-25 -20 -15
ctt ttg ttt tgw ynt gtt tta aag aca gag tct tgc tct gtg gcc cag 390
Leu Leu Phe Xaa Xaa Val Leu Lys Thr Glu Ser Cys Ser Val Ala Gln
-10 -5 1 5

gct gga ctg caa tgg tgc gat ctc agc tca ctg caa ctt cca gcc ycc 438
 Ala Gly Leu Gln Trp Cys Asp Leu Ser Ser Leu Gln Leu Pro Ala Xaa
 10 15 20
 tgg gtt caa agc gat tct cct gcc tca gcc tc 470
 Trp Val Gln Ser Asp Ser Pro Ala Ser Ala
 25 30

<210> 478
 <211> 172
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..172

<221> sig_peptide
 <222> 14..58
 <223> score 10.9
 seq LSVCLLLVTLALC/CY

<400> 478
 aaaacaagcc acc atg aag ctg tgc gtg tgt ctc ctg ctg gtc acg ctg 49
 Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu
 -15 -10 -5
 gcc ctc tgc tgc tac cag gcc aat gcc gag ttc tgc cca gct ctt gtt 97
 Ala Leu Cys Cys Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val
 1 5 10
 tct gag ctg tta gac ttc ttc ttc att agt gaa cct ctg ttc aag tta 145
 Ser Glu Leu Leu Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu
 15 20 25
 agt ctt gcc aaa ttt gat gcc cct cga 172
 Ser Leu Ala Lys Phe Asp Ala Pro Arg
 30 35

<210> 479
 <211> 270
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 87..269

<221> sig_peptide
 <222> 87..194
 <223> score 4.7
 seq SCFVPSLVGTALQ/QS

<400> 479
 agcagtccag agaagtgaag tgacttgccct gaagccacag agcctgcaag tgcgagggct 60
 gggattccaa tccaagctct gggcca atg gct ttg cat atc cta gaa tgc gag 113

<221> sig_peptide
 <222> 65..109
 <223> score 3.9
 seq ILVFLCRRLLLEA/SI

<400> 481
 atagattctc tctttgtgcc acaagactgc tgcagaagga tgggggcagt gggtgtatag 60
 ataa atg ttc att ttg gtg ttc ctg tgc aga aga tta tta cta gag gct 109
 Met Phe Ile Leu Val Phe Leu Cys Arg Arg Leu Leu Leu Glu Ala
 -15 -10 -5
 tct att cag cta ttt tgc tct acc tcc tct tcc aga aca agg ttt ctt 157
 Ser Ile Gln Leu Phe Cys Ser Thr Ser Ser Arg Thr Arg Phe Leu
 1 5 10 15
 gag atg gaa tct att tct gat gaa gat gct atg agt att gtt gaa atg 205
 Glu Met Glu Ser Ile Ser Asp Glu Asp Ala Met Ser Ile Val Glu Met
 20 25 30
 aca aca aag gat cta gaa tat tac ata aac tta gtt gat aaa atg gca 253
 Thr Thr Lys Asp Leu Glu Tyr Tyr Ile Asn Leu Val Asp Lys Met Ala
 35 40 45
 gcc a 257
 Ala

<210> 482
 <211> 299
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..297

<221> sig_peptide
 <222> 22..153
 <223> score 4.8
 seq SGLMQMLLLKVSA/HI

<400> 482
 ctctgccaat atcgtgtgtc c atg ctg aag atg gac gag agc acg ctg ctg 51
 Met Leu Lys Met Asp Glu Ser Thr Leu Leu
 -40 -35
 cgg gag gcc cag gag ctg agc ctg gag aag ctg cag cag gcc gtg agg 99
 Arg Glu Ala Gln Glu Leu Ser Leu Glu Lys Leu Gln Gln Ala Val Arg
 -30 -25 -20
 mag aac ggg ctg atg tcg ggg ctg atg cag atg ctg ctg ctg aag gtg 147
 Xaa Asn Gly Leu Met Ser Gly Leu Met Gln Met Leu Leu Lys Val
 -15 -10 -5
 tct gca cac atc asc gag cag ctg ggc atg gcc cca ggt ggc gag ttc 195
 Ser Ala His Ile Xaa Glu Gln Leu Gly Met Ala Pro Gly Gly Glu Phe
 1 5 10
 agg gag gsc ttc aag gag gcc agc aag gtg cct ttc tgc aag tdc cac 243
 Arg Glu Xaa Phe Lys Glu Ala Ser Lys Val Pro Phe Cys Lys Xaa His

catgtggctc caadktctgc atctggattt gggggwgttt tttggmatgg caccctcacc 180
tctctccctg cctgttttcc ccaaagtgga aaggaaggcc tttcaaacca gagtgtctca 240
ctcccctctg acctccagac cagatggggc atg agc cag cca gct cag cca ggc 294
Met Ser Gln Pro Ala Gln Pro Gly
-40 -35
tcc ctg tgt cct ggg agg aag tgt ccc atc ccc cat gcc cct tat ggg 342
Ser Leu Cys Pro Gly Arg Lys Cys Pro Ile Pro His Ala Pro Tyr Gly
-30 -25 -20
gag gga ggg cgt ctg atg ctc tct ctc tgc ctc ccc ccc atc ctg tca 390
Glu Gly Gly Arg Leu Met Leu Ser Leu Cys Leu Pro Pro Ile Leu Ser
-15 -10 -5
ggc aca ggt gac ggg ggc agc cca wgc gag ccc ttc tcc tgc tgc t 436
Gly Thr Gly Asp Gly Gly Ser Pro Xaa Glu Pro Phe Ser Cys Cys
1 5 10 15

<210> 485
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..303

<221> sig_peptide
<222> 106..210
<223> score 8.5
seq FVLFCSVLRRSLA/RS

<400> 485
tcctcactgt gccaccagg taacgcttgt ggctccttctc ctgtgtagca gcacccctctg 60
aaaggatgga gactctacaa agaggggaccg gtgcctgggc ctagg atg gaa gct ggc 117
Met Glu Ala Gly
-35
aaa cad tgg ccc atg ggc aaa tcc tgc cca cca cat ttt ttt gtt ttg 165
Lys Xaa Trp Pro Met Gly Lys Ser Cys Pro Pro His Phe Phe Val Leu
-30 -25 -20
ttt tgt ttt gtt tta ttc tgt tct gtt ttg aga cgg agt ctt gct cgg 213
Phe Cys Phe Val Leu Phe Cys Ser Val Leu Arg Arg Ser Leu Ala Arg
-15 -10 -5 1
tcg ccc agg ctg gag tgc agt ggc gcg atc ttg gct cac tgc aac ctc 261
Ser Pro Arg Leu Glu Cys Ser Gly Ala Ile Leu Ala His Cys Asn Leu
5 10 15
tgc acc ctg ggt tca agt gat tat cct gcc tca gcc tcc cta y 304
Cys Thr Leu Gly Ser Ser Asp Tyr Pro Ala Ser Ala Ser Leu
20 25 30

<210> 486
<211> 185
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> 32..184

<221> sig_peptide
<222> 32..133
<223> score 3.8
seq FHQMALXPGTSRA/QA

<400> 486
acgcggcaca cagtcaccagt gctcagtcac c atg tgt cct gca tgg ctc cca 52
Met Cys Pro Ala Trp Leu Pro
-30
tgt tgg acg gca cag acg gaa cat ctc gat cgt tac agg aag ttc cac 100
Cys Trp Thr Ala Gln Thr Glu His Leu Asp Arg Tyr Arg Lys Phe His
-25 -20 -15
cag atg gcg ctg tyt cca ggg aca tct agg gca cag gcc tta ctt tat 148
Gln Met Ala Leu Xaa Pro Gly Thr Ser Arg Ala Gln Ala Leu Leu Tyr
-10 -5 1 5
aac gaa gtc cta gag aga ttt atg ttc acc cgg ctg c 185
Asn Glu Val Leu Glu Arg Phe Met Phe Thr Arg Leu
10 15

<210> 487
<211> 194
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..194

<221> sig_peptide
<222> 30..134
<223> score 4.8
seq PWVLDIFLTLVFA/LG

<400> 487
agttgctaga aagcaatgcg cctattcac atg gag aat ctt ccc ttt cct cta 53
Met Glu Asn Leu Pro Phe Pro Leu
-35 -30
aaa tta ctt agt gcc tca tca cta aac acc ccc agc tcc aca cca tgg 101
Lys Leu Leu Ser Ala Ser Ser Leu Asn Thr Pro Ser Ser Thr Pro Trp
-25 -20 -15
gtg ttg gat atc ttc ctc acc ttg gtg ttt gcc ctg ggg ttc ttc ttc 149
Val Leu Asp Ile Phe Leu Thr Leu Val Phe Ala Leu Gly Phe Phe
-10 -5 1 5
cta tta ctc ccc tac ttc tct tac ctc cgt tgt gac aac cca cca 194
Leu Leu Leu Pro Tyr Phe Ser Tyr Leu Arg Cys Asp Asn Pro Pro
10 15 20

<210> 488
<211> 352

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 158..352

<221> sig_peptide
<222> 158..214
<223> score 6.6
seq MLMVVLLCQVLLG/GA

<400> 488
attatattca aatattcctt ttaggagcca ttccgtagtg ccatcccgag caacgcactg 60
ctgcagcttc cctgagcctt tccagcaagt ttgttcaaga ttggctgtca agaatacawgg 120
ghmtgttatd awatgchttg ttttctgtca agacacc atg att cct ggt aac cga 175
Met Ile Pro Gly Asn Arg
-15
atg ctg atg gtc gtt tta tta tgc caa gtc ctg cta gga ggc gcg agc 223
Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly Ala Ser
-10 -5 1
cat gct agt ttg ata cct gag acg ggg aag aaa aaa gtc gcc gag att 271
His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala Glu Ile
5 10 15
cag ggc cac gcg gga gga cgc cgc tca ggg cag agc cat gag ctc ctg 319
Gln Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu Leu Leu
20 25 30 35
crg rac ttc gag gcg aca ctt ctg cag atg ttt 352
Xaa Xaa Phe Glu Ala Thr Leu Leu Gln Met Phe
40 45

<210> 489
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 189..359

<221> sig_peptide
<222> 189..275
<223> score 6
seq LFMALPPVLSSHG/SR

<400> 489
acttgcaactt gcttggttggg gtcagagccc gtcctctaaac cagggctcca tatgggctgc 60
ctgtctgccg caacacagcc tagcggggaa acagtagaaa tgccacttct atgtatttat 120
catattttatt ttgagataat taacgaagac gttaaataaaa gccagactgc actgaccctt 180
ggggcgccc atg cga gac ccc ctc gcg gac atg gta cac agt tat tta tca 230
Met Arg Asp Pro Leu Ala Asp Met Val His Ser Tyr Leu Ser
-25 -20

tcg tct ttg ttc atg gcc ctt cca cca gtg ctg agc tca cat ggc agc	278
Ser Ser Leu Phe Met Ala Leu Pro Pro Val Leu Ser Ser His Gly Ser	
-15 -10 -5 1	
agg aac ctg aga atc tgg ggg agt cca ttt ggt gga gcg ctg act aag	326
Arg Asn Leu Arg Ile Trp Gly Ser Pro Phe Gly Gly Ala Leu Thr Lys	
5 10 15	
ggc aaa gca ccc cca acc cca gca caa cca gcc ct	361
Gly Lys Ala Pro Pro Thr Pro Ala Gln Pro Ala	
20 25	

<210> 490
 <211> 346
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 183..344

<221> sig_peptide
 <222> 183..239
 <223> score 6.2
 seq FLFLIIPISRSHG/KV

<400> 490	
tatacttttct agaadacatt tcaattttatt atgacaaaatt acgtcagtaa attcatttaa	60
cctttttgtc tttttaagaa actttttatga cctctattta cttaacttca tatataatca	120
aataaararca raagargtga aaagagaaga ttgcagccaa gaggaattcg ttacaaacat	180
gt atg aga ttt ttt aag ttt ttt ttg ttt tta att att cct att tca	227
Met Arg Phe Phe Lys Phe Phe Leu Phe Leu Ile Ile Pro Ile Ser	
-15 -10 -5	
cgt tca cat gga aaa gtc aga aag cat aac tac tct agg ccg ggc gcc	275
Arg Ser His Gly Lys Val Arg Lys His Asn Tyr Ser Arg Pro Gly Ala	
1 5 10	
gtg gca cac gcc tgt aat ccc agc act ctg gga ggc caa ggc aaa gtg	323
Val Ala His Ala Cys Asn Pro Ser Thr Leu Gly Gly Gln Gly Lys Val	
15 20 25	
gat ggc ttg agt cca gga gtt tt	346
Asp Gly Leu Ser Pro Gly Val	
30 35	

<210> 491
 <211> 190
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 18..188

<221> sig_peptide
 <222> 18..62
 <223> score 4.7

seq RCACFPFFPFAFC/HD

<400> 491
 ctctctcctg ttcgggtc atg gtg aga tgt gct tgc ttc ccc ttc ttc ccc 50
 Met Val Arg Cys Ala Cys Phe Pro Phe Phe Pro
 -15 -10 -5
 ttc gcc ttc tgc cat gac tgt aag ttt ctt ggg gcc tcc cag tca tgc 98
 Phe Ala Phe Cys His Asp Cys Lys Phe Leu Gly Ala Ser Gln Ser Cys
 1 5 10
 ttc ttg tta agc cgg caa aac tgt gta agc aca gga kga cct tca tcc 146
 Phe Leu Leu Ser Arg Gln Asn Cys Val Ser Thr Gly Xaa Pro Ser Ser
 15 20 25
 aaa tct gat atc aac tca agg tct gga tct tgt tca ctg gca ag 190
 Lys Ser Asp Ile Asn Ser Arg Ser Gly Ser Cys Ser Leu Ala
 30 35 40

<210> 492
 <211> 421
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 108..419
 <221> sig_peptide
 <222> 108..161
 <223> score 3.5
 seq ALEVIVTLSETAA/AM

<400> 492
 aatccctcgt tgagattgca gatactgttc caaagtattt gcgtcctcac ttggaagcaa 60
 ctctacagct aagtctaaag ttgtgtggag acactagcct caacaat atg caa cgc 116
 Met Gln Arg
 cag ctt gcc ctt gaa gtg atc gtc acc ctc tct gag act gca gct gct 164
 Gln Leu Ala Leu Glu Val Ile Val Thr Leu Ser Glu Thr Ala Ala Ala
 -15 -10 -5 1
 atg tta aga aaa cat acc aat att gtt gca cag act att cct cag atg 212
 Met Leu Arg Lys His Thr Asn Ile Val Ala Gln Thr Ile Pro Gln Met
 5 10 15
 tta gca atg atg gtt gat ttg gaa gaa gat gag gac tgg gca aat gca 260
 Leu Ala Met Met Val Asp Leu Glu Glu Asp Glu Asp Trp Ala Asn Ala
 20 25 30
 gat gaa cta gaa gat gat gat ttt gac agc aat gca gtt gca ggc gag 308
 Asp Glu Leu Glu Asp Asp Asp Phe Asp Ser Asn Ala Val Ala Gly Glu
 35 40 45
 agt gct cta gat cga atg gct tgc gga ctt ggt gga aag ctc gtt ctg 356
 Ser Ala Leu Asp Arg Met Ala Cys Gly Leu Gly Gly Lys Leu Val Leu
 50 55 60 65
 ccg atg atc aag gaa cac att atg caa atg ctt caa aat cgt aag ctg 404
 Pro Met Ile Lys Glu His Ile Met Gln Met Leu Gln Asn Arg Lys Leu
 70 75 80

tgt cct tca atg cta ga
Cys Pro Ser Met Leu
85

421

<210> 493
<211> 291
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 79..291

<221> sig_peptide
<222> 79..207
<223> score 6.2
seq LALGIPSITQAWG/LW

<400> 493
aagtattggg gatgctgagc tgcgggggtac gggcctgagg agggatggga gtaagaagtg 60
ctgtggaaac cgtcagcc atg aac cag gct gac cct cgg ctc aga gca gtg 111
Met Asn Gln Ala Asp Pro Arg Leu Arg Ala Val
-40 -35
tgc ttg tgg act ctc aca tct gca gcc atg agc aga ggc gac aac tgc 159
Cys Leu Trp Thr Leu Thr Ser Ala Ala Met Ser Arg Gly Asp Asn Cys
-30 -25 -20
acg gat cta ctc gca ctg gga atc ccc tcc ata acc cag gcc tgg gga 207
Thr Asp Leu Leu Ala Leu Gly Ile Pro Ser Ile Thr Gln Ala Trp Gly
-15 -10 -5
ctg tgg gtc ctc tta ggg gct gtg acg ctg cta ttt ctc atc tcg ctg 255
Leu Trp Val Leu Leu Gly Ala Val Thr Leu Leu Phe Leu Ile Ser Leu
1 5 10 15
gct gca cac ttg tcc cag tgg acc agg ggt cgg agc 291
Ala Ala His Leu Ser Gln Trp Thr Arg Gly Arg Ser
20 25

<210> 494
<211> 237
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 49..237

<221> sig_peptide
<222> 49..180
<223> score 5.2
seq XIYXFNFLRWSLA/LS

<400> 494
cataccagct ctctttcctt tttacatcct ttcactttta atctatctt atg tct ctg

57

<220>

<221> CDS

<222> 26..193

<221> sig_peptide

<222> 26..163

<223> score 6.5

seq WLFFLMLSCTPP/DR

<400> 496

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acttttgctt tatgttcagg ggtcc atg tgt agg atg tgc agg ttt gtt aca      52
                               Met Cys Arg Met Cys Arg Phe Val Thr
                               -45                               -40
tgg ata aac gtg tgc cat ggt gat ttg ctg cac aga tca tcc cgt cgc      100
Trp Ile Asn Val Cys His Gly Asp Leu Leu His Arg Ser Ser Arg Arg
                               -35                               -25
ctg ggt gtg aag ccg agc acg cat tgg cta ttc ttc ctg atg ctc tcc      148
Leu Gly Val Lys Pro Ser Thr His Trp Leu Phe Phe Leu Met Leu Ser
                               -20                               -10
ctt tgc acc cct cct gac aga ccc tgg tgt gtg ttg ttc ccc ccg ct      195
Leu Cys Thr Pro Pro Asp Arg Pro Trp Cys Val Leu Phe Pro Pro
-5                               1                               5                               10
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<210> 497

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 209..370

<221> sig_peptide

<222> 209..289

<223> score 6.6

seq LAFSFSFFPSSFS/SF

<400> 497

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atattgcctt agaactacat tgctaaacct ggtctttgta tctgcgaagt tctaacatct      120
tgccacagct tagttagctt tgagagggaa agggtagaat ccatttaagg agacaggtta      180
aaaaatgata tattttaagca tataggca atg gta gca cat gat tac caa aac      232
                               Met Val Ala His Asp Tyr Gln Asn
                               -25                               -20
ata att agc ctt ttc ttt ctt gct ttt tca ttt tct ttc ttt cct tct      280
Ile Ile Ser Leu Phe Phe Leu Ala Phe Ser Phe Ser Phe Phe Pro Ser
                               -15                               -10                               -5
tca ttt tct tct ttc ttt ctt ktc ttt ctt tct ttt ttc tct tct ttc      328
Ser Phe Ser Ser Phe Phe Leu Xaa Phe Leu Ser Phe Phe Ser Ser Phe
                               1                               5                               10
ttt ctc tct ctt ctt tct ttc cct tcc ttc ctc ccc ccc ggr      370
Phe Leu Ser Leu Leu Ser Phe Pro Ser Phe Leu Pro Pro Gly
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15

20

25

<210> 498
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 <213> Homo sapiens

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 <222> 200..400

<221> sig_peptide
 <222> 200..286
 <223> score 8.8
 seq VLFCFVFLRQSLA/LS

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 tccaaccctc ttcaagtact tcaggggttt aaaacttcag tggaggaaat aactgcacat 120
 gcggtggaaa aagcaagaga actcaaatta gaagtaaagc ctgaagatgg gactgaattg 180
 ctaaaatctc ctaacttta atg gat gag gag ttg gtt ctt atg aat gag caa 232
 Met Asp Glu Glu Leu Val Leu Met Asn Glu Gln
 -25 -20
 aga aac tgt ttt tct gtt ttg ttt tgt ttt gtt ttt ttg aga cag agt 280
 Arg Asn Cys Phe Ser Val Leu Phe Cys Phe Val Phe Leu Arg Gln Ser
 -15 -10 -5
 ctt gct ctg tca gcc agg ctg aag cgc agt ggc aca gtc tcg gct cac 328
 Leu Ala Leu Ser Ala Arg Leu Lys Arg Ser Gly Thr Val Ser Ala His
 1 5 10
 tgc aac ctc cgc ctc ccg ggc tca agc att tct tct gcc tca gcc tcc 376
 Cys Asn Leu Arg Leu Pro Gly Ser Ser Ile Ser Ser Ala Ser Ala Ser
 15 20 25 30
 cta gta gct ggg att aca ggc gtg t 401
 Leu Val Ala Gly Ile Thr Gly Val
 35

<210> 499
 <211> 215
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 23..214

<221> sig_peptide
 <222> 23..121
 <223> score 6
 seq LHQACLLAPSHP/QC

<400> 499
 cgccctcatc agctgtttgc ag atg cac ctc ctc cac cct ctg ctc cca atc 52

004220" 656EY550

004220" 656ET560

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Met His Leu Leu His Pro Leu Leu Pro Ile
-30 -25
ctg tgg tat cat cat tgg ggt ctg ggc ttc ctc cac cag gca tgc ctc 100
Leu Trp Tyr His His Trp Gly Leu Gly Phe Leu His Gln Ala Cys Leu
-20 -15 -10
ctc ctg gct cct tcc cac ccc cag tgc cac ctc ctg gag ccc tcc cac 148
Leu Leu Ala Pro Ser His Pro Gln Cys His Leu Leu Glu Pro Ser His
-5 1 5
ctg gga tac ccc cag cca tgc ccc cac cac cta tgc ctc ctg ggg ctg 196
Leu Gly Tyr Pro Gln Pro Cys Pro His His Leu Cys Leu Leu Gly Leu
10 15 20 25
cag gac atg gcc ccc cat c 215
Gln Asp Met Ala Pro His
30

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<210> 500
 <211> 298
 <212> DNA
 <213> Homo sapiens

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 <222> 57..296
 <221> sig_peptide
 <222> 57..146
 <223> score 5.4
 seq GLCWACXSSLGSC/EY

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Met
-30
acg acc ttc gtg ggc ctg cga cct cag ccg ggg gga agg ggc agg agt 107
Thr Thr Phe Val Gly Leu Arg Pro Gln Pro Gly Gly Arg Gly Arg Ser
-25 -20 -15
ggg ctc tgc tgg gcc tgc tgs agc tct ctt ggg agt tgt gaa tat gct 155
Gly Leu Cys Trp Ala Cys Xaa Ser Ser Leu Gly Ser Cys Glu Tyr Ala
-10 -5 1
tgc ttc cct ggg atg agc ttt tcc atc ttc aac aca caa gcc ggc cta 203
Cys Phe Pro Gly Met Ser Phe Ser Ile Phe Asn Thr Gln Ala Gly Leu
5 10 15
tcc aca ggg aaa gaa agt gga acc gag gct tcg cgg ctg cgg gag gag 251
Ser Thr Gly Lys Glu Ser Gly Thr Glu Ala Ser Arg Leu Arg Glu Glu
20 25 30 35
gga ggc aga gtc act att tac cgg gca cgg agt ttc tgt ggc gag ta 298
Gly Gly Arg Val Thr Ile Tyr Arg Ala Arg Ser Phe Cys Gly Glu
40 45 50

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<210> 501
 <211> 248
 <212> DNA
 <213> Homo sapiens

004220" 6555555555

<220>
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<222> 63..248

<221> sig_peptide
<222> 63..143
<223> score 5
seq LSCFYLLAIVSNA/VM

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atgttgttagc ttctgtcata atttccttcc cttttaaggc tgaataattt tccattgtgt 60
at atg tac cat att ttg ttc atc cat tca ttc att gat aga tac ttg 107
Met Tyr His Ile Leu Phe Ile His Ser Phe Ile Asp Arg Tyr Leu
-25 -20 -15
agt tgc ttc tac ctt ttg gca att gtg agt aat gct gtt atg aac atg 155
Ser Cys Phe Tyr Leu Leu Ala Ile Val Ser Asn Ala Val Met Asn Met
-10 -5 1
ggt gta caa atg tct gtt ttg agt cct tgt ttt gct ttc gtg cat tct 203
Gly Val Gln Met Ser Val Leu Ser Pro Cys Phe Ala Phe Val His Ser
5 10 15 20
att aaa aat gtt aag gtt ctt tgc ttt tta ctt ttt ttt ctc ttt 248
Ile Lys Asn Val Lys Val Leu Cys Phe Leu Leu Phe Phe Leu Phe
25 30 35

<210> 502
<211> 344
<212> DNA
<213> Homo sapiens

<220>
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<222> 173..343

<221> sig_peptide
<222> 173..253
<223> score 7.6
seq LLFLGFLIIAIQT/DV

<400> 502
tgagaatctg tttaagaagc agttggaatc cctgattcct tcttatataa ctaagcta 60
gattcttcct tttctacttt aggagaaaac tataattttt aaccctcca cccccaacgg 120
agggtgtaag aaagaagctc tctggactgc ttcataacag gcacacttaa ag atg tat 178
Met Tyr
gtg ggt gtt cct gtt tct cca cag cct cgt cag cat cta ttg ttt ctt 226
Val Gly Val Pro Val Ser Pro Gln Pro Arg Gln His Leu Leu Phe Leu
-25 -20 -15 -10
ggc ttt tta ata att gcc att cag act gat gtg aga wgg tat ctc att 274
Gly Phe Leu Ile Ile Ala Ile Gln Thr Asp Val Arg Xaa Tyr Leu Ile
-5 1 5
gtg gtt ttg att tgc att tat cta atg atc agt gat gtt gag ttt ttt 322
Val Val Leu Ile Cys Ile Tyr Leu Met Ile Ser Asp Val Glu Phe Phe

10 15 20 344
 ttc ata cgt ttt ttg gcc aca a
 Phe Ile Arg Phe Leu Ala Thr
 25 30

<210> 503
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 8..352

<221> sig_peptide
 <222> 8..145
 <223> score 9.8
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 Met Val Ser Lys Ile Val His Thr Leu Gly Met Lys Ile Ile
 -45 -40 -35
 gta aag aaa aga aaa aag cag gag tat ttg aac aaa tca cta aga btc 97
 Val Lys Lys Arg Lys Lys Gln Glu Tyr Leu Asn Lys Ser Leu Arg Xaa
 -30 -25 -20
 atg gaa caa tta ttg gca tta ctt cag gga ttg tct tgg tcc ttc tca 145
 Met Glu Gln Leu Leu Ala Leu Leu Gln Gly Leu Ser Trp Ser Phe Ser
 -15 -10 -5
 tta ttt tcw att tta gta caa gtg aaa cag cct cga aaa aag gtc atg 193
 Leu Phe Ser Ile Leu Val Gln Val Lys Gln Pro Arg Lys Lys Val Met
 1 5 10 15
 gct tgc aaa acc gct ttt aat aaa acc ggg ttc caa gaa gtg ttt gat 241
 Ala Cys Lys Thr Ala Phe Asn Lys Thr Gly Phe Gln Glu Val Phe Asp
 20 25 30
 cct cct cat tat gaa ctg ttt tca cta agg gac aaa gag att tct gca 289
 Pro Pro His Tyr Glu Leu Phe Ser Leu Arg Asp Lys Glu Ile Ser Ala
 35 40 45
 gac ctg gca gac ttg tcg gaa gaa ttg gac aac tac cag aag atg cgg 337
 Asp Leu Ala Asp Leu Ser Glu Glu Leu Asp Asn Tyr Gln Lys Met Arg
 50 55 60
 cgc tcc tcc acc gcc tc 354
 Arg Ser Ser Thr Ala
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<210> 504
 <211> 282
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 98..280

<221> sig_peptide
 <222> 98..145
 <223> score 7.5
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<400> 504
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 tttcctcatc tgtgaaacaa ctgataattt atatgac atg gaa ctt ctt ttt tgt 115
 Met Glu Leu Leu Phe Cys
 -15
 ttg tct gtt tgt ttg ttt gag gta gag tct cac tct gtc acc cag gct 163
 Leu Ser Val Cys Leu Phe Glu Val Glu Ser His Ser Val Thr Gln Ala
 -10 -5 1 5
 gga gtg cag tgg cac agt ctt ggc cca ctg aac tct ctg cct cct gga 211
 Gly Val Gln Trp His Ser Leu Gly Pro Leu Asn Ser Leu Pro Pro Gly
 10 15 20
 ttc aag cga ttt tcc tgc ctc agc ctt tca agt agc tgg gat tac agg 259
 Phe Lys Arg Phe Ser Cys Leu Ser Leu Ser Ser Trp Asp Tyr Arg
 25 30 35
 cat gca cca cca cct cca gca ta 282
 His Ala Pro Pro Pro Pro Ala
 40 45

<210> 505
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 43..369

<221> sig_peptide
 <222> 43..111
 <223> score 6.6
 seq VRLLXLXLLLIA/LE

<400> 505
 aatgtgtaca cgcccagctt cctgcctggt actctccaca gt atg cga aga ata 54
 Met Arg Arg Ile
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 tcc ctg act tct agc cct gtg cgc ctt ctt ttg tdt ctg cwg ttr cta 102
 Ser Leu Thr Ser Ser Pro Val Arg Leu Leu Leu Xaa Leu Xaa Leu Leu
 -15 -10 -5
 cta ata gcc ttg gag atc atg gtt ggt ggt cac tct ctt tgc ttc aac 150
 Leu Ile Ala Leu Glu Ile Met Val Gly Gly His Ser Leu Cys Phe Asn
 1 5 10
 ttc act ata aaa tca ttg tcc aga cct gga cag ccc tgg tgt gaa gcg 198
 Phe Thr Ile Lys Ser Leu Ser Arg Pro Gly Gln Pro Trp Cys Glu Ala
 15 20 25
 cat gtc ttc ttg aat aaa aat ctt ttc ctt cag tac aac agt gac aac 246

004220"066FT560

His Val Phe Leu Asn Lys Asn Leu Phe Leu Gln Tyr Asn Ser Asp Asn	
30 35 40 45	
aac atg gtc aaa cct ctg ggc ctc ctg ggg aag aag gta tat gcc acc	294
Asn Met Val Lys Pro Leu Gly Leu Leu Gly Lys Lys Val Tyr Ala Thr	
50 55 60	
agc act tgg gga gaa ttg acc caa acg ctg gga gaa gtg ggg cga gac	342
Ser Thr Trp Gly Glu Leu Thr Gln Thr Leu Gly Glu Val Gly Arg Asp	
65 70 75	
ctc agg atg ctc ctt tgt gac atc aaa	369
Leu Arg Met Leu Leu Cys Asp Ile Lys	
80 85	

<210> 506
 <211> 403
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 246..401

<221> sig_peptide
 <222> 246..389
 <223> score 7.4
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cctctccggt tcacgccatt ctcccgcctc agcctcccga gtagctkggr mctacaggcc	120
gcctgccacc atgcctggct aattttggtt ttgtattttt aatagagaca gggtttcacc	180
atgttagcca ggatggctct gatctcctga cctcgtaatc tgcccaaagt gctgggatta	240
caggc atg agc cac tgt gcc tgg ccc tct gtg tac ttt tta aaa ggc ctt	290
Met Ser His Cys Ala Trp Pro Ser Val Tyr Phe Leu Lys Gly Leu	
-45 -40 -35	
tct tgt ttg ttt tgg aca tct gat agg ctc ttt caa tat ggg aaa ttt	338
Ser Cys Leu Phe Trp Thr Ser Asp Arg Leu Phe Gln Tyr Gly Lys Phe	
-30 -25 -20	
tct tgt att ctt tct ttg atg ttt ctt ccc atc ttt ttt ccc tcc ttc	386
Ser Cys Ile Leu Ser Leu Met Phe Leu Pro Ile Phe Phe Pro Ser Phe	
-15 -10 -5	
tct tcc tac aac ata ac	403
Ser Ser Tyr Asn Ile	
1	

<210> 507
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 106..288

<221> sig_peptide
 <222> 106..189
 <223> score 4.5
 seq RFLSLSAADGXDX/SX

<400> 507
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 aggcggggagg ccgmsggmagg agctcttcct gcaggcgtgg aracc atg gtg ctc acg 117
 Met Val Leu Thr
 -25
 ctc gga gaa agt tgg ccg gta ttg gtg ggg agg agg ttt ctc agt ctg 165
 Leu Gly Glu Ser Trp Pro Val Leu Val Gly Arg Arg Phe Leu Ser Leu
 -20 -15 -10
 tcc gca gcc gac ggc asc gat gsc agc cam gac agc tgg gac gtg gag 213
 Ser Ala Ala Asp Gly Xaa Asp Xaa Ser Xaa Asp Ser Trp Asp Val Glu
 -5 1 5
 cgc gtc gcc gag tgg ccc tgg ctc tcc ggg acc att cga gct gtt tcc 261
 Arg Val Ala Glu Trp Pro Trp Leu Ser Gly Thr Ile Arg Ala Val Ser
 10 15 20
 cac acc gac gtt acc aag aag gat ctg aa 290
 His Thr Asp Val Thr Lys Lys Asp Leu
 25 30

<210> 508
 <211> 250
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 75..248

<221> sig_peptide
 <222> 75..221
 <223> score 7
 seq FGLFVSLVFLGQA/FT

<400> 508
 aactctttca aatatggaga ttaatcacca acttcttatt ttttgggcca gttggattca 60
 atttttttatt taac atg att ttt cta tat cgt tac tgt cga atg cta gaa 110
 Met Ile Phe Leu Tyr Arg Tyr Cys Arg Met Leu Glu
 -45 -40
 gaa ggc tct ttc cga ggt cgg aca gca gac ttt gta ttt atg ttc ctt 158
 Glu Gly Ser Phe Arg Gly Arg Thr Ala Asp Phe Val Phe Met Phe Leu
 -35 -30 -25
 ttt ggt gga ttc tta atg acc ctt ttt ggt ctg ttt gtg agc tta gtt 206
 Phe Gly Gly Phe Leu Met Thr Leu Phe Gly Leu Phe Val Ser Leu Val
 -20 -15 -10
 ttc ttg ggc cag gcc ttt aca ata atg ctc gtc tat gtg tgg ag 250
 Phe Leu Gly Gln Ala Phe Thr Ile Met Leu Val Tyr Val Trp
 -5 1 5

<210> 509
 <211> 361
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 60..359

<221> sig_peptide
 <222> 60..113
 <223> score 15.9
 seq LLCCLVLLTGVR/SP

<400> 509
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 atg cac agc tca gca ctg ctc tgt tgc ctg gtc ctc ctg act ggg gtg 107
 Met His Ser Ser Ala Leu Leu Cys Cys Leu Val Leu Leu Thr Gly Val
 -15 -10 -5
 agg gcc agc cca ggc cag ggc acc cag tct gag aac agc tgc acc cac 155
 Arg Ala Ser Pro Gly Gln Gly Thr Gln Ser Glu Asn Ser Cys Thr His
 1 5 10
 ttc cca ggc aac ctg cct aac atg ctt cga gat ctc cga gat gcc ttc 203
 Phe Pro Gly Asn Leu Pro Asn Met Leu Arg Asp Leu Arg Asp Ala Phe
 15 20 25 30
 agc aga gtg aag act ttc ttt caa atg aag gat cag ctg gac aac ttg 251
 Ser Arg Val Lys Thr Phe Phe Gln Met Lys Asp Gln Leu Asp Asn Leu
 35 40 45
 ttg tta aag gag tcc ttg ctg gag gac ttt aag ggt tac ctg ggt tgc 299
 Leu Leu Lys Glu Ser Leu Leu Glu Asp Phe Lys Gly Tyr Leu Gly Cys
 50 55 60
 caa gcc ttg tct gag atg atc cag ttt tac ctg gag gag gtg atg ccc 347
 Gln Ala Leu Ser Glu Met Ile Gln Phe Tyr Leu Glu Glu Val Met Pro
 65 70 75
 aag ctg aga acc aa 361
 Lys Leu Arg Thr
 80

<210> 510
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 13..183

<221> sig_peptide
 <222> 13..156
 <223> score 8.5
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<400> 510
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 Met Asp Gly Ser Met Asp Gly Trp Met Thr Gly Cys His
 -45 -40
 tct gtc acc caa gct gga gtg cag tgg tgt gat cac aga tca ctg cag 99
 Ser Val Thr Gln Ala Gly Val Gln Trp Cys Asp His Arg Ser Leu Gln
 -35 -30 -25 -20
 ctg caa ccc cct gca gat ttc tct gtg ttg tct ggg ctg gtc ttg aac 147
 Leu Gln Pro Pro Ala Asp Phe Ser Val Leu Ser Gly Leu Val Leu Asn
 -15 -10 -5
 tcc tgg gct caa aca atc atc ttg ctt cgg cct ccc t 184
 Ser Trp Ala Gln Thr Ile Ile Leu Leu Arg Pro Pro
 1 5

<210> 511
 <211> 414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 253..414
 <221> sig_peptide
 <222> 253..360
 <223> score 5
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 atgtatttct aattatataa atatttgacc ctctttgcct artttgtttt attcacttca 120
 actttgaccc tttatacttc tttttaaatt tcacttttctt atggttgttt ttctactttt 180
 cctcaatgcc ctttgtaaaa ttttcatttg aatctattat tctcccttgg acgtcttaat 240
 tctttctcta ct atg act ttt tct ttc ttt tgt ttc ttt cct ggg ttc aag 291
 Met Thr Phe Ser Phe Phe Cys Phe Phe Pro Gly Phe Lys
 -35 -30 -25
 cca ctc ctg ttt cat tac ttt ctt ttt wnk tcc ttt tct att tkd act 339
 Pro Leu Leu Phe His Tyr Phe Leu Phe Xaa Ser Phe Ser Ile Xaa Thr
 -20 -15 -10
 ctk ctt tgg ggc ttg aac tgt aag agg tcc tgg aac ata aat ttg aga 387
 Leu Leu Trp Gly Leu Asn Cys Lys Arg Ser Trp Asn Ile Asn Leu Arg
 -5 1 5
 att gtt gsa tca tac agt agt ggt tac 414
 Ile Val Xaa Ser Tyr Ser Ser Gly Tyr
 10 15

<210> 512
 <211> 328
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 113..328

<221> sig_peptide

<222> 113..184

<223> score 7.8

seq LMAGSSLSAGVSG/ED

<400> 512

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aatgaaa	at	tttccaaagg	attatgtgaa	attttcagat	gaagaagaat	tt atg aat		118
						Met Asn		
gaa gat	gag aag	gaa atg	aag gaa	att cta	atg gca	gga agt	agt tta	166
Glu Asp	Glu Lys	Glu Met	Lys Glu	Ile Leu	Met Ala	Gly Ser	Ser Leu	
-20			-15			-10		
tca gct	gga gtt	agt ggg	gaa gat	aaa acc	gag ata	ttg aat	ccc act	214
Ser Ala	Gly Val	Ser Gly	Glu Asp	Lys Thr	Glu Ile	Leu Asn	Pro Thr	
-5		1		5		10		
cca scg	atg gcc	aaa tct	ctg acc	ata gac	tgt ctg	gaa ttg	gca tta	262
Pro Xaa	Met Ala	Lys Ser	Leu Thr	Ile Asp	Cys Leu	Glu Leu	Ala Leu	
	15			20		25		
ccc cct	gaa ctg	gct ttt	caa ctt	aat gaa	tta ttt	ggt cct	ggt ggt	310
Pro Pro	Glu Leu	Ala Phe	Gln Leu	Asn Glu	Leu Phe	Gly Pro	Val Gly	
	30		35			40		
att gat	tca ggg	tct cta						328
Ile Asp	Ser Gly	Ser Leu						
	45							

<210> 513

<211> 351

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 27..350

<221> sig_peptide

<222> 27..95

<223> score 10

seq PLLGLLLSLPAGA/DV

<400> 513

accgagctgg	atttgtatgt	tgacac	atg cct	tct tgg	atc ggg	gct gtg	att	53
			Met Pro	Ser Trp	Ile Gly	Ala Val	Ile	
			-20					
ctt ccc	ctc ttg	ggg ctg	ctg ctc	tcc ctc	ccc gcc	ggg gcg	gat gtg	101
Leu Pro	Leu Leu	Gly Leu	Leu Leu	Ser Leu	Pro Ala	Gly Ala	Asp Val	
	-10		-5			1		
aag gct	cgg agc	tgc gga	gag gtc	cgc cag	gcg tac	ggt gcc	aag gga	149
Lys Ala	Arg Ser	Cys Gly	Glu Val	Arg Gln	Ala Tyr	Gly Ala	Lys Gly	
	5		10			15		
ttc agc	ctg gcg	gac atc	ccc tac	cag gag	atc gca	kgg gaa	cac tta	197

Phe	Ser	Leu	Ala	Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Xaa	Glu	His	Leu	
20					25					30						
aga	atc	tgt	cct	cag	gaa	tat	aca	tgc	tgc	acc	aca	gaa	atg	gar	gac	245
Arg	Ile	Cys	Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	
35				40				45							50	
aag	tta	agc	caa	caa	agc	aaa	ctc	gaa	ttt	gaa	aac	ctt	gtg	gaa	gag	293
Lys	Leu	Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	
			55					60					65			
aca	agc	cat	ttt	gtg	cgc	acc	act	ttt	gtg	tcc	agg	cat	aag	aaa	ttt	341
Thr	Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	
			70					75					80			
gac	ggt	agg	t													351
Asp	Gly	Arg														
			85													

<210> 514
 <211> 221
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 12..221
 <221> sig_peptide
 <222> 12..86
 <223> score 4.6
 seq LPTLLLLPVGAPG/KK

<400> 514																	
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	Met	Val	Leu	Gly	Ala	Leu	Asn	Leu	Pro	Ser	Gln	Glu	Leu				
	-25				-20						-15						
ccc	act	ctc	ctg	ctc	ctc	cca	gtg	ggg	gca	cct	ggr	aag	aaa	aaa	ggc	98	
Pro	Thr	Leu	Leu	Leu	Pro	Val	Gly	Ala	Pro	Gly	Lys	Lys	Lys	Lys	Gly		
	-10				-5					1							
atg	gaa	ggc	aaa	act	ccc	ttg	gac	ctg	ttt	gct	cat	ttt	ggc	cct	gag	146	
Met	Glu	Gly	Lys	Thr	Pro	Leu	Asp	Leu	Phe	Ala	His	Phe	Gly	Pro	Glu		
5				10				15					20				
cca	ggg	gac	cac	tca	gat	ccg	ctg	cct	ccc	tct	gca	ccc	tct	ccc	act	194	
Pro	Gly	Asp	His	Ser	Asp	Pro	Leu	Pro	Pro	Ser	Ala	Pro	Ser	Pro	Thr		
			25					30					35				
cgg	gag	ggg	gct	ctg	acc	ccg	ccc	cca								221	
Arg	Glu	Gly	Ala	Leu	Thr	Pro	Pro	Pro									
			40					45									

<210> 515
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 <213> Homo sapiens

<220>
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<222> 18..305

<221> sig_peptide

<222> 18..131

<223> score 4.8

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-35 -30
ctg gcc ttc cgg ccc cag atg gat ccc cgg cag cta tcc atg ctg 98
Leu Ala Phe Arg Pro Gln Met Asp Pro Arg Gln Leu Ser Met Met Leu
-25 -20 -15
atg ctg gcg cag tca aac ccg cag ctg ttc gcg ctt atg ggc acc cgg 146
Met Leu Ala Gln Ser Asn Pro Gln Leu Phe Ala Leu Met Gly Thr Arg
-10 -5 1 5
gca ggc atc gcc agg gag ctg gag cgt gtg gag cnd cag tct cgg ctg 194
Ala Gly Ile Ala Arg Glu Leu Glu Arg Val Glu Xaa Gln Ser Arg Leu
10 15 20
gag cag ctg agt gcg gca gag ctg cag agc agg aac cag ggc cac tgg 242
Glu Gln Leu Ser Ala Ala Glu Leu Gln Ser Arg Asn Gln Gly His Trp
25 30 35
gct gac tgg cta cag gcg tac aga gcc cgg ctg gac aag gac ctg gaa 290
Ala Asp Trp Leu Gln Ala Tyr Arg Ala Arg Leu Asp Lys Asp Leu Glu
40 45 50
ggc gct ggg gac kac 305
Gly Ala Gly Asp Xaa
55

<210> 516

<211> 367

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 67..366

<221> sig_peptide

<222> 67..183

<223> score 5.4

seq ILLTSCFYTLVSS/TF

<400> 516

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tctagc atg atc tca tcc tgt gga gtt aaa tac ttg ttt tca cat gcc 108
Met Ile Ser Ser Cys Gly Val Lys Tyr Leu Phe Ser His Ala
-35 -30
tcc tta ttt ttt atg gta ggg agt aca gga agt tta ata ctc tta act 156
Ser Leu Phe Phe Met Val Gly Ser Thr Gly Ser Leu Ile Leu Leu Thr
-25 -20 -15 -10

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tct tgt ttc tat acc ctt gtt tca tca acc ttt ctt caa aaa ctc tct      204
Ser Cys Phe Tyr Thr Leu Val Ser Ser Thr Phe Leu Gln Lys Leu Ser
          -5                      1                      5
tct ttg ctc ttg ata tta ttt acc gaa aca agt gty ctt atg tta aaa      252
Ser Leu Leu Leu Ile Leu Phe Thr Glu Thr Ser Val Leu Met Leu Lys
          10                      15                      20
aca ttt gta gct aat tct tgc tgt waa ttg tgg tct cac aat tgt att      300
Thr Phe Val Ala Asn Ser Cys Cys Xaa Leu Trp Ser His Asn Cys Ile
          25                      30                      35
aat ttc ttc aaa aag gtc ckg cct tct tat tgc kgc agc agt cta ctc      348
Asn Phe Phe Lys Lys Val Xaa Pro Ser Tyr Cys Xaa Ser Ser Leu Leu
          40                      45                      50                      55
ttc ctg gcc gta cct agg t      367
Phe Leu Ala Val Pro Arg
          60

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<210> 517
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 <212> DNA
 <213> Homo sapiens

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<221> sig_peptide
 <222> 58..102
 <223> score 4.5
 seq LLGAAAVAALGRG/RA

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atg aga ctc ctg gga gct gca gcc gtc gcg gct ctg ggg cgc gga agg      105
Met Arg Leu Leu Gly Ala Ala Val Ala Ala Leu Gly Arg Gly Arg
          -15          -10          -5                      1
gcc ccc gcc tcc cta ggc tgg cag agg aag cag gtt aat tgg aag gcc      153
Ala Pro Ala Ser Leu Gly Trp Gln Arg Lys Gln Val Asn Trp Lys Ala
          5                      10                      15
tgc cga tgg tct tca tca ggg gtg att cct aat gaa aaa ata cga aat      201
Cys Arg Trp Ser Ser Ser Gly Val Ile Pro Asn Glu Lys Ile Arg Asn
          20                      25                      30
att gga atc tca gct cac att gat tct ggg aa      233
Ile Gly Ile Ser Ala His Ile Asp Ser Gly
          35                      40

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<210> 518
 <211> 434
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 57..434

<221> sig_peptide
 <222> 57..101
 <223> score 4
 seq PTCATCAHPVTLA/QR

<400> 518
 anbkgccgcg tctgcaacgg agtcttcbbt ctccaattgc cttctgcccc atcacc atg 59
 Met
 -15
 ggc ccc acc tgc gcc acc tgc gcc cac cct gtg acc ctg gct cag cga 107
 Gly Pro Thr Cys Ala Thr Cys Ala His Pro Val Thr Leu Ala Gln Arg
 -10 -5 1
 cct tgg ccc tta atc gcc caa cgc cga ttc ctc aaa att ccg gct gcg 155
 Pro Trp Pro Leu Ile Ala Gln Arg Arg Phe Leu Lys Ile Pro Ala Ala
 5 10 15
 ctg aat cgg gct gct ttt gcc gcc gcc ccg gca gtt ggg ccc tgt ttc 203
 Leu Asn Arg Ala Ala Phe Ala Ala Ala Pro Ala Val Gly Pro Cys Phe
 20 25 30
 cgc cgg cgc cct ggg aga gcc ctc acc act cgg ctg ggc tcc ctg gcc 251
 Arg Arg Arg Pro Gly Arg Gly Leu Thr Thr Arg Leu Gly Ser Leu Ala
 35 40 45 50
 cct ccc ttc ccc tgg cct gag cac ccc tgc gcc chv ccg ctc ctc ctg 299
 Pro Pro Phe Pro Trp Pro Glu His Pro Cys Gly Xaa Pro Leu Leu Leu
 55 60 65
 aga agg cga caa tct ctt tgc acc tta gtg ttt cga gga cag aaa ggg 347
 Arg Arg Arg Gln Ser Leu Cys Thr Leu Val Phe Arg Gly Gln Lys Gly
 70 75 80
 cag aag ggt cac ttc gga gcc act cgc gcc gtt ttc acg tgt gtg tgt 395
 Gln Lys Gly His Phe Gly Ala Thr Arg Ala Val Phe Thr Cys Val Cys
 85 90 95
 aat ggg ggg agg ggg gct ccc gcc ttt ccc ctt ttc agc 434
 Asn Gly Gly Arg Gly Ala Pro Gly Phe Pro Leu Phe Ser
 100 105 110

<210> 519
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 <212> DNA
 <213> Homo sapiens

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 <222> 190..378

<221> sig_peptide
 <222> 190..306
 <223> score 4.6
 seq AFLSCLAFLVLDL/QE

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 agccatgagg ggctgtggca gggaggggca ggggtgtggaa agactcccct ggggcatgg 120

tggagatgtg ctgaggtctt ctccctgac gtcttctcct ccctgctgac cgacggctac 180
 cagaackag atg gag tct ccg cag ctc cac tgc att ctc aac agc aac agc 231
 Met Glu Ser Pro Gln Leu His Cys Ile Leu Asn Ser Asn Ser
 -35 -30
 gtg gcc tgc agc ttt gcc gtg gga gcc ggc ttc ctg gcc ttc ctc agc 279
 Val Ala Cys Ser Phe Ala Val Gly Ala Gly Phe Leu Ala Phe Leu Ser
 -25 -20 -15 -10
 tgc ctg gcc ttc ctc gtc ctg gac aca cag gag acc cgc att gcc ggc 327
 Cys Leu Ala Phe Leu Val Leu Asp Thr Gln Glu Thr Arg Ile Ala Gly
 -5 1 5
 acc cgc ttc aag aca gcc ttc cag ctc ctg gac hkc atc ctg gct gtt 375
 Thr Arg Phe Lys Thr Ala Phe Gln Leu Leu Asp Xaa Ile Leu Ala Val
 10 15 20
 ctc t 379
 Leu

<210> 520
 <211> 369
 <212> DNA
 <213> Homo sapiens

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 <222> 210..368

<221> sig_peptide
 <222> 210..287
 <223> score 6.3
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 gacccctggg cgaaggcctg gacttgacaga tgtgtgttcc ctgtgcgggt ggacagaggg 120
 ggcccttatg accacattg cagccccatt ccaccacccc ttcctcccca gagcagtctc 180
 tgccgagggga cagcacctgt gtcccttcg atg cca caa cag cca gtt gaa cag 233
 Met Pro Gln Gln Pro Val Glu Gln
 -25 -20
 ggg agc cct ttg ctc agg cag ctt ctc ctg cct ctc cct cct ttc tcc 281
 Gly Ser Pro Leu Leu Arg Gln Leu Leu Leu Pro Leu Pro Pro Phe Ser
 -15 -10 -5
 ttc cct gcc cca tcc ccg tgc cct tct tgg cct gtg gcg ctg ggg agc 329
 Phe Pro Ala Pro Ser Pro Cys Pro Ser Trp Pro Val Ala Leu Gly Ser
 1 5 10
 cat ggt gtg gca tac tgg ggc tcc tgc tcc ttg ggs cac t 369
 His Gly Val Ala Tyr Trp Gly Ser Cys Ser Leu Gly His
 15 20 25

<210> 521
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 <212> DNA
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<220>

<221> CDS
<222> 54..257

<221> sig_peptide
<222> 54..173
<223> score 3.9
seq CVYVCVCISVCAC/VY

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Met
-40
cgt gtg tgt gcg cat cag tgt ctg cat gtg tgt atr tgt gtg tat gta 104
Arg Val Cys Ala His Gln Cys Leu His Val Cys Xaa Cys Val Tyr Val
-35 -30 -25
tgt stg tgc gcg cgc atc tgt gtg tgt gca tgt gtg tat gta tgt gtg 152
Cys Xaa Cys Ala Arg Ile Cys Val Cys Ala Cys Val Tyr Val Cys Val
-20 -15 -10
tgc atc tct gtg tgt gca tgt gtg tat gtg tgt gtg cat ctg tgt gtg 200
Cys Ile Ser Val Cys Ala Cys Val Tyr Val Cys Val His Leu Cys Val
-5 1 5
tgt gca tgt gtg cat gcg tgt gta tgt gtg tgt gcg tgc gtg cat ctg 248
Cys Ala Cys Val His Ala Cys Val Cys Val Cys Ala Cys Val His Leu
10 15 20 25
tgt gtg tgc 257
Cys Val Cys

<210> 522
<211> 231
<212> DNA
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<222> 62..229

<221> sig_peptide
<222> 62..109
<223> score 11.3
seq PLLLSSLLGGSQA/MD

<400> 522
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g atg cta ctg cca ctg ctg ctg tcm tgc ctg ctg ggc ggg tcc cag gct 109
Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln Ala
-15 -10 -5
atg gat ggg aga ttc tgg ata cga gtg cag gag tca gtg atg gtg ccg 157
Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met Val Pro
1 5 10 15
gag ggc ctg tgc atc tct gtn kcc ctg ctc ttt ctc cta ccc ccg aca 205
Glu Gly Leu Cys Ile Ser Val Xaa Leu Leu Phe Leu Leu Pro Pro Thr
20 25 30

aga ctg gac agg gtc tac ccc agc cg
 Arg Leu Asp Arg Val Tyr Pro Ser
 35 40

231

<210> 523
 <211> 257
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> 60..257

<221> sig_peptide
 <222> 60..170
 <223> score 4.5
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<400> 523
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 atg ctt att act cgk tta cag tct ggt ata gat ttt gca atc cag ctt 107
 Met Leu Ile Thr Arg Leu Gln Ser Gly Ile Asp Phe Ala Ile Gln Leu
 -35 -30 -25
 gat gaa agc act gat att gga agc tgc aca aca ctt tta gtt tat gtc 155
 Asp Glu Ser Thr Asp Ile Gly Ser Cys Thr Thr Leu Leu Val Tyr Val
 -20 -15 -10
 aga tat gcg tgg caa gat gat ttt ttg gag gat ttt ttg tgt ttt tta 203
 Arg Tyr Ala Trp Gln Asp Asp Phe Leu Glu Asp Phe Leu Cys Phe Leu
 -5 1 5 10
 aat tta acc tca cac cta agt gga tta gat att ttt aca gaa tta gaa 251
 Asn Leu Thr Ser His Leu Ser Gly Leu Asp Ile Phe Thr Glu Leu Glu
 15 20 25
 agg cgc 257
 Arg Arg

<210> 524
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 79..354

<221> sig_peptide
 <222> 79..180
 <223> score 5.2
 seq LWSSCWLAPLADG/ML

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 ctggaaacgc gagcgggg atg gta ggt ggt ttg gac ccg ccg ggc cgc cgt 111

004220"666T50

004220 "665T560

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Arg	Phe	Gln	Lys	Gly	Phe	Asp	Trp	Arg	Asn	Leu	Trp	agg
		-20						-15				-10
ctg	gct	cct	ctg	gct	gat	ggc	atg	ttg	agg	tac	atg	ggc
Leu	Ala	Pro	Leu	Ala	Asp	Gly	Met	Leu	Arg	Tyr	Met	Gly
		-5					1				5	
cga	ngg	gca	tcc	aat	cca	gag	ggg	tcc	act	cta	gag	gcc
Arg	Xaa	Ala	Ser	Asn	Pro	Glu	Gly	Ser	Thr	Leu	Glu	Ala
10					15				20			
gca	cca	trg	gcc	agt	gtg	tca	cca	agt	gta	akh	mtc	cct
Ala	Pro	Xaa	Ala	Ser	Val	Ser	Pro	Ser	Val	Xaa	Xaa	Pro
				30				35				40
tgg	gca	gca	aaa	atg	gag	acc	gtg	agc	cca	gca	aca	agt
Trp	Ala	Ala	Lys	Met	Glu	Thr	Val	Ser	Pro	Ala	Thr	Ser
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159
207
255
303
351
354

ggc
Gly

<210> 525
<211> 173
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..171

<221> sig_peptide
<222> 16..156
<223> score 3.6
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	Met	Val	Glu	Lys	Lys	Thr	Ser	Gly	Ser	Leu	Ser	Val
					-45					-40		
gcc	cag	gct	gga	atg	caa	tgg	cgc	gat	ctc	agc	tcg	ctg
Ala	Gln	Ala	Gly	Met	Gln	Trp	Arg	Asp	Leu	Ser	Ser	Leu
					-30				-25			-20
cct	ccc	ggg	ttc	aag	cga	ttc	ttg	tgc	ctc	agc	ctc	ccg
Pro	Pro	Gly	Phe	Lys	Arg	Phe	Leu	Cys	Leu	Ser	Leu	Pro
				-15				-10				-5
att	aca	ggc	atg	tgc	cac	cac	acc	ct				
Ile	Thr	Gly	Met	Cys	His	His	Thr					
		1					5					

51
99
147
173

<210> 526
<211> 427
<212> DNA
<213> Homo sapiens

004220"666T560

<220>
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<222> 275..427

<221> sig_peptide
<222> 275..394
<223> score 4.2
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tgttttgtct aaaattcata gatgctgaac tgtgtatatt tggtgtcaag tttgaaaggt 120
acttgggttt ttgggggtgt taggaggtag ggtggatggt actattaaat acatttagac 180
tttttaaaat aagtgttaact gatcatttcc aacaaatatt tactatgtcc atacttgtgc 240
tccaaaagac aattctgtct tcctcttgag atac atg tct cgg ggc ccc tgt agg 295
Met Ser Arg Gly Pro Cys Arg
-40 -35
tct ggt ctg aga ggg tcc cca tgg gtg gct gtg tcw gct ggc gct ttc 343
Ser Gly Leu Arg Gly Ser Pro Trp Val Ala Val Ser Ala Gly Ala Phe
-30 -25 -20
ttg gac act cct ctg ctc tca gga ctg tgt gta gca gtc tgc gct cag 391
Leu Asp Thr Pro Leu Leu Ser Gly Leu Cys Val Ala Val Cys Ala Gln
-15 -10 -5
yaa ggc cat gtt ggt gtg atg ggc ttc ggc tca gat 427
Xaa Gly His Val Gly Val Met Gly Phe Gly Ser Asp
1 5 10

<210> 527
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<212> DNA
<213> Homo sapiens

<220>
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<222> 79..249

<221> sig_peptide
<222> 79..210
<223> score 4
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agcagccgag gcccaga atg gcc aag ttt ctt tcc sva gac caa att aat 111
Met Ala Lys Phe Leu Ser Xaa Asp Gln Ile Asn
-40 -35
gag tac aag gaa tgc ttc tcc ctg tat gac arg cag cag agg ggg aag 159
Glu Tyr Lys Glu Cys Phe Ser Leu Tyr Asp Xaa Gln Gln Arg Gly Lys
-30 -25 -20
ata aaa gcc acc gmc ctc atg gtg gcc atg mgg tgc ctg ggg gcc agc 207
Ile Lys Ala Thr Xaa Leu Met Val Ala Met Arg Cys Leu Gly Ala Ser
-15 -10 -5

ccg asg cca ggg gag gtg cag cgg cns tgc aga ccc acg gga ta
 Pro Xaa Pro Gly Glu Val Gln Arg Xaa Cys Arg Pro Thr Gly
 1 5 10

251

<210> 528
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 <212> DNA
 <213> Homo sapiens

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 <222> 28..246

<221> sig_peptide
 <222> 28..69
 <223> score 3.8
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 Met Leu Asp Ser Leu Leu Ala Leu Gly
 -10
 ggc ctg gtg ctg ctt cgg gat tcc gtg gag tgg gag ggg cgc agt ctc 102
 Gly Leu Val Leu Leu Arg Asp Ser Val Glu Trp Glu Gly Arg Ser Leu
 -5 1 5 10
 ttg aag gcg ctt gks aag aaa tct gca ctg tgt ggg gag caa gtg cat 150
 Leu Lys Ala Leu Xaa Lys Lys Ser Ala Leu Cys Gly Glu Gln Val His
 15 20 25
 atc ctg ggc tgt gaa gtg agy gab gaa gag ttt cgt gaa rgt ttt gac 198
 Ile Leu Gly Cys Glu Val Ser Xaa Glu Glu Phe Arg Glu Xaa Phe Asp
 30 35 40
 tct sat atc arc aat cgg ctg gtt tac cat grc ttc ttc aga gac cct c 247
 Ser Xaa Ile Xaa Asn Arg Leu Val Tyr His Xaa Phe Phe Arg Asp Pro
 45 50 55

<210> 529
 <211> 467
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 285..467

<221> sig_peptide
 <222> 285..350
 <223> score 3.8
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 agatacagtc agtcatcttc ttcagggtta cctcaaagt tccaaggtct tacacctact 120

004220"666T560

catcatattc agggaactga gactccacac acctcacttt gaggctggaa tatgctgaaa	180
ctgcctccac aaactcatta ttctggacca agacttacag cctaaagtga aggacatttc	240
caaagaaatt ttctcctcac tgatgcctct cctgctgcaa tgca atg acc ctg gct	296
Met Thr Leu Ala	
-20	
atg tac aag aca tac ttt ggc ttg ctc ctg gga aac ctt tgc tct gta	344
Met Tyr Lys Thr Tyr Phe Gly Leu Leu Leu Gly Asn Leu Cys Ser Val	
-15 -10 -5	
aag agc act gag ann ttg cta cca ttg ctg gct tca agc act ttg tcc	392
Lys Ser Thr Glu Xaa Leu Leu Pro Leu Leu Ala Ser Ser Thr Leu Ser	
1 5 10	
cca ttc att tcc aag atg gag tct tgc tct tgt tac cca ggt tgg agt	440
Pro Phe Ile Ser Lys Met Glu Ser Cys Ser Cys Tyr Pro Gly Trp Ser	
15 20 25 30	
gca atg gca caa tct cgg ctc act gca	467
Ala Met Ala Gln Ser Arg Leu Thr Ala	
35	
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<222> 17..358	
<221> sig_peptide	
<222> 17..130	
<223> score 3.5	
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Met Ser Ser Met Trp Ser Glu Tyr Thr Ile Gly Gly	
-35 -30	
gtg aag att tac ttt cct tat aaa gct tac ccg tca cag ctt gct atg	100
Val Lys Ile Tyr Phe Pro Tyr Lys Ala Tyr Pro Ser Gln Leu Ala Met	
-25 -20 -15	
atg aat tct att ctc aga gga tta aac agc aag caa cat tgt ttg ttg	148
Met Asn Ser Ile Leu Arg Gly Leu Asn Ser Lys Gln His Cys Leu Leu	
-10 -5 1 5	
gag agt ccc aca gga agt gga aaa agc tta gcc tta ctt tgt tct gct	196
Glu Ser Pro Thr Gly Ser Gly Lys Ser Leu Ala Leu Leu Cys Ser Ala	
10 15 20	
tta gca tgg caa caa tct ctt agt ggg aaa cca gca gat gag ggc gta	244
Leu Ala Trp Gln Gln Ser Leu Ser Gly Lys Pro Ala Asp Glu Gly Val	
25 30 35	
agt gaa aaa gct gaa gta caa ttg tca tgt tgt tgt gca tgc cat tca	292
Ser Glu Lys Ala Glu Val Leu Ser Cys Cys Cys Ala Cys His Ser	
40 45 50	
aag gat ttt aca aac aat gac atg aac caa gga act tca cgt cat ttc	340
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359

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<210> 531
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<212> DNA
<213> Homo sapiens
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<221> CDS  
<222> 41..205
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<221> sig_peptide
<222> 41..175
<223> score 5
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[illegible]

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<210> 532
<211> 457
<212> DNA
<213> Homo sapiens
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<220>  
<221> CDS  
<222> 139..456
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<221> sig_peptide
<222> 139..240
<223> score 3.6
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ccagaccagt gtcctaaa atg ttt scc cta tgt ttt ctt aca gtg gkt ttt 171
Met Phe Xaa Leu Cys Phe Leu Thr Val Xaa Phe
-30 -25
atc att tca aat ctt ttt ttt ttg ara cgg rgt ctt gct ctg tcg ctc 219
Ile Ile Ser Asn Leu Phe Phe Leu Xaa Arg Xaa Leu Ala Leu Ser Leu
-20 -15 -10
agg ctg gak tgc akt ggc rcg atc tcg gct cac tgc aac ctc cgc ctc 267
Arg Leu Xaa Cys Xaa Gly Xaa Ile Ser Ala His Cys Asn Leu Arg Leu
-5 1 5
cca ggt tca agc aat tct cct gcc tca gcc tcc cga gta gct ggg att 315
Pro Gly Ser Ser Asn Ser Pro Ala Ser Ala Ser Arg Val Ala Gly Ile
10 15 20 25
ama ggc gtg cac cac cac gcc cgg cwa att ttt gta ttt twa gtg gas 363
Xaa Gly Val His His His Ala Arg Xaa Ile Phe Val Phe Xaa Val Xaa
30 35 40
acg ggg ttt cac cat gtt ggw mag gct ggt ctc gra gtt cht gac ctc 411
Thr Gly Phe His His Val Gly Xaa Ala Gly Leu Xaa Val Xaa Asp Leu
45 50 55
rtg atc ctc ctg cct ccg cct ccc aaa gtg ctg gga tta cag gcg t 457
Xaa Ile Leu Leu Pro Pro Pro Lys Val Leu Gly Leu Gln Ala
60 65 70

<210> 533
<211> 447
<212> DNA
<213> Homo sapiens

<220>
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<222> 273..446

<221> sig_peptide
<222> 273..329
<223> score 5.9
seq PXXLLILAHITQS/CP

<400> 533
gtatttggtta aatgctacaa gagtgactgg gatcataagt gttacgggag tttggcaaag 60
aagcaggagg tagttagtgt aactgttaat gtgattataa gactaatata tttgtkggr 120
agataactta ccaagtttgg tttgtggaaa atttggattg agaaggaaat tgtatgtttc 180
cgttagaagt agaacaacaa caacaaaata tctcccatca tttgtttggt actatctggc 240
ctccccagtg ctgcttgga gaatcatgaa ac atg atg aat caa aca cat cct 293
Met Met Asn Gln Thr His Pro
-15
trm rtg ttg ctc atc ctg gca cat att aca cag agt tgc cca tgg gcc 341
Xaa Xaa Leu Leu Ile Leu Ala His Ile Thr Gln Ser Cys Pro Trp Ala
-10 -5 1
cat gta gga gca gct cca tct gcc ctt cta ata cat agg tgg gar ctg 389
His Val Gly Ala Ala Pro Ser Ala Leu Leu Ile His Arg Trp Glu Leu
5 10 15 20
agg ggg tgc tcg tat ttg aaa ctg ttt ttg gtt atg gtg ctc ata ttt 437
Arg Gly Cys Ser Tyr Leu Lys Leu Phe Leu Val Met Val Leu Ile Phe

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25 30 35 447
gaa atg ctt t
Glu Met Leu

<210> 534
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 230..418

<221> sig_peptide
<222> 230..307
<223> score 5.6
seq LWCLLPASFTHS/LG

<400> 534
gatgtctgag gtggcatgac aacacatggc aggattaata tcatttgcac ttattttggt 60
atztatatta aatataatgc agtattttaa ttcgcagaca agtcagctcc cccattatck 120
akgttttaat attkatttgt gtccactttc gaggtgaaac tgactgtatt cagcatttca 180
gcccgtgttt aaggtggctt gtccctgaaa ggtggagtgt tggggattc atg caa aca 238
Met Gln Thr
-25
ttt gag gaa ggg cac ctc cca gaa aac ttt ctt tgg tgc ctt tta cct 286
Phe Glu Glu Gly His Leu Pro Glu Asn Phe Leu Trp Cys Leu Leu Pro
-20 -15 -10
cct gct tct ttt act cac tca ttg ggg ttt tgc cag gnc tta cac tgc 334
Pro Ala Ser Phe Thr His Ser Leu Gly Phe Cys Gln Xaa Leu His Cys
-5 1 5
tct ttc ctc aac ttc ttt ccc tct ttg ccg ctt ttc tat ttt gtc gtt 382
Ser Phe Leu Asn Phe Phe Pro Ser Leu Pro Leu Phe Tyr Phe Val Val
10 15 20 25
cca tgc ttg agc atg gcc ttc ccc tcc ctc tcc tgt ca 420
Pro Cys Leu Ser Met Ala Phe Pro Ser Leu Ser Cys
30 35

<210> 535
<211> 318
<212> DNA
<213> Homo sapiens

<220>
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<222> 153..317

<221> sig_peptide
<222> 153..257
<223> score 4.9
seq LFIFIGSLQPVPT/RF

004220"666E7560

<400> 535
 cacacacaaa ctctcaagtg gcctaattcc ctctcaccaa accaatcaca atacagataa 60
 aagagaataa cttgtgttca tttttgtaca aacaaaaaag atataaattg tgaatgrtgc 120
 atgrttttta awtvmccaag taaactgggc aa atg ctt ctg cat tat tta aag 173
 Met Leu Leu His Tyr Leu Lys
 -35 -30
 cta aaa ggt gat cag tgg aaa ctt tcc tct gtt agt act cta ata ctt 221
 Leu Lys Gly Asp Gln Trp Lys Leu Ser Ser Val Ser Thr Leu Ile Leu
 -25 -20 -15
 ttt ata ttt atc ggc tca cta caa cct gtg cct acc agg ttc aag cga 269
 Phe Ile Phe Ile Gly Ser Leu Gln Pro Val Pro Thr Arg Phe Lys Arg
 -10 -5 1
 ttc tcc tgt ctc gdc cac ctg agt agc cga gac cac agg caa gca cta c 318
 Phe Ser Cys Leu Xaa His Leu Ser Ser Arg Asp His Arg Gln Ala Leu
 5 10 15 20

<210> 536
 <211> 471
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 114..470
 <221> sig_peptide
 <222> 114..167
 <223> score 11
 seq LLLWASLLTGAWP/SF

<400> 536
 gcgagaccag agcgagcgaa cgaaccgcgg cgggtccggag agccccgagc gcassnagga 60
 cctgggtttc tagagagtgg agcctgcttc ctgggcccta ggccccctcc aca atg 116
 Met
 ctt gtc gcc ggt ctt ctt ctc tgg gct tcc cta ctg acc ggg gcc tgg 164
 Leu Val Ala Gly Leu Leu Leu Trp Ala Ser Leu Leu Thr Gly Ala Trp
 -15 -10 -5
 cca tcc ttc ccc acc cag gac cac ctc ccg gcc acg ccc cgg gtc cgg 212
 Pro Ser Phe Pro Thr Gln Asp His Leu Pro Ala Thr Pro Arg Val Arg
 1 5 10 15
 ctc tca ttc aaa gag ctg aag gcc aca ggc acc gcc cac ttc ttc aac 260
 Leu Ser Phe Lys Glu Leu Lys Ala Thr Gly Thr Ala His Phe Phe Asn
 20 25 30
 ttc ctg ctc aac aca acc gac tac cga atc ttg ctc aag gac gag gac 308
 Phe Leu Leu Asn Thr Thr Asp Tyr Arg Ile Leu Leu Lys Asp Glu Asp
 35 40 45
 cac gac cgc atg tac gtg ggc agc aag gac tac gtg ctg tcc ctg gac 356
 His Asp Arg Met Tyr Val Gly Ser Lys Asp Tyr Val Leu Ser Leu Asp
 50 55 60
 ctg cac gac atc aac cgc gag ccc ctc att ata cac tgg gca gcc tcc 404
 Leu His Asp Ile Asn Arg Glu Pro Leu Ile Ile His Trp Ala Ala Ser
 65 70 75
 cca cag cgc atc gag gaa tgc gtg ctc tca ggc aag gat gtc aac ggc 452

Pro Gln Arg Ile Glu Glu Cys Val Leu Ser Gly Lys Asp Val Asn Gly
 80 85 90 95
 gag tgt ggg aac ttc gtc a
 Glu Cys Gly Asn Phe Val
 100

471

<210> 537
 <211> 344
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 149..343

<221> sig_peptide
 <222> 149..214
 <223> score 4.2
 seq TAYWLSFMSWAQS/SS

<400> 537
 tgtatactga gggttcaggaa ctgctggaga gatgactggg caccaagagg atgacagtga 60
 ctcagctggc atcccttagc tgggtcatgg cagagctgag tggccactcc tgtctctgac 120
 cccagcttca gtgctcttta tctcctcc atg cct cct cag tgc tgc tct 172
 Met Pro Pro Gln Ser Cys Cys Ser
 -20 -15
 aag act gct tac tgg ctt tcc ttc atg tcc tgg gca cag agc agt tct 220
 Lys Thr Ala Tyr Trp Leu Ser Phe Met Ser Trp Ala Gln Ser Ser Ser
 -10 -5 1
 ttt ggt agc aga htt gag tcc act tcc ccc tgc aca gat cac tgc tca 268
 Phe Gly Ser Arg Xaa Glu Ser Thr Ser Pro Cys Thr Asp His Cys Ser
 5 10 15
 gga ccc aga gag gag cag ctc tgc tcc agc agg gtt ttc cat tgc atc 316
 Gly Pro Arg Glu Glu Gln Leu Cys Ser Ser Arg Val Phe His Cys Ile
 20 25 30
 aca cac cca aac ggt agg atc cac cgg t 344
 Thr His Pro Asn Gly Arg Ile His Arg
 35 40

<210> 538
 <211> 221
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 1..219

<221> sig_peptide
 <222> 1..66
 <223> score 6.2
 seq ILVLTNLVNLNA/SN

004220" 666ET50

<400> 538
 atg aca gaa tca aat tca cac ata tca ata tta gta cta acc ttg aat 48
 Met Thr Glu Ser Asn Ser His Ile Ser Ile Leu Val Leu Thr Leu Asn
 -20 -15 -10
 gta aat ggg ctt aat gca tca aat aaa agg cac aga gtg gca agt tgg 96
 Val Asn Gly Leu Asn Ala Ser Asn Lys Arg His Arg Val Ala Ser Trp
 -5 1 5 10
 ata atg aag caa aac aca atg gta tgc tgt att caa gag acc cat ccc 144
 Ile Met Lys Gln Asn Thr Met Val Cys Cys Ile Gln Glu Thr His Pro
 15 20 25
 cca tgc aat gat gcc cat agg ctc aaa gta aag gaa tgg aga aaa atc 192
 Pro Cys Asn Asp Ala His Arg Leu Lys Val Lys Glu Trp Arg Lys Ile
 30 35 40
 tgc caa gca aac aga aaa cag aag aaa ga 221
 Cys Gln Ala Asn Arg Lys Gln Lys Lys
 45 50

<210> 539
 <211> 431
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 171..431
 <221> sig_peptide
 <222> 171..314
 <223> score 3.8
 seq NSLLLLLLCLYIYP/HS

<400> 539
 actctgaaag cagtcttcac agaaactttt cacagaagtc aaatagttta agcaaattct 60
 agatacatgg tagagaccag gagaaaatat gaataacttt cttctaaaca aggagctcag 120
 tggataaacc atacctctag attccttgct tccattttcc cagaaacaag atg agg 176
 Met Arg
 aag aga aag atc agt gtg tgt caa caa act tgg gcc tta tta tgc aag 224
 Lys Arg Lys Ile Ser Val Cys Gln Gln Thr Trp Ala Leu Leu Cys Lys
 -45 -40 -35
 aac ttt ctt aaa aaa tgg aga atg aaa aga gag tcc tta atg gaa tgg 272
 Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser Leu Met Glu Trp
 -30 -25 -20 -15
 ctg aat tca ttg ctc cta cta ctt tgt ttg tat ata tat cct cat agt 320
 Leu Asn Ser Leu Leu Leu Leu Leu Cys Leu Tyr Ile Tyr Pro His Ser
 -10 -5 1
 cat caa gta aat gaw tdd tct tca ctg ctt acc atg gac ctg gga cgg 368
 His Gln Val Asn Xaa Xaa Ser Ser Leu Leu Thr Met Asp Leu Gly Arg
 5 10 15
 gta gat rnn tkt aat gaa tcc aga ttt tct gtt gta tac aca cct gtc 416
 Val Asp Xaa Xaa Asn Glu Ser Arg Phe Ser Val Val Tyr Thr Pro Val
 20 25 30
 acc aac acg acc cct 431

Thr Asn Thr Thr Pro
35

<210> 540
<211> 343
<212> DNA
<213> Homo sapiens

<220>
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<222> 42..341

<221> sig_peptide
<222> 42..161
<223> score 5.9
seq VVLAWGLLNVSMA/GM

<400> 540
ccagagagag tggcgcgagc tgcgttttcc ggccagagga c atg atg cag ggg gag 56
Met Met Gln Gly Glu
-40
gca cac cct agt gct tcc ctt att gac aga acc atc aag atg aga aaa 104
Ala His Pro Ser Ala Ser Leu Ile Asp Arg Thr Ile Lys Met Arg Lys
-35 -30 -25 -20
gaa aca gag gct agg aaa gtg gtc tta gcc tgg gga ctc cta aat gta 152
Glu Thr Glu Ala Arg Lys Val Val Leu Ala Trp Gly Leu Leu Asn Val
-15 -10 -5
tct atg gct gga atg ata tat act gaa atg act gga aaa ttg att agt 200
Ser Met Ala Gly Met Ile Tyr Thr Glu Met Thr Gly Lys Leu Ile Ser
1 5 10
tca tac tac aat gtg aca tac tgg ccc ctc tgg tat ady gag ctt gcc 248
Ser Tyr Tyr Asn Val Thr Tyr Trp Pro Leu Trp Tyr Xaa Glu Leu Ala
15 20 25
ctt gca tct ctc ttc agc ctt aat gcc tta ttt gat ttt tgg aga tat 296
Leu Ala Ser Leu Phe Ser Leu Asn Ala Leu Phe Asp Phe Trp Arg Tyr
30 35 40 45
ttc aaa tat act gtg gca cca aca agt ctg gtt gtt agt cct gga cg 343
Phe Lys Tyr Thr Val Ala Pro Thr Ser Leu Val Val Ser Pro Gly
50 55 60

<210> 541
<211> 286
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 121..285

<221> sig_peptide
<222> 121..222
<223> score 7.2
seq LLLFSLLVSPPTC/KV

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 aaaactcttt cttcggtctg cgagctgaga ggagcaggta gaggggcaga ggcgggactg 60
 tcgtctgggg gagcgcgcca ggaggtctct caggccgacc ccagaccctg gctggccagg 120
 atg aag tat ctc cgg cac cgg cgg ccc aat gcc acc ctc att ctg gcc 168
 Met Lys Tyr Leu Arg His Arg Arg Pro Asn Ala Thr Leu Ile Leu Ala
 -30 -25 -20
 atc ggc gct ttc acc ctc ctc ctc ttc agt ctg cta gtg tca cca ccc 216
 Ile Gly Ala Phe Thr Leu Leu Leu Phe Ser Leu Leu Val Ser Pro Pro
 -15 -10 -5
 acc tgc aag gtc cag gag cag cca ccg gcg atc ccc gag gcc ctg gcc 264
 Thr Cys Lys Val Gln Glu Gln Pro Pro Ala Ile Pro Glu Ala Leu Ala
 1 5 10
 tgg chc act cca cct acc cga t 286
 Trp Xaa Thr Pro Pro Thr Arg
 15 20

<210> 542
 <211> 300
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 104..298
 <221> sig_peptide
 <222> 104..175
 <223> score 4.8
 seq ILSLFCWDTESLA/PS

<400> 542
 actctcacga gaacagcatg tgggaaacca gggaaactgt ccccatgac cagtgcctc 60
 ccaccaggtc cctcccttga cacaacagag attacaattt gag atg aga ttt gga 115
 Met Arg Phe Gly
 tgg aga cac aga gcc aaa acs ata tta agc ctg ttc tgc tgg gac aca 163
 Trp Arg His Arg Ala Lys Thr Ile Leu Ser Leu Phe Cys Trp Asp Thr
 -20 -15 -10 -5
 gaa tca ctt gct cca tct cat aca ttg atg atg att aat ttg tat gtg 211
 Glu Ser Leu Ala Pro Ser His Thr Leu Met Met Ile Asn Leu Tyr Val
 1 5 10
 tac ctt cca aaa aag atg gtt gtg ttt gaa tgg agg cct tct gga cag 259
 Tyr Leu Pro Lys Lys Met Val Val Phe Glu Trp Arg Pro Ser Gly Gln
 15 20 25
 gaa aat aat cac atc ctt cct gag ata atg agc aca ctc gt 300
 Glu Asn Asn His Ile Leu Pro Glu Ile Met Ser Thr Leu
 30 35 40

<210> 543
 <211> 404
 <212> DNA
 <213> Homo sapiens



<220>
<221> CDS
<222> 147..404

<221> sig_peptide
<222> 147..278
<223> score 3.5
seq AVVMLMVAIFAGT/MQ

<400> 543
agtctggaaa gccgctgcct aaggaagagg tggcagtgcg gattcagggtg gtcctttgcc 60
attccaaaag aaagctggat tgccttacca aatctccagg ttttcgtta tacctcttca 120
ctcaggctct gcccagaact caagga atg ttt acc ctt gcg gaa gtt gca tca 173
Met Phe Thr Leu Ala Glu Val Ala Ser
-40

ctt aat gac att cag cca act tac cga atc ctg aaa cca tgg tgg gat 221
Leu Asn Asp Ile Gln Pro Thr Tyr Arg Ile Leu Lys Pro Trp Trp Asp
-35 -30 -25 -20

gtg ttt atg gat tac cta gct gtt gtt atg tta atg gta gcc atc ttt 269
Val Phe Met Asp Tyr Leu Ala Val Val Met Leu Met Val Ala Ile Phe
-15 -10 -5

gca gga acc atg caa ctt acc aaa gat cag gtg gtc tgt ttg cca gta 317
Ala Gly Thr Met Gln Leu Thr Lys Asp Gln Val Val Cys Leu Pro Val
1 5 10

ttg cca tct cct gta aat tca aav kca cat aca cca cca gga aat gcc 365
Leu Pro Ser Pro Val Asn Ser Xaa Xaa His Thr Pro Pro Gly Asn Ala
15 20 25

gag gtc acc acc aac atc cca aag atg gaa gca gcc act 404
Glu Val Thr Thr Asn Ile Pro Lys Met Glu Ala Ala Thr
30 35 40

<210> 544
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 150..329

<221> sig_peptide
<222> 150..248
<223> score 3.8
seq WSLALSSRLECNG/AI

<400> 544
agagccaccg ggctggggac cggggagcgg aggctgaaat ccccagacgc cggttttctg 60
ggctgggctt tctgccttac tcactccttc tccctcttcc tggattttac cgaccgttcg 120
cgaaacagct ttccacasaa tggagcttc atg tcc tcg tgc agg aag tac tca 173
Met Ser Ser Cys Arg Lys Tyr Ser
-30

tcg act gat gtg gca gac ttt gct ccc tgg caa aaa tgg agt ctc gct	221
Ser Thr Asp Val Ala Asp Phe Ala Pro Trp Gln Lys Trp Ser Leu Ala	
-25 -20 -15 -10	
ctg tca tcc agg ctg gag tgc aat ggc gcc atc tct gct tac tgc aac	269
Leu Ser Ser Arg Leu Glu Cys Asn Gly Ala Ile Ser Ala Tyr Cys Asn	
-5 1 5	
ctc tgc ttc ccg ggt tca agc gaa tct gct tcc cga gtt caa gcg att	317
Leu Cys Phe Pro Gly Ser Ser Glu Ser Ala Ser Arg Val Gln Ala Ile	
10 15 20	
ctc ctg cct cag c	330
Leu Leu Pro Gln	
25	

<210> 545
 <211> 420
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 253..420
 <221> sig_peptide
 <222> 253..321
 <223> score 6.2
 seq LCNLSIFFCCSVS/QP

<400> 545	
catatattaa gacatatcag aatttttagaa ctctcataca atcctggaac acatattaac	60
aacaaatctc tatcagtata acccaaagga agctaaacac cacctcacac ttgacaatgt	120
ttcctgtata atbcaaacat tacaaataag cctaataataa gcctaatatg tcaactctga	180
acttcaggaa gcctaataatc caaaaagtta gtttaagggtc aaaagttttt gaattaactt	240
ttttccatta gt atg gtc ata tct ttc tta cta att tgt aag tta tgt aat	291
Met Val Ile Ser Phe Leu Leu Ile Cys Lys Leu Cys Asn	
-20 -15	
tta tca att ttt ttt tgt tgt tct gtt tcc caa cct cta tgt cag ata	339
Leu Ser Ile Phe Phe Cys Cys Ser Val Ser Gln Pro Leu Cys Gln Ile	
-10 -5 1 5	
aag aat cac cca ggc cag aca caa tgg ctc atg ctt gta atc cca aca	387
Lys Asn His Pro Gly Gln Thr Gln Trp Leu Met Leu Val Ile Pro Thr	
10 15 20	
ctt tgg gaa gcc aag gtg gga gaa ttg ctt gaa	420
Leu Trp Glu Ala Lys Val Gly Glu Leu Leu Glu	
25 30	

<210> 546
 <211> 327
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 87..326

<221> sig_peptide

<222> 87..128

<223> score 5.7

seq NVLIIVFVAFAFG/FL

<400> 546

tatcttctct ccagtctaaa gcctcactga acaaactgtc cttgactgtc agtgctcagg 60
gaactgctct gccacccttc tcttca atg aat gtg tta atc att gtt ttt gtt 113
Met Asn Val Leu Ile Ile Val Phe Val

-10

gca ttt gct ttt ggg ttc ytg gtc atg aag tct ttg ctt aag cca atg 161
Ala Phe Ala Phe Gly Phe Leu Val Met Lys Ser Leu Leu Lys Pro Met
-5 1 5 10

tcg aga agg gtt ttt ctg atg tta tct tct agg att ttt atg gtt tca 209
Ser Arg Arg Val Phe Leu Met Leu Ser Ser Arg Ile Phe Met Val Ser
15 20 25

ggc ctt aga ttt aag tcc ttg atc cat ctt gag ttg att ttt gta tat 257
Gly Leu Arg Phe Lys Ser Leu Ile His Leu Glu Leu Ile Phe Val Tyr
30 35 40

aag ttg aga gat gag gat cca gtt tca ttc ttc tac atg tgg ctt gcc 305
Lys Leu Arg Asp Glu Asp Pro Val Ser Phe Phe Tyr Met Trp Leu Ala
45 50 55

aat tat ccc agc acc att tgt t 327
Asn Tyr Pro Ser Thr Ile Cys
60 65

<210> 547

<211> 338

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 166..336

<221> sig_peptide

<222> 166..222

<223> score 4.2

seq LLSLAAYLSGPHQ/EP

<400> 547

aaatgtcttc cacagctttg ccagtgaggc cacatggctc ctgacatacg taacccagga 60
tgggatgcct tgttgagtc tctcagatat ggagcaaat gggccatgtg cagtcaagac 120
gccatctamc ctgggcagct tgcctaagcc tcgagggacc tgcca atg atg gat ctg 177
Met Met Asp Leu

aga cct ctt ctg tcc ctg gct gcc tat ctg tct ggt cct cat caa gaa 225
Arg Pro Leu Leu Ser Leu Ala Ala Tyr Leu Ser Gly Pro His Gln Glu
-15 -10 -5 1

ccc agt gtt ccc acc cga gat gga gac gtg aat aat ctt cct aag cct 273
Pro Ser Val Pro Thr Arg Asp Gly Asp Val Asn Asn Leu Pro Lys Pro
5 10 15

aat cct gcc aga agc gtg aag caa ggg gga ath tgg aag gcg gaa cag 321
 Asn Pro Ala Arg Ser Val Lys Gln Gly Gly Ile Trp Lys Ala Glu Gln
 20 25 30
 gaa aga gtg gaa gtg ga 338
 Glu Arg Val Glu Val
 35

<210> 548
 <211> 381
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 88..381

<221> sig_peptide
 <222> 88..174
 <223> score 5.8
 seq LHAXAGAAASVIA/AD

<400> 548
 acttatctgc agactttag gcagcaactc accctcactc agaggtcttc tggttctgga 60
 aacaactcta gctcagcctt ctccacc atg agc ctc aga ctt gat acc acc cct 114
 Met Ser Leu Arg Leu Asp Thr Thr Pro
 -25
 tcc tgt aac agt gcg aga cca ctt cat gcc ytt gca ggt gck gct gct 162
 Ser Cys Asn Ser Ala Arg Pro Leu His Ala Xaa Ala Gly Ala Ala Ala
 -15 -10 -5
 -20
 tct gtc att gct gct gac tgc tct ggc ttc ctc cac caa agg aca act 210
 Ser Val Ile Ala Ala Asp Cys Ser Gly Phe Leu His Gln Arg Thr Thr
 1 5 10
 aag aga aac ttg gcg aaa ggc aaa gag gaa agt cta gac agt gac ttg 258
 Lys Arg Asn Leu Ala Lys Gly Lys Glu Glu Ser Leu Asp Ser Asp Leu
 15 20 25
 tat gct gaa ctc cgc tgc atg tgt ata aag aca acc tct gga att cat 306
 Tyr Ala Glu Leu Arg Cys Met Cys Ile Lys Thr Thr Ser Gly Ile His
 30 35 40
 ccc aaa aac atc caa agt ttg gaa gtg atc ggg aaa gga acc cat tgc 354
 Pro Lys Asn Ile Gln Ser Leu Glu Val Ile Gly Lys Gly Thr His Cys
 45 50 55 60
 aac caa gtc gaa gtg ata gcc aca ctc 381
 Asn Gln Val Glu Val Ile Ala Thr Leu
 65

<210> 549
 <211> 357
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 54..356

004220"656E560

<221> sig_peptide
 <222> 54..134
 <223> score 5.9
 seq ALALAXAPDLAQA/PL

<400> 549
 agtgcagaag gttctgggaa gtaggagacc ccactggctt tgggtccccta aga atg 56
 Met
 gac tct gct gcc tgt gct gct gct gcc acc cct gtt cca gcc ctg gct 104
 Asp Ser Ala Ala Cys Ala Ala Ala Thr Pro Val Pro Ala Leu Ala
 -25 -20 -15
 ttg gcc hta gct cca gac cta gca caa gcc cca ctg gca ctc cct ggc 152
 Leu Ala Xaa Ala Pro Asp Leu Ala Gln Ala Pro Leu Ala Leu Pro Gly
 -10 -5 1 5
 ctg tta agc cca tct tgc ctt ctc tcc tct gga caa gaa gta aat ggg 200
 Leu Leu Ser Pro Ser Cys Leu Leu Ser Ser Gly Gln Glu Val Asn Gly
 10 15 20
 agt gaa aga gga act tgt ctc tgg agg ccc tgg ctg tct tcc aca aat 248
 Ser Glu Arg Gly Thr Cys Leu Trp Arg Pro Trp Leu Ser Ser Thr Asn
 25 30 35
 gac tcc cca agg cag atg agg aag ctg gtg gat ttg gct gct ggt ggg 296
 Asp Ser Pro Arg Gln Met Arg Lys Leu Val Asp Leu Ala Ala Gly Gly
 40 45 50
 gca acg gct gct gag gtc acc aag gct gaa tcc atr ntc cat cac cct 344
 Ala Thr Ala Ala Glu Val Thr Lys Ala Glu Ser Xaa Xaa His His Pro
 55 60 65 70
 gtc agg ctc ttc t
 Val Arg Leu Phe 357

<210> 550
 <211> 448
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 150..446

<221> sig_peptide
 <222> 150..272
 <223> score 6.5
 seq IAVLVLYFLFVLA/VG

<400> 550
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 acctoctagt gccttagaag ccaactgacag cccccagggc aggtgagccc tgcactctgga 120
 ataaggatcc agaggtctcg ttcaggacc atg gag agc ggc acc agc agc cct 173
 Met Glu Ser Gly Thr Ser Ser Pro
 -40 -35
 cag cct cca cag tta gat ccc ctg gat gcg ttt ccc cag aag ggc ttg 221
 Gln Pro Pro Gln Leu Asp Pro Leu Asp Ala Phe Pro Gln Lys Gly Leu

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	-30	-25	-20	
gag cct ggg gac atc gcg gtg cta gtt ctg tac ttc ctc ttt gtc ctg				269
Glu Pro Gly Asp Ile Ala Val Leu Val Leu Tyr Phe Leu Phe Val Leu				
	-15	-10	-5	
gct gtt gga cta tgg tcc aca gtg aag asc aaa aga gac aca gtg aaa				317
Ala Val Gly Leu Trp Ser Thr Val Lys Xaa Lys Arg Asp Thr Val Lys				
1 5 10 15				
ggc tac ttc ctg gct gga ggg gac atg gtg tgg tgg cca gtg ggt rca				365
Gly Tyr Phe Leu Ala Gly Gly Asp Met Val Trp Trp Pro Val Gly Xaa				
	20	25	30	
tcc ttg ttt gcc agc aat gtt gga agt gga cat ttc att ggc ctg gca				413
Ser Leu Phe Ala Ser Asn Val Gly Ser Gly His Phe Ile Gly Leu Ala				
	35	40	45	
ggg tca ggt gct gct acg ggc att tct gta tca gc				448
Gly Ser Gly Ala Ala Thr Gly Ile Ser Val Ser				
	50	55		

<210> 551
 <211> 363
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 139..363
 <221> sig_peptide
 <222> 139..213
 <223> score 4.8
 seq LWFPSMLFSLSL/SN

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taataaaaaat gaaccccggtt acagagtcac catcatgtct cttctcacca ccctctgaat	60
ctgcattagc cagtcaacta gccctttcag cgtcatgtga ccagcgcgcc ccattcagct	120
tggctggtgt cgtttcac atg acc cag gct ggc cag tcg tca ggt tgc acc	171
Met Thr Gln Ala Gly Gln Ser Ser Gly Cys Thr	
	-25 -20 -15
gcc ctt tgg ttc ccg agc atg ctg ttt tct ctc agc ctt ctc tcc aac	219
Ala Leu Trp Phe Pro Ser Met Leu Phe Ser Leu Ser Leu Leu Ser Asn	
	-10 -5 1
ctt aac caa atc ggc agc agc cac ctc gac cgc cca cac att cct ggc	267
Leu Asn Gln Ile Gly Ser Ser His Leu Asp Arg Pro His Ile Pro Gly	
	5 10 15
caa tca gct cag ctg ttt att tac caa atg tct tca caa caa cta cag	315
Gln Ser Ala Gln Leu Phe Ile Tyr Gln Met Ser Ser Gln Gln Leu Gln	
	20 25 30
cag cag cct tcg gct aac aaa aaa gca ggv aaa atc cnt aac acc cca	363
Gln Gln Pro Ser Ala Asn Lys Lys Ala Gly Lys Ile Xaa Asn Thr Pro	
	35 40 45 50

<210> 552
 <211> 263
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 11..262

<221> sig_peptide

<222> 11..103

<223> score 3.6

seq LFIYLVFVECLLC/TR

<400> 552

agggtaatgg atg gga att gat att ttc tat cct tca cac atc cca gac 49
Met Gly Ile Asp Ile Phe Tyr Pro Ser His Ile Pro Asp
-30 -25 -20
ttt cat cct att cat tta ttc att tat cta gtg ttt gta gag tgc ctt 97
Phe His Pro Ile His Leu Phe Ile Tyr Leu Val Phe Val Glu Cys Leu
-15 -10 -5
ctg tgt acc agg aac tgr gaw agk ttg tcc kga ttc aac tgt gat aac 145
Leu Cys Thr Arg Asn Xaa Xaa Xaa Leu Ser Xaa Phe Asn Cys Asp Asn
1 5 10
gct caa ata atc ttc aca aca ggc tca tcc tct agt gga gga aat aaa 193
Ala Gln Ile Ile Phe Thr Thr Gly Ser Ser Ser Ser Gly Gly Asn Lys
15 20 25 30
cca ttt aaa agt agt tta tgt aca gta cat aga ggc caa gaa agg gaa 241
Pro Phe Lys Ser Ser Leu Cys Thr Val His Arg Gly Gln Glu Arg Glu
35 40 45
aga ata gag tgc caa ggg aat g 263
Arg Ile Glu Cys Gln Gly Asn
50

<210> 553

<211> 362

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 192..362

<221> sig_peptide

<222> 192..323

<223> score 6.9

seq LNLLSSWSSMAQS/RL

<400> 553

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agtggatagg ggtagacttt tcacacgggg acaaattatt acaggatatt tgcgccccct 120
gttccgagtc actcggggcc atcggggttac ttcagcaggt tctctgcatt acggaccctt 180
ttgaggctca g atg gag cct tgc tct gtc acc cag gct ggt gtg caa tgg 230
Met Glu Pro Cys Ser Val Thr Gln Ala Gly Val Gln Trp
-40 -35

cac aat ctc gac tca ctg caa cct cca tct cca agg ttc aag tta ttc	278
His Asn Leu Asp Ser Leu Gln Pro Pro Ser Pro Arg Phe Lys Leu Phe	
-30 -25 -20	
tcc tgc ctc aac ctc ctg agt agc tgg agt tca atg gca cag tct cga	326
Ser Cys Leu Asn Leu Leu Ser Ser Trp Ser Ser Met Ala Gln Ser Arg	
-15 -10 -5 1	
ctc act gca acc tcc atc tcc aag ccg ccg ccg ccc	362
Leu Thr Ala Thr Ser Ile Ser Lys Pro Pro Pro Pro	
5 10	

<210> 554
 <211> 385
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 194..385

<221> sig_peptide
 <222> 194..334
 <223> score 7.6
 seq LXLGEGLTFLCLC/QV

<400> 554	
agt gag agc tagtcttggt actatctggt tttgtttctt actgtttgtc tgtttatggt	60
tggttgcaag aaaattgtgt tgtaaattat cccttgcttt ctctattagt taatagcctt	120
ccccttctgt agtaaagtaa msagsetttt kcctgttcaa atattttagg cttgtttttt	180
gttttgattg tac atg cct gtg tgt ttt tat tcc tta att tgt ttc ttt	229
Met Pro Val Cys Phe Tyr Ser Leu Ile Cys Phe Phe	
-45 -40	
att tat ttc tgt ttg tta tct cca aga gaa aca ata gaa gag gtg gcc	277
Ile Tyr Phe Cys Leu Leu Ser Pro Arg Glu Thr Ile Glu Glu Val Ala	
-35 -30 -25 -20	
ctc ttc cag ttt tct ctg cth mtc ttg gga gag ggt ctc acc ttt ctt	325
Leu Phe Gln Phe Ser Leu Leu Xaa Leu Gly Glu Gly Leu Thr Phe Leu	
-15 -10 -5	
tgc ctc tgc cag gta atg acg aat aan atg caa ctg ctg ttc ttg agt	373
Cys Leu Cys Gln Val Met Thr Asn Xaa Met Gln Leu Leu Phe Leu Ser	
1 5 10	
ggg gta gtc tgt	385
Gly Val Val Cys	
15	

<210> 555
 <211> 411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..410

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<221> sig_peptide
 <222> 126..176
 <223> score 4.6
 seq ILLWEACTGRCQA/SL

<400> 555
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 aaagttggaa aaatggaaag tgggagctgt gaggcacgtg ttacacccac actttcctcc 120
 tacag atg cag tgt tgg att ttg ttg tgg gag gca tgc aca ggt agg tgc 170
 Met Gln Cys Trp Ile Leu Leu Trp Glu Ala Cys Thr Gly Arg Cys
 -15 -10 -5
 cag gcc tcc cta ctc tct ccc tgg ccc aga ggt ggc agg ggc aag tta 218
 Gln Ala Ser Leu Leu Ser Pro Trp Pro Arg Gly Gly Arg Gly Lys Leu
 1 5 10
 gtg gca gtg gtg gct gca aaa tgg ttg gca gca atc tgt ggg att tgg 266
 Val Ala Val Val Ala Ala Lys Trp Leu Ala Ala Ile Cys Gly Ile Trp
 15 20 25 30
 gct atc aaa gaa atg cca agc cat ggc cac agt ctt caa gca ggg gca 314
 Ala Ile Lys Glu Met Pro Ser His Gly His Ser Leu Gln Ala Gly Ala
 35 40 45
 ggg gaa ggt gca ctg gtg acc tgg agc ctg caa acc tca ttt ggt gtg 362
 Gly Glu Gly Ala Leu Val Thr Trp Ser Leu Gln Thr Ser Phe Gly Val
 50 55 60
 aag cag tat aag tgg gga gtt gtg tgg cat gaa gca aac ctg ttg ctt c 411
 Lys Gln Tyr Lys Trp Gly Val Val Trp His Glu Ala Asn Leu Leu Leu
 65 70 75

<210> 556
 <211> 472
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 289..471

<221> sig_peptide
 <222> 289..402
 <223> score 4.4
 seq LELLTSGDPLASA/SQ

<400> 556
 cataacacca ggttaaata ttttttatat ctcccaaaga agtatttttc aatctgcaga 60
 tcatgacccc ttagtagatt gtgaaacaca ttagtggatt atgacaagca tttttagaaa 120
 aatgaaaaag gattaggaag tgtaggatg cattgcatta ttgaaataat tgtttttgag 180
 atggagtttc gctcttggtt gccgaggtctg gactgcaatg gcccgatctg cctcccggtt 240
 tcgggtgatt ctctctgctc agcctctctga gtagctggga ttacagac atg ctc cac 297
 Met Leu His
 cat gcc tgg cta att ttg tat tta gtt tta gta gag atg ggg ttt ctc 345
 His Ala Trp Leu Ile Leu Tyr Leu Val Leu Val Glu Met Gly Phe Leu
 -35 -30 -25 -20
 cat gtt ggt cag gct ggt ctt gaa ctc ctg acc tca ggt gat cca ctt 393

004220"666E7560

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His Val Gly Gln Ala Gly Leu Glu Leu Leu Thr Ser Gly Asp Pro Leu
      -15                      -10                      -5
gcc tcg gcc tcc caa agt gct ggg gat aca ggc atg aac ccc tgt gcc      441
Ala Ser Ala Ser Gln Ser Ala Gly Asp Thr Gly Met Asn Pro Cys Ala
      1                      5                      10
cgg cct aat ttt tgt att ttt agt aga gat g
Arg Pro Asn Phe Cys Ile Phe Ser Arg Asp
      15                      20

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<210> 557
 <211> 419
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 114..419

<221> sig_peptide
 <222> 114..188
 <223> score 4.4
 seq VVSWLVSAEGSHP/DP

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<400> 557
attccactct tcctggactg cagaggagtc gccgatccca cttgggtccg gagtcagggc      60
cttcaggggt ccgggaacgc cgccatcccg agtgggtgaag gaggagatct cgg atg      116
                                         Met
                                         -25
aca atg cca agc tac cat gct tca atg gcc sgg gtg tgg tcc tgg ctg      164
Thr Met Pro Ser Tyr His Ala Ser Met Ala Xaa Val Val Ser Trp Leu
      -20                      -15                      -10
gtg tca gct gag ggc tca cac cca gac cca gcc ccc ttc tgd gct gat      212
Val Ser Ala Glu Gly Ser His Pro Asp Pro Ala Pro Phe Xaa Ala Asp
      -5                      1                      5
aac cca tcg gag ctg cca cca cct atg gag cgc acg gga ggc atc ggg      260
Asn Pro Ser Glu Leu Pro Pro Pro Met Glu Arg Thr Gly Gly Ile Gly
      10                      15                      20
gac tcc cga ccc cca tcc ttc cac cct cat gct ggt ggg ggs agc cag      308
Asp Ser Arg Pro Pro Ser Phe His Pro His Ala Gly Gly Gly Ser Gln
      25                      30                      35                      40
gag aac ctg gac aat gac aca gag acg gac tct ttg gtg tct gcc cag      356
Glu Asn Leu Asp Asn Asp Thr Glu Thr Asp Ser Leu Val Ser Ala Gln
      45                      50                      55
cga gag cgg cca cgc cgg agg gat ggc cca gag cat gca acc cgg cta      404
Arg Glu Arg Pro Arg Arg Arg Asp Gly Pro Glu His Ala Thr Arg Leu
      60                      65                      70
aat gga act gcg aag
Asn Gly Thr Ala Lys
      75

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<210> 558
 <211> 397
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 53..397

<221> sig_peptide

<222> 53..121

<223> score 5.9

seq TLKFLTLLQKSNA/KR

<400> 558

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Met Met
aca gca cct gtt cta gca gct cag act ctg aag ttt ttg acg tta ttg 106
Thr Ala Pro Val Leu Ala Ala Gln Thr Leu Lys Phe Leu Thr Leu Leu
-20 -15 -10
cag aaa tca aac gca aaa agg scc aac ctt gac cga ctt cat gat gaa 154
Gln Lys Ser Asn Ala Lys Arg Xaa Asn Leu Asp Arg Leu His Asp Glu
-5 1 5 10
ctt tgg tac aac gat cca ggc cag atg aat gat gga cca ctc tgc aaa 202
Leu Trp Tyr Asn Asp Pro Gly Gln Met Asn Asp Gly Pro Leu Cys Lys
15 20 25
tgc agc gca aag gca aga cgc aca gga att agg cac agc att tat cct 250
Cys Ser Ala Lys Ala Arg Arg Thr Gly Ile Arg His Ser Ile Tyr Pro
30 35 40
gga gaa gag gcc atc aag ccc tgt cgt cct atg acc aac aat gct ggc 298
Gly Glu Glu Ala Ile Lys Pro Cys Arg Pro Met Thr Asn Asn Ala Gly
45 50 55
aga ctt ttc cac tac cgg atc aca gtm tcc ccg cct acg aac ttt tta 346
Arg Leu Phe His Tyr Arg Ile Thr Val Ser Pro Pro Thr Asn Phe Leu
60 65 70 75
act gac agg cca act gtt ata gaa tac gat gat cac gag tat atc ttt 394
Thr Asp Arg Pro Thr Val Ile Glu Tyr Asp Asp His Glu Tyr Ile Phe
80 85 90
gaa 397
Glu

<210> 559

<211> 385

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 204..383

<221> sig_peptide

<222> 204..287

<223> score 7.7

seq LVMCFLSYFGTFA/VE

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 ttggttaattt tcagctcaca aatgatgaag aaatccataa cgtcggaact tccttgacct 60
 ttggatttgg cacattgacc tgctggatcc aggctgcgct gacactcaag gtcaacatca 120
 asaataagg acggagagtt ggaattccac gggttattct gtcggcatct atcactctct 180
 gtgtggtcct ctacttcac ctc atg gcc caa agc atc cac atg tat gca gcc 233
 Met Ala Gln Ser Ile His Met Tyr Ala Ala
 -25 -20
 agg gtc cag tgg ggc ctg gtc atg tgc ttc ctg tct tat ttt ggc acc 281
 Arg Val Gln Trp Gly Leu Val Met Cys Phe Leu Ser Tyr Phe Gly Thr
 -15 -10 -5
 ttt gcc gtg gag ttc cgg cat tac cgc tat gag att gtt tgc tct gag 329
 Phe Ala Val Glu Phe Arg His Tyr Arg Tyr Glu Ile Val Cys Ser Glu
 1 5 10
 tac cag gag aat ttc cta agc ttc tca gaa agc ctg tca gaa gct tct 377
 Tyr Gln Glu Asn Phe Leu Ser Phe Ser Glu Ser Leu Ser Glu Ala Ser
 15 20 25 30
 gaa tat ca 385
 Glu Tyr

<210> 560
 <211> 452
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 47..451
 <221> sig_peptide
 <222> 47..106
 <223> score 10.6
 seq LLTLLALLAHTSA/VA

<400> 560
 acgggcccgg cgcgaggagg agcgaasagc gcgggcagcg agcgag atg cag cac 55
 Met Gln His
 -20
 cga ggc ttc ctc ctc ctc acc ctc ctc gcc ctg ctg ggc cac acc tcc 103
 Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala His Thr Ser
 -15 -10 -5
 gcg gtc gcc aaa aag ava gat aag gtg aag aag ggc ggc ccg ggg ctc 151
 Ala Val Ala Lys Lys Xaa Asp Lys Val Lys Lys Gly Gly Pro Gly Leu
 1 5 10 15
 ggg ctg ggc ggt ggc gac tgc aga gtg aaa att gcc acc aag gcc aac 199
 Gly Leu Gly Gly Gly Asp Cys Arg Val Lys Ile Ala Thr Lys Ala Asn
 20 25 30
 cct tgg gat gga aaa tca cta aag cct gac agt gtc cgg tcc cag ctg 247
 Pro Trp Asp Gly Lys Ser Leu Lys Pro Asp Ser Val Arg Ser Gln Leu
 35 40 45
 gag acg tca ttg aag agg ctg cag tgt ccc caa gtg gac ctc ttc tac 295
 Glu Thr Ser Leu Lys Arg Leu Gln Cys Pro Gln Val Asp Leu Phe Tyr
 50 55 60
 cta cac gca cct gac cac ggc acc hnn ggt gga asa gac gct gca tgc 343

Leu His Ala Pro Asp His Gly Thr Xaa Gly Gly Xaa Asp Ala Ala Cys
 65 70 75
 ctg cca gcg gct gca cca gga ggg aag ttc gtg gmg ctt ggc ctc tcc 391
 Leu Pro Ala Ala Ala Pro Gly Gly Lys Phe Val Xaa Leu Gly Leu Ser
 80 85 90 95
 aaa tst gct agc tgg gaa gtg gcc gag atc tgt acc tct gca aga gca 439
 Lys Xaa Ala Ser Trp Glu Val Ala Glu Ile Cys Thr Ser Ala Arg Ala
 100 105 110
 atg gct gga tcc t 452
 Met Ala Gly Ser
 115

<210> 561
 <211> 478
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 325..477

<221> sig_peptide
 <222> 325..444
 <223> score 3.9
 seq CVNLLLGFEFVIS/RS

<400> 561
 taaaacttag ggggaagatt tgccctctcac tttttttctt ggaaaatgtg ggcagcaatt 60
 ttaaagagaa catgaaaatg gagtaggttg aaaccaacat tcagaacttc ctttcatgga 120
 ttgaaactta aagctgaggg aggktttrag ggtggarktr aggaagggct agaagatagc 180
 aaatttcaga gtcatatcag agaatatgaa ctgtcagtgt ttccaatgtt tctcttggt 240
 ctgcacagca cttccaagcc cttttgctca ctgttttgct tctgccacac ctaggagaag 300
 attcagagct tgctgaggca aaac atg cga tat ttc caa ggg cct tcc ccc 351
 Met Arg Tyr Phe Gln Gly Pro Ser Pro
 -40 -35
 tat tct gaa ata gaa att gag ctt tgt gat cat gtg tat tca ttc caa 399
 Tyr Ser Glu Ile Glu Ile Glu Leu Cys Asp His Val Tyr Ser Phe Gln
 -30 -25 -20
 ggt cta tgt gtt aac ctt ttg cta gga ttt gaa cct gtt att agt agg 447
 Gly Leu Cys Val Asn Leu Leu Leu Gly Phe Glu Pro Val Ile Ser Arg
 -15 -10 -5 1
 agc cgr mgc agt tca ctt gct gtt gag tct a 478
 Ser Arg Xaa Ser Ser Leu Ala Val Glu Ser
 5 10

<210> 562
 <211> 412
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..412

<221> sig_peptide
 <222> 5..91
 <223> score 11.4
 seq LCLLGCLLSHAAA/AP

<400> 562
 tacg atg gag gcg cta atg gcc cgg ggc gcg ctc acg ggt ccc ctg agg 49
 Met Glu Ala Leu Met Ala Arg Gly Ala Leu Thr Gly Pro Leu Arg
 -25 -20 -15
 gcg ctc tgt ctc ctg ggc tgc ctg ctg agc cac gcc gcc gcc gcg ccg 97
 Ala Leu Cys Leu Leu Gly Cys Leu Leu Ser His Ala Ala Ala Ala Pro
 -10 -5 1
 tcg ccc atc atc aag ttc ccc ggc gat gtc gcc ccc aaa amg gwc aaa 145
 Ser Pro Ile Ile Lys Phe Pro Gly Asp Val Ala Pro Lys Xaa Xaa Lys
 5 10 15
 rag ttg gca stg caa tac ctg aas anc ttc tat ggc tgc ccc aak rag 193
 Xaa Leu Ala Xaa Gln Tyr Leu Xaa Xaa Phe Tyr Gly Cys Pro Xaa Xaa
 20 25 30
 agc tgc aac ctg ttt gtg ctg aag gac aca cta aag aag atg cag aag 241
 Ser Cys Asn Leu Phe Val Leu Lys Asp Thr Leu Lys Lys Met Gln Lys
 35 40 45 50
 ttc ttt gga ctg ccc cag aca ggt gat ctt gac cag aat acc atc gan 289
 Phe Phe Gly Leu Pro Gln Thr Gly Asp Leu Asp Gln Asn Thr Ile Xaa
 55 60 65
 ncc atg cgg aag cca cgc tgc ggc aas cca gat gtg gcc ars tac aac 337
 Xaa Met Arg Lys Pro Arg Cys Gly Xaa Pro Asp Val Ala Xaa Tyr Asn
 70 75 80
 ttc ttc cct cgc aag nnc aag tgg gac aag aac cag atc aca tac agg 385
 Phe Phe Pro Arg Lys Xaa Lys Trp Asp Lys Asn Gln Ile Thr Tyr Arg
 85 90 95
 atc att ggc tac aca sct gat ctg gac 412
 Ile Ile Gly Tyr Thr Xaa Asp Leu Asp
 100 105

<210> 563
 <211> 458
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 185..457

<221> sig_peptide
 <222> 185..298
 <223> score 6.3
 seq PCVSLWAPRXFA/SS

<400> 563
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 aatgctatgt ccaggggaaa aatattccca attccaggta aaagatcaga aacagatatc 120

acctgsawtt tgttccacct tcaccccagg cttcagctat acttaggtat tactctctgg 180
 tccc atg aac cat ctc atg cct ttg act gtg ctg cac tca gtg ctt gaa 229
 Met Asn His Leu Met Pro Leu Thr Val Leu His Ser Val Leu Glu
 -35 -30 -25
 atg ctc cgc aca ccc cgc aca cct ccc tgg ccc tgt gta tcc ctt cta 277
 Met Leu Arg Thr Pro Arg Thr Pro Pro Trp Pro Cys Val Ser Leu Leu
 -20 -15 -10
 tgg gcg ccc aga gsa ttt gct tcc tct tgc tct caa gca ttt acc act 325
 Trp Ala Pro Arg Xaa Phe Ala Ser Ser Cys Ser Gln Ala Phe Thr Thr
 -5 1 5
 ctg can kgc aat tgc ttg ctt act aat cca tct ccc aca cta gat tgt 373
 Leu Xaa Xaa Asn Cys Leu Leu Thr Asn Pro Ser Pro Thr Leu Asp Cys
 10 15 20 25
 gac ctc cct gag ggc tca gaa ata tta aat tct tct ctg tat cct cat 421
 Asp Leu Pro Glu Gly Ser Glu Ile Leu Asn Ser Ser Leu Tyr Pro His
 30 35 40
 tgc cta ctc agt gct tgg aac aca cga cac tca aca a 458
 Cys Leu Leu Ser Ala Trp Asn Thr Arg His Ser Thr
 45 50

<210> 564
 <211> 502
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> 324..500
 <221> sig_peptide
 <222> 324..398
 <223> score 4.3
 seq ALYLSLNLYFANS/LY

<400> 564
 gtctaggctc ttcaagttag gattcatatc tatgacatgt gctgtacagt gcttctactg 60
 tgaggtagtc tcccagacag aaaccacatg ggccttcagg catagatggt cagtaaataa 120
 ttactttaca gtggtgtcat ttcttaggag acmcagagtr agaccttaag tgagatctta 180
 cctacctcct cccatccaat ctatccatac aagggtggac cttaaagcagc cttgagctta 240
 ataatgatgt gtgttagaac aaggatactg agattagact aagntgggtc ttttaagtcag 300
 ccgtctctga caaagggcac aca atg tac tgt ctg arg tgt gtg gag aaa ata 353
 Met Tyr Cys Leu Xaa Cys Val Glu Lys Ile
 -25 -20
 gca aaa gct ctt tat ctc agc ctt aat tta tat ttt gca aat tca ctt 401
 Ala Lys Ala Leu Tyr Leu Ser Leu Asn Leu Tyr Phe Ala Asn Ser Leu
 -15 -10 -5 1
 tat tat atg tgt gtg tgt tca tac ata tac ttt tat tta tkt att tat 449
 Tyr Tyr Met Cys Val Cys Ser Tyr Ile Tyr Phe Tyr Leu Xaa Ile Tyr
 5 10 15
 ktk tat kkt tta ata aaa ann dng tct tat tat gtt gcc cag act ggt 497
 Xaa Tyr Xaa Leu Ile Lys Xaa Xaa Ser Tyr Tyr Val Ala Gln Thr Gly
 20 25 30
 ctc aa 502

Leu

<210> 565
<211> 218
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 7..216

<221> sig_peptide
<222> 7..120
<223> score 7.9
seq LPFLSLFWPWAPG/AV

<400> 565
aggagc atg ggt ggt ttt ttt ccc cct acc gag gtc cgt gag gtg tgt 48
Met Gly Gly Phe Phe Pro Pro Thr Glu Val Arg Glu Val Cys
-35 -30 -25
gct aac caa ggg gcg gct cac aac cgt gac aga ctg cca ttc ctg agt 96
Ala Asn Gln Gly Ala Ala His Asn Arg Asp Arg Leu Pro Phe Leu Ser
-20 -15 -10
ctc ttc tgg cca tgg gcc ccc gga gcc gtg agc gtc ggg cag gcg cgg 144
Leu Phe Trp Pro Trp Ala Pro Gly Ala Val Ser Val Gly Gln Ala Arg
-5 1 5
tac aga aca cca acg aca ksa gcg ccc tca gca agc gtt ccc tgg ccg 192
Tyr Arg Thr Pro Thr Thr Xaa Ala Pro Ser Ala Ser Val Pro Trp Pro
10 15 20
cgc gcg ggt acg tgc agg acc cct ac 218
Arg Ala Gly Thr Cys Arg Thr Pro
25 30

<210> 566
<211> 271
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..269

<221> sig_peptide
<222> 63..122
<223> score 7.2
seq LALWLGAVGVGVA/EP

<400> 566
gggctggctc ggagasctga ggggcgcaca cccgcttcgc agggccaggg tgacacggad 60
gc atg cga cgg ctg ctg atc cct ctg gcc ctg tgg ctg ggt gcg gtg 107
Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly Ala Val
-20 -15 -10

ggc gtg ggc gtc gcc gar cct cca ssg gaa gcc cag cgc cgg ggc htg 155
 Gly Val Gly Val Ala Glu Pro Pro Xaa Glu Ala Gln Arg Arg Gly Xaa
 -5 1 5 10
 cag gtg gcc ctg gag gaa ttt cac aag cac ccg ccc gtg cag tgg gcc 203
 Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp Ala
 15 20 25
 ttc cag gag acc agt gtg gag agc gcc gtg gac acg ccw ntc cca gct 251
 Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Xaa Pro Ala
 30 35 40
 gga ata ttt gtg agg ccg gt
 Gly Ile Phe Val Arg Pro
 45 271

<210> 567
 <211> 295
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 60..293
 <221> sig_peptide
 <222> 60..140
 <223> score 3.6
 seq RVLGXSLRRCEA/AG

<400> 567 59
 gaggagaccg caagttgagt ggaggaggcg gcgggtggggc cccgrvacca ggtgcctcc 107
 atg gca ggc tct gaa gag ctg ggg ctc cgg gaa gac acg ctg agg gtc
 Met Ala Gly Ser Glu Glu Leu Gly Leu Arg Glu Asp Thr Leu Arg Val
 -25 -20 -15
 cta gct ggc cyt tcc ctt agg cgt tgt gag gct gcc ggg tct cct gtt 155
 Leu Ala Gly Xaa Ser Leu Arg Arg Cys Glu Ala Ala Gly Ser Pro Val
 -10 -5 1 5
 cca act cca cct aga agc cct gcc caa gaa gag ccr ncr gac ttc ctg 203
 Pro Thr Pro Pro Arg Ser Pro Ala Gln Glu Glu Pro Xaa Asp Phe Leu
 10 15 20
 agc cgc ctt cga aga tgt ctt ccc tgc tcs ntg ggg cga gga gca gcc 251
 Ser Arg Leu Arg Arg Cys Leu Pro Cys Ser Xaa Gly Arg Gly Ala Ala
 25 30 35
 ccc tct gag tcc cct cgg cct tgc tct ctg ccc atc cgc ccc tc 295
 Pro Ser Glu Ser Pro Arg Pro Cys Ser Leu Pro Ile Arg Pro
 40 45 50

<210> 568
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 139..369

<221> sig_peptide
 <222> 139..261
 <223> score 9.5
 seq LIIFLSFLPFINS/SF

<400> 568
 caagtgggat aggtcctgtg acagaattgt gtgatacagg tcaaacagga gttgggttat 60
 ggggaaaatg ccagttgaaa tatgttttga tctttggaga aacctatttt ttcatttaac 120
 ctgttcttta aatccagt atg ttc cag aac ata caa aaa tgt tta aat gtt 171
 Met Phe Gln Asn Ile Gln Lys Cys Leu Asn Val
 -40 -35
 cca ttt gta aga gga tat cat gta ttt tat atc aat tta aat gca gtt 219
 Pro Phe Val Arg Gly Tyr His Val Phe Tyr Ile Asn Leu Asn Ala Val
 -30 -25 -20 -15
 atc cta atc att ttt ctt tca ttt tta ccc ttt att aac tct tca ttt 267
 Ile Leu Ile Ile Phe Leu Ser Phe Leu Pro Phe Ile Asn Ser Ser Phe
 -10 -5 1
 gtt tac aaa aca aat cca ctc tat gac gca atc tct aat tat gtg ttt 315
 Val Tyr Lys Thr Asn Pro Leu Tyr Asp Ala Ile Ser Asn Tyr Val Phe
 5 10 15
 tct ttc agg tat cca aac ctt gra asc ttt gct cta gat gtc agg ctt 363
 Ser Phe Arg Tyr Pro Asn Leu Xaa Xaa Phe Ala Leu Asp Val Arg Leu
 20 25 30
 gtt ttt
 Val Phe
 35 369

<210> 569
 <211> 269
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..267

<221> sig_peptide
 <222> 46..111
 <223> score 10.3
 seq FLLLLLLLLLTRW/AP

<400> 569
 agtccccggg cgcctcctgg agagcaagga cgcgggggag cagag atg atc cga gcc 57
 Met Ile Arg Ala
 -20
 gcg cgg ccg ccg ctg ttc ctg ctg ctg ctg ctg ctg ctg ctc act 105
 Ala Pro Pro Pro Leu Phe Leu Leu Leu Leu Leu Leu Leu Thr
 -15 -10 -5
 aga tgg gct cct cac aga gca atg gcc cct tcc tgg tcc agc cas atg 153
 Arg Trp Ala Pro His Arg Ala Met Ala Pro Ser Trp Ser Ser Xaa Met
 1 5 10

001220"66ET550

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gtg tca ccc tgg agt aca acc cct att ctt gga atc tgr ttg cca atg      201
Val Ser Pro Trp Ser Thr Thr Pro Ile Leu Gly Ile Xaa Leu Pro Met
15                      20                      25                      30
tgt tat acc tgg agt ccc cag ctg ggg tgg gct tct cct act ccg atg      249
Cys Tyr Thr Trp Ser Pro Gln Leu Gly Trp Ala Ser Pro Thr Pro Met
                      35                      40                      45
aca agt ttt atg caa ctt gt
Thr Ser Phe Met Gln Leu
                      50

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<210> 570
 <211> 257
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 37..255

<221> sig_peptide
 <222> 37..168
 <223> score 4.8
 seq LTFCLVDLSNVDS/GM

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<400> 570
caattttgga ataagtgtga tgtggtggtg agaaga atg tat att ttg ttg att      54
                      Met Tyr Ile Leu Leu Ile
                      -40
tgg ggt gga gag ttc tgt aga tgt cta tta ggt ctg ctt ggt gca gag      102
Trp Gly Gly Glu Phe Cys Arg Cys Leu Leu Gly Leu Leu Gly Ala Glu
                      -35                      -30                      -25
ctg agt tca att ccc tgg ata tcc ttg tta act ttc tgt ctt gtt gat      150
Leu Ser Ser Ile Pro Trp Ile Ser Leu Leu Thr Phe Cys Leu Val Asp
                      -20                      -15                      -10
ctg tct aat gtt gac agt ggg atg tta aag tct ccc att att att gtg      198
Leu Ser Asn Val Asp Ser Gly Met Leu Lys Ser Pro Ile Ile Ile Val
                      -5                      1                      5                      10
tgg gag tct aag tct ctt tgt agg tct cta agg act tgc ctt atg aat      246
Trp Glu Ser Lys Ser Leu Cys Arg Ser Leu Arg Thr Cys Leu Met Asn
                      15                      20                      25
ctg ggt gca gt
Leu Gly Ala

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<210> 571
 <211> 249
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 53..247

<221> sig_peptide

<222> 53..190
 <223> score 3.5
 seq RWLCLQAYLASFS/LE

<400> 571
 cgtgtcctca ggattttcct cttgggctgg acagtttgct cccctggagg gt atg agc 58
 Met Ser
 -45

ctg act gct agt ggg cca aga gct gcc tgg gag gaa agg gtg ggg ggt 106
 Leu Thr Ala Ser Gly Pro Arg Ala Ala Trp Glu Glu Arg Val Gly Gly
 -40 -35 -30

ctc cac act tgg ggt gcc aac att cct acc gcc cct gat tcc cag cgg 154
 Leu His Thr Trp Gly Ala Asn Ile Pro Thr Ala Pro Asp Ser Gln Arg
 -25 -20 -15

tgg ctc tgt ctt cag gcg tac ctg gca tcc ttc agt ctt gag agc ccc 202
 Trp Leu Cys Leu Gln Ala Tyr Leu Ala Ser Phe Ser Leu Glu Ser Pro
 -10 -5 1

cac aga atc tac ctk gaa tct cct ccc acg ctc ctt ttc ccc ccg cc 249
 His Arg Ile Tyr Leu Glu Ser Pro Pro Thr Leu Leu Phe Pro Pro
 5 10 15

<210> 572
 <211> 350
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 194..349

<221> sig_peptide
 <222> 194..316
 <223> score 9.9
 seq ILPFLLFPFPVNA/RS

<400> 572
 tagtgatcct tttccttctc ccactccgta agtttctatc cttggcctcc tattcttttt 60
 actacatata tactttatat atacatatat acttggaaca ggcttaatga gttccaaggt 120
 ttcaagtata atagaaggat agtttcccta atatttcttc aaaacagatt tctcttctga 180
 aatccagagt cat atg tcc agt tgg atg tat ctt gga tac ccc att gtc 229
 Met Ser Ser Trp Met Tyr Leu Gly Tyr Pro Ile Val
 -40 -35 -30

acc tca aac act act tgt cta aaa ctg atc tca tca tct ttt ccc caa 277
 Thr Ser Asn Thr Thr Cys Leu Lys Leu Ile Ser Ser Ser Phe Pro Gln
 -25 -20 -15

atc ctt cct ttt ctt cta ttt ccc ttc cca gtg aat gcc aga tct cac 325
 Ile Leu Pro Phe Leu Leu Phe Pro Phe Pro Val Asn Ala Arg Ser His
 -10 -5 1

tya gtt gct caa act aaa agc ccg a 350
 Xaa Val Ala Gln Thr Lys Ser Pro
 5 10

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<210> 573
 <211> 201
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 10..201

<221> sig_peptide
 <222> 10..132
 <223> score 5
 seq RLLLLILSGCLVYG/TA

<400> 573
 gaggcaacc atg gcg gga gga atg aaa gtg gcg gtc tgc ccg gca gtt ggt 51
 Met Ala Gly Gly Met Lys Val Ala Val Ser Pro Ala Val Gly
 -40 -35 -30
 ccc ggg ccc tgg ggc tgc gga gtc ggg ggc ggt ggg aca gtg cgg cta 99
 Pro Gly Pro Trp Gly Ser Gly Val Gly Gly Gly Gly Thr Val Arg Leu
 -25 -20 -15
 ctc ttg atc ctc tcc ggc tgc ttg gtc tac ggc aca gct gaa act gat 147
 Leu Leu Ile Leu Ser Gly Cys Leu Val Tyr Gly Thr Ala Glu Thr Asp
 -10 -5 1 5
 gta aat gtg gtc atg ctt cag gaa tcc caa gtt tgt gaa aag cgt gcc 195
 Val Asn Val Val Met Leu Gln Glu Ser Gln Val Cys Glu Lys Arg Ala
 10 15 20
 201
 agc ctc
 Ser Leu

<210> 574
 <211> 236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 60..236

<221> sig_peptide
 <222> 60..101
 <223> score 5.4
 seq FLSSLPLYSPPC/DY

<400> 574
 tagtggttat gatcccttga ctggctcctg agttattgcc catatgtggt cccagggtcc 59
 atg ttc ttg agt ctg agc ccc ttg tat agt ccc tgt cct tgt gat tat 107
 Met Phe Leu Ser Leu Ser Pro Leu Tyr Ser Pro Cys Pro Cys Asp Tyr
 -10 -5 1
 atc ctt atg cct ggt aac aaa ccc cta tcc cat gta cat gtc ctg agt 155
 Ile Leu Met Pro Gly Asn Lys Pro Leu Ser His Val His Val Leu Ser
 5 10 15

cca tac ccc aaa act gta tcc tca tgc cca tgc tgg aga atc tat gtt 203
 Pro Tyr Pro Lys Thr Val Ser Ser Cys Pro Cys Trp Arg Ile Tyr Val
 20 25 30
 ctt aag ttc ttg ctg tgt ccc tat aga cga ggg 236
 Leu Lys Phe Leu Leu Cys Pro Tyr Arg Arg Gly
 35 40 45

<210> 575
 <211> 351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 28..351

<221> sig_peptide
 <222> 28..87
 <223> score 6.8
 seq GLLWMLFVSELRA/AT

<400> 575 54
 avcagttgga gctggtgcac aggaagg atg agg aag acc agg ctc tgg ggg ctg
 Met Arg Lys Thr Arg Leu Trp Gly Leu
 -20 -15
 ctg tgg atg ctc ttt gtc tca gaa ctc cga gct gca act aaa tta act 102
 Leu Trp Met Leu Phe Val Ser Glu Leu Arg Ala Thr Lys Leu Thr
 -10 -5 1 5
 gag gaa aag tat gaa ctg aaa gag ggg cag acc ctg gat gtg aaa tgt 150
 Glu Glu Lys Tyr Glu Leu Lys Glu Gly Gln Thr Leu Asp Val Lys Cys
 10 15 20
 gac tac acg cta gag aag ttt gcc agc agc cag aaa gct tgg cag ata 198
 Asp Tyr Thr Leu Glu Lys Phe Ala Ser Ser Gln Lys Ala Trp Gln Ile
 25 30 35
 ata agg gac gga gag atg ccc aag acc ctg gca tgc aca gag agg cct 246
 Ile Arg Asp Gly Glu Met Pro Lys Thr Leu Ala Cys Thr Glu Arg Pro
 40 45 50
 tca aag aat tcc cat cca gtc caa gtg ggg agg atc ata cta gaa gac 294
 Ser Lys Asn Ser His Pro Val Gln Val Gly Arg Ile Ile Leu Glu Asp
 55 60 65
 tac cat gat cat ggt tta ctg cgc gtc cga atg gtc aac ctt caa gtg 342
 Tyr His Asp His Gly Leu Leu Arg Val Arg Met Val Asn Leu Gln Val
 70 75 80 85
 vaa gat tct 351
 Xaa Asp Ser

<210> 576
 <211> 314
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 86..313

<221> sig_peptide

<222> 86..160

<223> score 3.5

seq IFLGKSLFSLLEA/MI

<400> 576

gagccaggga ctcgggtgcc tggggcagac gaggccggt tctccgcgga cagctaggga 60
gagtgtcctg ggtgtcagcc agaac atg tct ttc aac ctg caa tca tca aag 112
Met Ser Phe Asn Leu Gln Ser Ser Lys

-25

-20

aaa ctg ttc att ttc tta gga aaa tca ctg ttt agt ctt ctg gag gct 160
Lys Leu Phe Ile Phe Leu Gly Lys Ser Leu Phe Ser Leu Leu Glu Ala
-15 -10 -5

atg att ttt gcc tta ctc cca aag cca cgg aag aac gtt gct ggt gaa 208
Met Ile Phe Ala Leu Leu Pro Lys Pro Arg Lys Asn Val Ala Gly Glu
1 5 10 15

ata gtc ctc atc aca ggt gct gga agt gga ctc gga agg ctc tta gcc 256
Ile Val Leu Ile Thr Gly Ala Gly Ser Gly Leu Gly Arg Leu Leu Ala
20 25 30

ttg cag ttt gcc cgg ctg gga tct gtt ctt gtt ctc tgg gat atc aat 304
Leu Gln Phe Ala Arg Leu Gly Ser Val Leu Val Leu Trp Asp Ile Asn
35 40 45

aag gag ggg a 314
Lys Glu Gly
50

<210> 577

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 17..406

<221> sig_peptide

<222> 17..79

<223> score 5.1

seq PLLLLLPLLNVEP/SG

<400> 577

acccagggtcc ccagcg atg tct cca cca ccg ctg ctg caa ccc ctg ctg ctg 52
Met Ser Pro Pro Pro Leu Leu Gln Pro Leu Leu Leu
-20 -15 -10

ctg ctg cct ctg ctg aat gtg gag cct tcc ggg gcc aca ctg atc cgc 100
Leu Leu Pro Leu Leu Asn Val Glu Pro Ser Gly Ala Thr Leu Ile Arg
-5 1 5

atc cct ctt cat cga gtc caa cct gga cgc agg atc ctg aac cta ctg 148
Ile Pro Leu His Arg Val Gln Pro Gly Arg Arg Ile Leu Asn Leu Leu
10 15 20

agg gga tgg aka gaa cca gca gag ctc ccc aag ttg ggg gcc cca tcc 196
 Arg Gly Trp Xaa Glu Pro Ala Glu Leu Pro Lys Leu Gly Ala Pro Ser
 25 30 35
 cct ggg gac aag ccc atc ttc gta cct ctc tcg aac tac agg gat gtg 244
 Pro Gly Asp Lys Pro Ile Phe Val Pro Leu Ser Asn Tyr Arg Asp Val
 40 45 50 55
 cag tat ttt ggg gaa att ggg ctg gga acg cct cca caa aac ttc act 292
 Gln Tyr Phe Gly Glu Ile Gly Leu Gly Thr Pro Pro Gln Asn Phe Thr
 60 65 70
 gtt gcc ttt gac act ggc tcc tcc aat ctc tgg gtc ccg tcc agg aga 340
 Val Ala Phe Asp Thr Gly Ser Ser Asn Leu Trp Val Pro Ser Arg Arg
 75 80 85
 tgc cac tty ttc agt gtg ccc tgc tgg tta cac acc gat ttg atc cca 388
 Cys His Phe Phe Ser Val Pro Cys Trp Leu His Thr Asp Leu Ile Pro
 90 95 100
 aag cct cta gct cct tcc a 407
 Lys Pro Leu Ala Pro Ser
 105

<210> 578

<211> 356

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 17..355

<221> sig_peptide

<222> 17..70

<223> score 10.4

seq LLQWLLLLLPTLC/GP

<400> 578

aggctgcaga ggtgcc atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg 52
 Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu
 -15 -10

ctg ctg ccc acg ctc tgt ggc cca ggc act gct gcc tgg amc acc tca 100
 Leu Leu Pro Thr Leu Cys Gly Pro Gly Thr Ala Ala Trp Xaa Thr Ser
 -5 1 5 10

tcc ttg gcc tgt gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag 148
 Ser Leu Ala Cys Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu
 15 20 25

caa gca ttr mag tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg 196
 Gln Ala Leu Xaa Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp
 30 35 40

gga cat gwg gga gcc gat gac cta tgc caa gag tgt gag gac atc gtc 244
 Gly His Xaa Gly Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val
 45 50 55

cac atc ctt aac aag atg gcc aag gag gcb att ttc cag gac acg atg 292
 His Ile Leu Asn Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met
 60 65 70

agg aag ttc ctg gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc 340

Arg Lys Phe Leu Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu
 75 80 85 90
 atg ccc cag tgc acc a
 Met Pro Gln Cys Thr
 95

356

<210> 579
 <211> 314
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 111..314

<221> sig_peptide
 <222> 111..236
 <223> score 7.2
 seq ILFSLSFLLVIIIT/FP

<400> 579
 atactttctc ctctcccctc tcccaagcac atctgagttg ctgcctgttc ttcacactta 60
 gctccaaacc catgaaaaat tgccaagtat aaaagcttct caagaatgag atg gat 116
 Met Asp
 tct agg gtg tct tca cct gag aag caa gat aaa gag aat ttc gtg ggt 164
 Ser Arg Val Ser Ser Pro Glu Lys Gln Asp Lys Glu Asn Phe Val Gly
 -40 -35 -30 -25
 gtc aac aat aaa cgg ctt ggt gta tgt ggc tgg atc ctg ttt tcc ctc 212
 Val Asn Asn Lys Arg Leu Gly Val Cys Gly Trp Ile Leu Phe Ser Leu
 -20 -15 -10
 tct ttc ctg ttg gtg atc att acc ttc ccc atc tcc ata tgg atg tgc 260
 Ser Phe Leu Leu Val Ile Ile Thr Phe Pro Ile Ser Ile Trp Met Cys
 -5 1 5
 ttg aag atc att aag gmg tat gaa cgt gmt gtt gta ttc cgt ctg gga 308
 Leu Lys Ile Ile Lys Xaa Tyr Glu Arg Xaa Val Val Phe Arg Leu Gly
 10 15 20
 cga cat 314
 Arg His
 25

<210> 580
 <211> 369
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 147..368

<221> sig_peptide
 <222> 147..269
 <223> score 3.5
 seq QLLGCLQCCWLQS/GR

004220" 556E7560

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<400> 580
ccaattttgt agttatctga tctgaaggaa gatgtgtgtg gaggtgttta gtgatgtttt 60
ccgatgacgg tgattcccc taaatctacg tattaaatac aatggaacag gatccacagt 120
tcaccacctaa taatatagtt tactga atg ttt tat gta gct atg acc aaa act 173
Met Phe Tyr Val Ala Met Thr Lys Thr
-40
cac aaa agg atc aga agc ctc tgt aac atc cac cat ggt ttg ttc cag 221
His Lys Arg Ile Arg Ser Leu Cys Asn Ile His His Gly Leu Phe Gln
-30 -25 -20
ttt act cag cag ctc ctg ggc tgt ctt cag tgc tgt tgg ctg caa tca 269
Phe Thr Gln Gln Leu Leu Gly Cys Leu Gln Cys Cys Trp Leu Gln Ser
-15 -10 -5
ggc aga gcc cca gct acc tat tac ctt gtg gag agt att gaa aag tca 317
Gly Arg Ala Pro Ala Thr Tyr Tyr Leu Val Glu Ser Ile Glu Lys Ser
1 5 10 15
gca cat ggc tct gta tta ngt act tat gat caa act cag act cgc ata 365
Ala His Gly Ser Val Leu Xaa Thr Tyr Asp Gln Thr Gln Thr Arg Ile
20 25 30
ggc a
Gly

<210> 581
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..302

<221> sig_peptide
<222> 84..173
<223> score 5.8
seq KLLFVLFLRQCLT/LL

<400> 581
cacatgtcca aaaagaaatt cttgtttcca gattcaataa ccccatasra atctgcattc 60
acttccttcc ccaagctttc cct atg arg gac gkg gta rca tca tct atc cag 113
Met Xaa Asp Xaa Val Xaa Ser Ser Ile Gln
-30 -25
gca ctt aga ctt aac att aag aag ttg ctc ttt gtt ttg ttt ttg aga 161
Ala Leu Arg Leu Asn Ile Lys Lys Leu Leu Phe Val Leu Phe Leu Arg
-20 -15 -10 -5
cag tgt ctc act ctg ttg ccc agg ctg gag tgt agt ggc acg gtc tgc 209
Gln Cys Leu Thr Leu Leu Pro Arg Leu Glu Cys Ser Gly Thr Val Ser
1 5 10
gct cac tgc aac ctc tgc ctc ctg ggt tca agc aat tct cct gcc tca 257
Ala His Cys Asn Leu Cys Leu Gly Ser Ser Asn Ser Pro Ala Ser
15 20 25
gcc tcc caa gta gct gga tta ctg tca tgt gcc act ttg ccc ggc tg 304
Ala Ser Gln Val Ala Gly Leu Leu Ser Cys Ala Thr Leu Pro Gly

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30

35

40

<210> 582
 <211> 271
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..271

<221> sig_peptide
 <222> 35..82
 <223> score 14.8
 seq SLPLLLLLLLGAWA/IP

<400> 582
 acagactaca cttgctgaac tggctcctgg ggcc atg agg ctg tca ctg cca ctg 55
 Met Arg Leu Ser Leu Pro Leu
 -15 -10
 ctg ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc ggg gac 103
 Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu Gly Asp
 -5 1 5
 agg gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag gag atg 151
 Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu Glu Met
 10 15 20
 tac tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc aga gct 199
 Tyr Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys Arg Ala
 25 30 35
 gtg gct tac cag gtg agt cct tca cca ctg tca cct gcc ctg ctc aca 247
 Val Ala Tyr Gln Val Ser Pro Ser Pro Leu Ser Pro Ala Leu Leu Thr
 40 45 50 55
 ccc ctt ctc aag cca gcc ccc acc 271
 Pro Leu Leu Lys Pro Ala Pro Thr
 60

<210> 583
 <211> 290
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 128..289

<221> sig_peptide
 <222> 128..274
 <223> score 8.5
 seq IVFLLLRVSPCLG/PS

<400> 583
 agatatcact gtcttggttt cacttagatc ctacttaca agtgagggtt attaacagaa 60

taaagccttc ctttaaagct ttataataat catatttatt aataatgctg ttgtgcatac 120
 ttatagt atg cat ata ttc agc ata tgt tgc atg tst tca gaa tta cat 169
 Met His Ile Phe Ser Ile Cys Cys Met Xaa Ser Glu Leu His
 -45 -40
 aag atg aaa tcc ctt tca ttg caa ctt gca agt gag aaa aga tcc tta 217
 Lys Met Lys Ser Leu Ser Leu Gln Leu Ala Ser Glu Lys Arg Ser Leu
 -35 -30 -25 -20
 gtg gct ctg gtg gaa gaa ata gta ttt ctt ctt ctc agg gtg tct ccc 265
 Val Ala Leu Val Glu Glu Ile Val Phe Leu Leu Arg Val Ser Pro
 -15 -10 -5
 tgc ctt ggc ccc tcc cab aag ccc c 290
 Cys Leu Gly Pro Ser Xaa Lys Pro
 1 5

<210> 584
 <211> 317
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 160..315
 <221> sig_peptide
 <222> 160..228
 <223> score 3.7
 seq TNLLCLTFQRCQS/YN

<400> 584
 tacatcagaa accagaggcg gaaaactttc cacggtgata tgcataaaca aatatttcat 60
 attttttaca gaaagtctgg ctattgccta tagaaagaca aaaactggta acagccttat 120
 tccagctaaa tttgaatgcc aggttgacac taatcatgg atg ctt tcc cag agc 174
 Met Leu Ser Gln Ser
 -20
 ttt cag aaa aac aaa acc aac ctg ttg tgt tta act ttc caa aga tgt 222
 Phe Gln Lys Asn Lys Thr Asn Leu Leu Cys Leu Thr Phe Gln Arg Cys
 -15 -10 -5
 cag agt tac aat tgg ctg aat att ttt gaa gct aca tat atg acg act 270
 Gln Ser Tyr Asn Trp Leu Asn Ile Phe Glu Ala Thr Tyr Met Thr Thr
 1 5 10
 ctc ttc att tca gta att aam aca aat ttt tta aaa aga tac ctc ct 317
 Leu Phe Ile Ser Val Ile Xaa Thr Asn Phe Leu Lys Arg Tyr Leu
 15 20 25

<210> 585
 <211> 252
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 45..251

<221> sig_peptide
 <222> 45..89
 <223> score 3.6
 seq VVEASSSVRLASS/EV

<400> 585
 gcagctgttt cggttaactgc tttgcctccc ggctcccgca gwgg atg ctg gtg gtg 56
 Met Leu Val Val
 -15
 gag gct tct tcc tca gtg cgg ctg gca agt tcg gag gtg act tcc tgg 104
 Glu Ala Ser Ser Ser Val Arg Leu Ala Ser Ser Glu Val Thr Ser Trp
 -10 -5 1 5
 tct atc ctg gtg acc ccc tcc gct tcc acg ccc att ata tcg ctc agt 152
 Ser Ile Leu Val Thr Pro Ser Ala Ser Thr Pro Ile Ile Ser Leu Ser
 10 15 20
 gct ggg ccc ctg agg aca cca tcc cac tcc aag acc tgg ttg ctg ctg 200
 Ala Gly Pro Leu Arg Thr Pro Ser His Ser Lys Thr Trp Leu Leu Leu
 25 30 35
 ggc gcc ttg gaa cca gcg tca gaa aga ccc tgc tcc tct gtt ctc cgc 248
 Gly Ala Leu Glu Pro Ala Ser Glu Arg Pro Cys Ser Ser Val Leu Arg
 40 45 50
 agc c 252
 Ser

<210> 586
 <211> 196
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 31..195

<221> sig_peptide
 <222> 31..135
 <223> score 5.4
 seq LVVVCYL SWRVSS/RS

<400> 586
 tactcaaaat ctacatttca gttagttgat atg cct ctt aag aat ctg ttc tct 54
 Met Pro Leu Lys Asn Leu Phe Ser
 -35
 gtt ggt ctg tgg gat cct tac aat tta ctg aag aaa cat gtt ttg gtt 102
 Val Gly Leu Trp Asp Pro Tyr Asn Leu Leu Lys Lys His Val Leu Val
 -25 -20 -15
 gtt gtc tgc tat tta tcc tgg aga gtg tct tcc aga agt tgg act ttg 150
 Val Val Cys Tyr Leu Ser Trp Arg Val Ser Ser Arg Ser Trp Thr Leu
 -10 -5 1 5
 ctg att aca cct gta aca ctt cat gct tct ctg tcc acc cag gcc c 196
 Leu Ile Thr Pro Val Thr Leu His Ala Ser Leu Ser Thr Gln Ala
 10 15 20

004220" 066E1560

<210> 587
 <211> 276
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 56..274

 <221> sig_peptide
 <222> 56..127
 <223> score 5.3
 seq LFHLLFLPHYIET/FK

<400> 587
 catttcttac tgccttacgc tcattcctgag gtccaccttg gtctctaaaa acacc atg 58
 Met
 tgt tct cat gcc tcc atg tct ttt cac aca ctg ttc cat ttg ctc ttc 106
 Cys Ser His Ala Ser Met Ser Phe His Thr Leu Phe His Leu Leu Phe
 -20 -15 -10
 ctc cca cat tac att gaa act ttc aag cct cag tcg aaa cat tgc ttc 154
 Leu Pro His Tyr Ile Glu Thr Phe Lys Pro Gln Ser Lys His Cys Phe
 -5 1 5
 ttc tgg ata gca gcc ttc ttg aca tcc ctc ctc act ccc cag tcc cta 202
 Phe Trp Ile Ala Ala Phe Leu Thr Ser Leu Leu Thr Pro Gln Ser Leu
 10 15 20 25
 cag ggc ttc cat agc tct tta tgt gca ctt cga tcc cag cat ttt cca 250
 Gln Gly Phe His Ser Ser Leu Cys Ala Leu Arg Ser Gln His Phe Pro
 30 35 40
 tcg act tgt aat tgt ttc tgc tac ct 276
 Ser Thr Cys Asn Cys Phe Cys Tyr
 45

<210> 588
 <211> 273
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 106..273

 <221> sig_peptide
 <222> 106..156
 <223> score 3.8
 seq TVLSGCASRGTTG/LP

<400> 588
 gaaattcaga cgtttgcac ctttctggcc taaaaatcaa gtccagagcc tgggtgactg 60
 tgtgaactgt cacctgtcag tgcctcccat cctgtccagg ccttg atg gag agc ttc 117
 Met Glu Ser Phe
 -15

004220" 66E7560

```

act gtt ttg tca ggc tgt gcc agc aga ggc aca act ggg ctg cca cag      165
Thr Val Leu Ser Gly Cys Ala Ser Arg Gly Thr Thr Gly Leu Pro Gln
      -10                      -5                      1
gag gtg cat gtc ctg aat ctc cgc act gca ggc cag ggg cct ggc cag      213
Glu Val His Val Leu Asn Leu Arg Thr Ala Gly Gln Gly Pro Gly Gln
      5                      10                      15
cta cag aga gag gtc aca ctt cac ctg aat ccc atc tcc tca gtc cac      261
Leu Gln Arg Glu Val Thr Leu His Leu Asn Pro Ile Ser Ser Val His
20                      25                      30                      35
atc cac cac aac
Ile His His Asn

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<210> 589
 <211> 197
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 19..195

 <221> sig_peptide
 <222> 19..96
 <223> score 8.7
 seq LLLLDVPTAAVQA/SP

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<400> 589
acctttgccc ctgctgcg atg acc ctg tgc cca ctt ctg ctg ttc ctg cca      51
                      Met Thr Leu Ser Pro Leu Leu Leu Phe Leu Pro
                      -25                      -20
ccg ctg ctg ctg ctg ctg gac gtc ccc acg gcg gcg gtg cag gcg tcm      99
Pro Leu Leu Leu Leu Leu Asp Val Pro Thr Ala Ala Val Gln Ala Ser
-15                      -10                      -5                      1
cct ctg caa gcg tta gac ttc ttt ggg aat ggg cca cca gtt aac tac      147
Pro Leu Gln Ala Leu Asp Phe Phe Gly Asn Gly Pro Pro Val Asn Tyr
      5                      10                      15
aag aca ggc aat cta tac ctg cgg ggg ccc ctg aag aag tcc aat gca      195
Lys Thr Gly Asn Leu Tyr Leu Arg Gly Pro Leu Lys Lys Ser Asn Ala
20                      25                      30
ca

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<210> 590
 <211> 291
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 20..289

 <221> sig_peptide
 <222> 20..70
 <223> score 5.5

SECRET

[illegible]

tgc agc acc aca gcc acc at
Cys Ser Thr Thr Ala Thr
25 30

<210> 592
<211> 218
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..217

<221> sig_peptide
<222> 2..85
<223> score 8
seq IVFCFVFLRQSLA/LS

<400> 592
t atg att cgt ttt tct ttg att tgg aag ctt atg ata gat ttt ata atc 49
Met Ile Arg Phe Ser Leu Ile Trp Lys Leu Met Ile Asp Phe Ile Ile
-25 -20 -15
gtt ttt tgt ttt gtt ttt ttg aga cag agt ctt gct ctg tca ccc agg 97
Val Phe Cys Phe Val Phe Leu Arg Gln Ser Leu Ala Leu Ser Pro Arg
-10 -5 1
ctg gag tgc agt ggc gcg atc tca gst cac agc aac cty csg cyt ccs 145
Leu Glu Cys Ser Gly Ala Ile Ser Xaa His Ser Asn Leu Xaa Xaa Pro
5 10 15 20
gct ttc aag caa ttc tcc tgc ctc agc ctc ctg agt agc tgg gac tgc 193
Ala Phe Lys Gln Phe Ser Cys Leu Ser Leu Ser Ser Trp Asp Cys
25 30 35
agg tgc ccc acc atg ccc gac tgt t 218
Arg Cys Pro Thr Met Pro Asp Cys
40

<210> 593
<211> 224
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 32..223

<221> sig_peptide
<222> 32..76
<223> score 6.7
seq LFVLFLFLFFSFL/FF

<400> 593
tgccccagcct agattttttg cccattttta a atg aga tta ttt gtc tta ttt 52
Met Arg Leu Phe Val Leu Phe

<222> 51..131
 <223> score 5.9
 seq ITLFICFFETGSC/SV

<400> 595
 cccagaattc ctgtatgttc aaaactatcg tttgtagcct ttgtgtgtga atg atg 56
 Met Met
 gct tgg ctt gtt tta aaa caa aaa aat cgc tgg ctc ata act tta ttc 104
 Ala Trp Leu Val Leu Lys Gln Lys Asn Arg Trp Leu Ile Thr Leu Phe
 -25 -20 -15 -10
 att tgt ttt ttt gag aca ggg tct tgc tct gtt gct cag gct gga gtg 152
 Ile Cys Phe Phe Glu Thr Gly Ser Cys Ser Val Ala Gln Ala Gly Val
 -5 1 5
 cag tgg cat gat cac agc tca ctg cgg ctt cca ccc tgg ggc tca agc 200
 Gln Trp His Asp His Ser Ser Leu Arg Leu Pro Pro Trp Gly Ser Ser
 10 15 20
 tat cct ccc acc tta gcc tcc caa cag gtg cgc 233
 Tyr Pro Pro Thr Leu Ala Ser Gln Gln Val Arg
 25 30

<210> 596
 <211> 314
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 159..314
 <221> sig_peptide
 <222> 159..215
 <223> score 7
 seq STVVLQVLTQATS/QD

<400> 596
 gacgccarac atggcgtggt cctagaagcc gcttttcggca tcagtaggcg gcggcgtggg 60
 gtctggcack gtggggagag ggamcaaccg acgccacttc gtgttgggaa gtgggagcgg 120
 ganrgccggg caattcccga ccgaaccaaa cggtttcc atg gat ctc aat agt gcc 176
 Met Asp Leu Asn Ser Ala
 -15
 agc act gtt gtt ctt cag gtg tta aca cag gcc acc agt cag gat act 224
 Ser Thr Val Val Leu Gln Val Leu Thr Gln Ala Thr Ser Gln Asp Thr
 -10 -5 1
 gct gtg tta aaa cca gct gag gag cag ttg aag cag tgg gag aca cag 272
 Ala Val Leu Lys Pro Ala Glu Glu Gln Leu Lys Gln Trp Glu Thr Gln
 5 10 15
 cca gdw ttc tat tca gtg ttg ctg aat att ttc acc aac cac 314
 Pro Gly Phe Tyr Ser Val Leu Leu Asn Ile Phe Thr Asn His
 20 25 30

<210> 597
 <211> 325

004220"666ET560

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..324

<221> sig_peptide
<222> 133..189
<223> score 7.9
seq LLLALLLPGGDNA/DA

<400> 597
agttgctgtc agcgggctkat ggggaagatt gttggtagaa ggaagtcaga atataggtac 60
agagggataa gtttgctaag aacagagatc agcaaacagc ttttctgaga gaaagaaaca 120
tctgcaaattg ac atg ctg ttt ctg cag ttt ctg ctg cta gct ctt ctt ctc 171
Met Leu Phe Leu Gln Phe Leu Leu Leu Ala Leu Leu Leu
-15 -10
cca ggt ggt gac aat gca gac gca tcc cag gaa cac gtc tcc ttc cat 219
Pro Gly Gly Asp Asn Ala Asp Ala Ser Gln Glu His Val Ser Phe His
-5 1 5 10
gtc atc cag atc ttc tca ttt gtc aac caa tcc tgg gca cga ggt cag 267
Val Ile Gln Ile Phe Ser Phe Val Asn Gln Ser Trp Ala Arg Gly Gln
15 20 25
ggc tca gga tgg ctg gaa kag ttg cag act cat ggc tgg gac agt gaa 315
Gly Ser Gly Trp Leu Glu Xaa Leu Gln Thr His Gly Trp Asp Ser Glu
30 35 40
tca gac act g 325
Ser Asp Thr
45

<210> 598
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..232

<221> sig_peptide
<222> 50..97
<223> score 3.5
seq LQALLVVALHSHP/AE

<400> 598
gtactcggca kcgcggaat aaagtttgct gatttggtgt ctacgctgg atg cct ggg 58
Met Pro Gly
-15
ttg cag gcc ctg ctt gtg gtg gcg ctc cac agt cat ccg gct gaa gaa 106
Leu Gln Ala Leu Leu Val Val Ala Leu His Ser His Pro Ala Glu Glu
-10 -5 1

004220" 022400

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gac ctg ttg gac tgg atc ttc tcg gga cgg agt ctc act ctg tcg ccc      154
Asp Leu Leu Asp Trp Ile Phe Ser Gly Arg Ser Leu Thr Leu Ser Pro
      5              10              15
agg ctg gag tgc agt ggc aca atc tcg gct cac tgc aag ctc cgc ctc      202
Arg Leu Glu Cys Ser Gly Thr Ile Ser Ala His Cys Lys Leu Arg Leu
      20              25              30              35
cca gat att gtt ttg tat tta ccc atg cgt      232
Pro Asp Ile Val Leu Tyr Leu Pro Met Arg
              40              45

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<210> 599
 <211> 394
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 122..394

<221> sig_peptide
 <222> 122..268
 <223> score 6.4
 seq AVSFAPLIQPCHS/ES

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<400> 599
caagtttgac ttctgtgaac cttcctttgt tactgggaat tgcctggaga tttctccgga      60
ttgttctcag tatgatcgtg tatactgtgg ggctggcgtg cagaaagagc atgaagagta      120
c atg aag aat ctt ctc aaa gtg gga ggg atc ctt gtc atg cca ctg gaa      169
Met Lys Asn Leu Leu Lys Val Gly Gly Ile Leu Val Met Pro Leu Glu
      -45              -40              -35
gag aag ttg act aag ata aca cgc aca ggt cct tca gct tgg gaa acc      217
Glu Lys Leu Thr Lys Ile Thr Arg Thr Gly Pro Ser Ala Trp Glu Thr
      -30              -25              -20
aad aag att ctt gct gtt tct ttt gct cct ctg atc cag ccc tgc cat      265
Xaa Lys Ile Leu Ala Val Ser Phe Ala Pro Leu Ile Gln Pro Cys His
      -15              -10              -5
tca gag tca gga aaa tca aga ctt gtc cag tta cca cca gtg gca gtt      313
Ser Glu Ser Gly Lys Ser Arg Leu Val Gln Leu Pro Pro Val Ala Val
      1              5              10              15
cgn agc ctc cag gac ttg gct cgc atc gcc atc cgg ggc acc att aaa      361
Arg Ser Leu Gln Asp Leu Ala Arg Ile Ala Ile Arg Gly Thr Ile Lys
      20              25              30
aag att att cat cag gaa act gtg agc aaa aac      394
Lys Ile Ile His Gln Glu Thr Val Ser Lys Asn
      35              40

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<210> 600
 <211> 232
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

004220 6667560

<222> 64..231

<221> sig_peptide

<222> 64..171

<223> score 4.6

seq TLLWCFSALLPT/IV

<400> 600
 atcaatgtcg tcctcttcat cctcctcttc ttcctcacca ctccagccat catcatcacc 60
 acc atg gac aag ttc aac gtc acc aag cct gtg gag tac ctc aac aac 108
 Met Asp Lys Phe Asn Val Thr Lys Pro Val Glu Tyr Leu Asn Asn
 -35 -30 -25
 ccc atc atc acc cag ttc ttc ccc acc ctg ctg ctg tgg tgc ttc tcg 156
 Pro Ile Ile Thr Gln Phe Phe Pro Thr Leu Leu Leu Trp Cys Phe Ser
 -20 -15 -10
 gcc ctc ctt ccc acc atc gtc tac tac tca gcc ttc ttt gaa gcc cac 204
 Ala Leu Leu Pro Thr Ile Val Tyr Tyr Ser Ala Phe Phe Glu Ala His
 -5 1 5 10
 tgg aca cgc tct ggg gag aac agg acc t 232
 Trp Thr Arg Ser Gly Glu Asn Arg Thr
 15 20

<210> 601

<211> 278

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 56..277

<221> sig_peptide

<222> 56..184

<223> score 3.5

seq QHWLLGGFPRTLQ/QA

<400> 601
 aggatccggg ctggaagcct ctgggagtg tgcctccagc caagaagttg gtgag atg 58
 Met
 gca aag cag tat ata gag aaa agt ctt ttg gtt cca gac cat gtg atc 106
 Ala Lys Gln Tyr Ile Glu Lys Ser Leu Leu Val Pro Asp His Val Ile
 -40 -35 -30
 aca cgc cta atg atg tcc gag ttg gag aac agg cgt ggc cag cac tgg 154
 Thr Arg Leu Met Met Ser Glu Leu Glu Asn Arg Arg Gly Gln His Trp
 -25 -20 -15
 ctc ctt ggt ggt ttt cct agg aca tta gga caa gcc gaa gcc ctg gac 202
 Leu Leu Gly Gly Phe Pro Arg Thr Leu Gly Gln Ala Glu Ala Leu Asp
 -10 -5 1 5
 aaa atc tgt gaa gtg gat cta gtg atc agt ttg aat att cca ttt gaa 250
 Lys Ile Cys Glu Val Asp Leu Val Ile Ser Leu Asn Ile Pro Phe Glu
 10 15 20
 aca ctt aaa gat cgt ctc agc cgc cag a 278

Thr Leu Lys Asp Arg Leu Ser Arg Gln
 25 30

<210> 602
 <211> 206
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 9..206

<221> sig_peptide
 <222> 9..143
 <223> score 3.6
 seq ALLELIDSPECLS/KC

<400> 602
 ctgggaag atg gcg ctg cac ttc cag agt ttg gct gaa ttg gaa rtg tta 50
 Met Ala Leu His Phe Gln Ser Leu Ala Glu Leu Glu Xaa Leu
 -45 -40 -35
 tgt act cat ctc tac ata ggg act gat ctt aca caa aga ata gag gct 98
 Cys Thr His Leu Tyr Ile Gly Thr Asp Leu Thr Gln Arg Ile Glu Ala
 -30 -25 -20
 gag aaa gca ctc ttg gaa ctt att gac agt cca gaa tgt ctc agc aag 146
 Glu Lys Ala Leu Leu Glu Leu Ile Asp Ser Pro Glu Cys Leu Ser Lys
 -15 -10 -5 1
 tgt caa ctt tta tta gaa caa gga aca aca tcc tat gct cag ctc ctt 194
 Cys Gln Leu Leu Leu Glu Gln Gly Thr Thr Ser Tyr Ala Gln Leu Leu
 5 10 15
 gca gca acc gkv 206
 Ala Ala Thr Xaa
 20

<210> 603
 <211> 205
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 24..203

<221> sig_peptide
 <222> 24..110
 <223> score 7.6
 seq PTLAIALAANAWA/FV

<400> 603
 ccatatgggt ggtgtggatc gtc atg tat act tac ggc aac aag cag cac aac 53
 Met Tyr Thr Tyr Gly Asn Lys Gln His Asn
 -25 -20

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agt ccc acc tgg gat gac ccc acg ctg gcc atc gcc ctc gcc gcc aat      101
Ser Pro Thr Trp Asp Asp Pro Thr Leu Ala Ile Ala Leu Ala Ala Asn
               -15                      -10                      -5
gcc tgg gcc ttc gtc ctc ttc tac gtc atc ccc gag gtc tcc cag gtg      149
Ala Trp Ala Phe Val Leu Phe Tyr Val Ile Pro Glu Val Ser Gln Val
               1                      5                      10
acc aag tcc agc cca gag caa agc tac cag ggg gac atg tac ccc acc      197
Thr Lys Ser Ser Pro Glu Gln Ser Tyr Gln Gly Asp Met Tyr Pro Thr
               15                      20                      25
cgg gac tt
Arg Asp
30

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<210> 604
<211> 319
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 150..317

<221> sig_peptide
<222> 150..278
<223> score 6.1
      seq SAATLASLGGTSS/RR

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<400> 604
actctcgtgc caagcatgtc tctccaaatg gctgctctct ggcgttcttc acactcccc      60
tgaagttcat ctaagatctt cattcttcaw aggcggaagc ccggctcgct gcaaaacggg      120
cggcccgcgc ggaggctcgc gagatccgc atg aag gag ctg gag cgg cag cag      173
                        Met Lys Glu Leu Glu Arg Gln Gln
                        -40
aag gag gta gaa gag aga cca gaa aaa gat ttt act gag aag ggg tct      221
Lys Glu Val Glu Glu Arg Pro Glu Lys Asp Phe Thr Glu Lys Gly Ser
-35                      -30                      -25                      -20
cgt aac atg ccg ggc ctg tct gca gcc acg ctg gcc tct ctg ggt ggg      269
Arg Asn Met Pro Gly Leu Ser Ala Ala Thr Leu Ala Ser Leu Gly Gly
-15                      -10                      -5
act tcc tct cgg aga ggc agc gga gac acc tcc atc tcc atc gac ccc      317
Thr Ser Ser Arg Arg Gly Ser Gly Asp Thr Ser Ile Ser Ile Asp Pro
               1                      5                      10
ga

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<210> 605
<211> 284
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> 65..283

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<221> sig_peptide
 <222> 65..172
 <223> score 5.3
 seq ALYIMCVPHSVWG/CA

<400> 605
 agtccagagg cctggccctg ccaagaaggc gctctccgga atcaacacct gggggcttgg 60
 aagg atg ttt cgc tca gat cga atg tgg arc tgc cat tgg aaa tgg aag 109
 Met Phe Arg Ser Asp Arg Met Trp Xaa Cys His Trp Lys Trp Lys
 -35 -30 -25
 ccc agt cct ctc ctg ttc tta ttt gct tta tat atc atg tgt gtt cct 157
 Pro Ser Pro Leu Leu Phe Leu Phe Ala Leu Tyr Ile Met Cys Val Pro
 -20 -15 -10
 cac tca gtg tgg gga tgt gcc aac tgc cga gtg gtt ttg tcc aac cct 205
 His Ser Val Trp Gly Cys Ala Asn Cys Arg Val Val Leu Ser Asn Pro
 -5 1 5 10
 tct ggg acc ttt act tct cca tgc tac cct aac gac tac cca aac agc 253
 Ser Gly Thr Phe Thr Ser Pro Cys Tyr Pro Asn Asp Tyr Pro Asn Ser
 15 20 25
 cag gct tgc atg tgg acg ctc cga gac ccc a 284
 Gln Ala Cys Met Trp Thr Leu Arg Asp Pro
 30 35

<210> 606
 <211> 383
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 5..382

<221> sig_peptide
 <222> 5..94
 <223> score 10.6
 seq GLLCCAALSLLWA/GP

<400> 606
 ttca atg cac aga tac aga aga ccc ctc cgt cat gca gca tct gcc atg 49
 Met His Arg Tyr Arg Arg Pro Leu Arg His Ala Ala Ser Ala Met
 -30 -25 -20
 agc atc ggc ctc ctg tgc tgt gca gcc ttg tct ctc ctg tgg gca ggt 97
 Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala Gly
 -15 -10 -5 1
 cca gtg aat gct ggt gtc act cag acc cca aaa ttc cag gtc ctg aag 145
 Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu Lys
 5 10 15
 aca gga cag agc atg aca ctg cag tgt gcc cag gat atg aac cat gaa 193
 Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His Glu
 20 25 30
 tac atg tcc tgg tat cga caa gac cca ggc atg ggg ctg agg ctg att 241
 Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu Ile

004220 " 054399 " 024400

35	40	45	
cat tac tca gtt ggt gct ggt atc act gac caa gga gaa gtc ccc aat			289
His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro Asn			
50	55	60	65
ggc tac aat gtc tcc aga tca acc aca gag gat ttc ccg ctc agg ctg			337
Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg Leu			
	70	75	80
ctg tcg gct gct ccc tcc cag aca tct gtg tac ttc tgt gcc agc a			383
Leu Ser Ala Ala Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser			
	85	90	95

<210> 607
 <211> 392
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 3..392

<221> sig_peptide
 <222> 3..146
 <223> score 5.7
 seq LLLFFGKLLVVGG/VG

<400> 607	
tc atg atc gcc atc tac ggg aag aat ttc tgt gtc tca gcc aaa aat	47
Met Ile Ala Ile Tyr Gly Lys Asn Phe Cys Val Ser Ala Lys Asn	
	-45
gcg ttc atg cta ctc atg cga aac att gtc agg gtg gtc gtc ctg gac	95
Ala Phe Met Leu Leu Met Arg Asn Ile Val Arg Val Val Val Leu Asp	
	-30
aaa gtc aca gac ctg ctg ctg ttc ttt ggg aag ctg ctg gtg gtc gga	143
Lys Val Thr Asp Leu Leu Leu Phe Phe Gly Lys Leu Leu Val Val Gly	
	-15
ggc gtg ggg gtc ctg tcc ttc ttt ttt ttc tcc ggt cgc atc ccg ggg	191
Gly Val Gly Val Leu Ser Phe Phe Phe Phe Ser Gly Arg Ile Pro Gly	
	1
ctg ggt aaa gac ttt aag agc ccc cac ctc aac tat tac tgg ctg ccc	239
Leu Gly Lys Asp Phe Lys Ser Pro His Leu Asn Tyr Tyr Trp Leu Pro	
	20
ayc atg acc tcc atc ctg ggg gcc tat gtc atc gcc agy ggc ttc ttc	287
Xaa Met Thr Ser Ile Leu Gly Ala Tyr Val Ile Ala Ser Gly Phe Phe	
	35
agc gtt ttc ggc atg tgt gtg gac acg ctc ttc ctc tgc ttc ctg gaa	335
Ser Val Phe Gly Met Cys Val Asp Thr Leu Phe Leu Cys Phe Leu Glu	
	50
gac ctg gag cgg aca acg gct ccc tgg acg gcc cta cta cat gtc caa	383
Asp Leu Glu Arg Thr Thr Ala Pro Trp Thr Ala Leu Leu His Val Gln	
	65
gag ctt cta	
Glu Leu Leu	
	80

<210> 608
 <211> 245
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 18..245

 <221> sig_peptide
 <222> 18..86
 <223> score 6.2
 seq PLPLLLLLQPGLP/LF

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 atctatatat agtacta atg gat ttg gtg tgc wtc ccc ctt agc gtc ccc 50
 Met Asp Leu Val Cys Xaa Pro Leu Ser Val Pro
 -20 -15
 ctc cct ctg ctc ctc ctc ctt cag cct ggt ctc ccc ctc ttc tct gcc 98
 Leu Pro Leu Leu Leu Leu Leu Gln Pro Gly Leu Pro Leu Phe Ser Ala
 -10 -5 1
 ctc cac ccc cgt ctc tgc act gag mta cat was maa mca agg gta gtt 146
 Leu His Pro Arg Leu Cys Thr Glu Xaa His Xaa Xaa Xaa Arg Val Val
 5 10 15 20
 tac tgt ctg ttt tgt ttt ctg ggt ttt cag tgt cct agc gga atg caa 194
 Tyr Cys Leu Phe Cys Phe Leu Gly Phe Gln Cys Pro Ser Gly Met Gln
 25 30 35
 gta ggc agc cag ccc gtc tgt tcc ctc tcc gcc cca ccc cgc ccc gcg 242
 Val Gly Ser Gln Pro Val Cys Ser Leu Ser Ala Pro Pro Arg Pro Ala
 40 45 50
 ccc 245
 Pro

<210> 609
 <211> 336
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 100..336

 <221> sig_peptide
 <222> 100..156
 <223> score 9.9
 seq ILFLVFLLAGLRS/KA

<400> 609
 ccagatctgt tctgcaacat tcaccgttct ctgcatccag ctctgcttat ctgctgttac 60
 cttggacacc agagcagcta taggtatctg ccagragcw atg aaa tca ttc agc 114
 Met Lys Ser Phe Ser

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                                     -15
cgg atc ctc ttc ctc gtc ttc ctc ctc gcc ggc ctg agg tcc aag gcc      162
Arg Ile Leu Phe Leu Val Phe Leu Leu Ala Gly Leu Arg Ser Lys Ala
                                     -10      -5      1
gct ccc tca gcc cct ctg cct ttg ggc tgt ggc ttt ccg gac atg gcc      210
Ala Pro Ser Ala Pro Leu Pro Leu Gly Cys Gly Phe Pro Asp Met Ala
      5      10      15
cac ccc tct gag act tcc cct ctg aag ggt gct tct gaa aat tcc aaa      258
His Pro Ser Glu Thr Ser Pro Leu Lys Gly Ala Ser Glu Asn Ser Lys
      20      25      30
cga gat cgc ctt aac cca gaa ttt cct ggg act cct tac cct gag cct      306
Arg Asp Arg Leu Asn Pro Glu Phe Pro Gly Thr Pro Tyr Pro Glu Pro
35      40      45      50
tcc aag cta cct cat acg gtt tcc ctg gaa      336
Ser Lys Leu Pro His Thr Val Ser Leu Glu
      55      60

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<210> 610
 <211> 373
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 109..372

<221> sig_peptide
 <222> 109..153
 <223> score 7.5
 seq AVLLALLMAGLAL/QP

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<400> 610
actggctcca ggaaaccgc tggtgttgac tgtgggcagt ccagcctctc cccatttgag      60
gccatataaa nnacctgagg ccctctccac cacagcccac cagtgacc atg aag gct      117
                                     -15
gtg ctg ctt gcc ctg ttg atg gca ggc ttg gcc ctg cag cca ggc act      165
Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln Pro Gly Thr
      -10      -5      1
gcc ctg ctg tgc tac tcc tgg arr gcc cag gtg rgc aac gag gac tgc      213
Ala Leu Leu Cys Tyr Ser Trp Xaa Ala Gln Val Xaa Asn Glu Asp Cys
      5      10      15      20
ctg cag gtg gag aac tgc acc cag ctg ggg gag cag tgc tgg acc gcg      261
Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys Trp Thr Ala
      25      30      35
cgc atc cgc gca gtt ggc ctc ctg acc gtc atc agc aaa ggc tgc agc      309
Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys Gly Cys Ser
      40      45      50
ttg aac tgc gtg gat sac tca cag gac tac tac gtg ggc aag aag aac      357
Leu Asn Cys Val Asp Xaa Ser Gln Asp Tyr Tyr Val Gly Lys Lys Asn
      55      60      65
atc acg tgc tgt gac a
Ile Thr Cys Cys Asp

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70

<210> 611
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..457

<221> sig_peptide
<222> 74..157
<223> score 9.5
seq LVXFSLLTAILG/AV

<400> 611
ccataccaaa ttaaagtgact gccataaagt atattttact cacaggacag attacaatag 60
ccttgataga atc atg gca tcc aaa ggg atg cgc cat ttt tgc ttg att 109
Met Ala Ser Lys Gly Met Arg His Phe Cys Leu Ile
-25 -20
tca gag cag ttg gtg tyc ttt agt ctt ctt gca aca gcg att ttg gga 157
Ser Glu Gln Leu Val Xaa Phe Ser Leu Leu Ala Thr Ala Ile Leu Gly
-15 -10 -5
gca gtt tcc tgg cag cca aca aat gga att ttc ttg agc atg ttt cta 205
Ala Val Ser Trp Gln Pro Thr Asn Gly Ile Phe Leu Ser Met Phe Leu
1 5 10 15
atc gtt ttg cca ttg gaa tcc atg gct cat ggg ctc ttc cat gaa ttg 253
Ile Val Leu Pro Leu Glu Ser Met Ala His Gly Leu Phe His Glu Leu
20 25 30
ggg aac tgt tta gga gga aca tct gtt gga tat gct att gtg att ccc 301
Gly Asn Cys Leu Gly Gly Thr Ser Val Gly Tyr Ala Ile Val Ile Pro
35 40 45
acc aac ttc tgc agt cct gat ggt cag cca aca ctg ctt ccc cca gaa 349
Thr Asn Phe Cys Ser Pro Asp Gly Gln Pro Thr Leu Leu Pro Pro Glu
50 55 60
cat gta cag gag tta aat ttg agg tct act ggc atg ctc aat gct atc 397
His Val Gln Glu Leu Asn Leu Arg Ser Thr Gly Met Leu Asn Ala Ile
65 70 75 80
caa aga ttt ttt gca tat cat atg att gag acc tat gga tgt gac tat 445
Gln Arg Phe Phe Ala Tyr His Met Ile Glu Thr Tyr Gly Cys Asp Tyr
85 90 95
tcc aca agt gga ct 459
Ser Thr Ser Gly
100

<210> 612
<211> 213
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 35..211

<221> sig_peptide

<222> 35..166

<223> score 3.7

seq LAERLGLFEELWA/AQ

<400> 612

ctgtttgagg atgtaggcac tgggtgaag gaac atg gcc ctg tat cag agg tgg 55
Met Ala Leu Tyr Gln Arg Trp
-40

cgg tgt ctc cgg ctc caa ggt tta cag gct tgc agg cta cac acg gca 103
Arg Cys Leu Arg Leu Gln Gly Leu Gln Ala Cys Arg Leu His Thr Ala
-35 -30 -25

ggt gtg tgc acc cct cca cgc tgg tta gca gag cgg ctt ggc ctt ttt 151
Val Val Ser Thr Pro Pro Arg Trp Leu Ala Glu Arg Leu Gly Leu Phe
-20 -15 -10

gag gag ctg tgg gct gct cag gta aag aga tta gca agc atg gca cag 199
Glu Glu Leu Trp Ala Ala Gln Val Lys Arg Leu Ala Ser Met Ala Gln
-5 1 5 10

aag gaa ccc cag ac 213
Lys Glu Pro Gln
15

<210> 613

<211> 334

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 136..333

<221> sig_peptide

<222> 136..222

<223> score 13

seq LLLVLLLVTXRS/MP

<400> 613

atttgtcgg cgctgggtccc ctcagagggg tctgtctgct gccggtgcct tggaccctcc 60
ccctcgcttc sngttctact gccccaggag cccggcgggt ccgggactcc cgkccgtgcc 120
ggtgcgggag ccggc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc 171
Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly
-25 -20

cct ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg asc cgg 219
Pro Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Xaa Arg
-15 -10 -5

tca atg cct gcc tcc tca ccg gca gcc tct tgc ttc tac tgc gcg tct 267
Ser Met Pro Ala Ser Ser Pro Ala Ala Ser Ser Phe Tyr Cys Ala Ser
1 5 10 15

tca gct btg agc cgg tgc cct ctt gca ggg ccc tgc agg tgc tca agc 315
Ser Ala Xaa Ser Arg Cys Pro Leu Ala Gly Pro Cys Arg Cys Ser Ser

20
ccc ggg acc gca ttt ctg c
Pro Gly Thr Ala Phe Leu
35

25

30

334

<210> 614
<211> 307
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 43..306

<221> sig_peptide
<222> 43..186
<223> score 5.4
seq ILLEVFVWNLQG/LP

<400> 614
astttcttcct gccaaagagaa caatgccgag aaacagagcg aa atg ktt cca aat 54
Met Xaa Pro Asn
-45
aat ttt tgg caa aaa ctt gga aga aaa aaa ccc cgc ata ttt acc tgt 102
Asn Phe Trp Gln Lys Leu Gly Arg Lys Lys Pro Arg Ile Phe Thr Cys
-30
acc cag agc tcc aca ggt gag gcg gca gtt aaa gca gaa aat cta att 150
Thr Gln Ser Ser Thr Gly Glu Ala Ala Val Lys Ala Glu Asn Leu Ile
-15
ctt ctg gaa gtt ttt gtc tgg aac gga ctc cag ggt ctt cct tcg gag 198
Leu Leu Glu Val Phe Val Trp Asn Gly Leu Gln Gly Leu Pro Ser Glu
-10
ctg tca gat aca agt gga tcc tct aag aaa ctt ggg agc ctt gtg ggc 246
Leu Ser Asp Thr Ser Gly Ser Ser Lys Lys Leu Gly Ser Leu Val Gly
5 10 15 20
tgg tgg aga act ctc aag atg gca cca gcc tgt cta tgg tct atg tgg 294
Trp Trp Arg Thr Leu Lys Met Ala Pro Ala Cys Leu Trp Ser Met Trp
25 30 35
gaa tca ccg cca c
Glu Ser Pro Pro
40

<210> 615
<211> 344
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..342

<221> sig_peptide
<222> 133..246

<223> score 3.6
seq LSWLITWFGHXL/DF

<400> 615
ttgtggtcac atttctgctg gtggtaggcg agaggctggc aacatccctg gtagaaaaat 60
tatctaccca ccacctcagg gattttatgg atccavcaat ggracaacac camgcatata 120
ttaaactatc tg atg ccc atc att gac cag gtg aat cca gag ctc cat gac 171
Met Pro Ile Ile Asp Gln Val Asn Pro Glu Leu His Asp
-35 -30
ttc atg cag agt gct gag gta ggg acc atc ttt gcc ctc agc tgg ctc 219
Phe Met Gln Ser Ala Glu Val Gly Thr Ile Phe Ala Leu Ser Trp Leu
-25 -20 -15 -10
atc acc tgg ttt ggg cat gwm ctg tct gac ttc agg cac gtc gtg cgg 267
Ile Thr Trp Phe Gly His Xaa Leu Ser Asp Phe Arg His Val Val Arg
-5 1 5
tta tat gac ttc ttc ctr gcc tgc cac cca ctg atg ccg att tac ttt 315
Leu Tyr Asp Phe Phe Leu Ala Cys His Pro Leu Met Pro Ile Tyr Phe
10 15 20
gca gcc gtg att gtg ttg tat cgc gag ca 344
Ala Ala Val Ile Val Leu Tyr Arg Glu
25 30

<210> 616
<211> 390
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..388

<221> sig_peptide
<222> 83..142
<223> score 3.9
seq FLAPSSGVQPTLA/MP

<400> 616
cactgaaaga gtaatacagc ctcatggggg tggatcgaat cctctggaag gcactcagca 60
tcttcaagat gtaccttacg tc atg gtg agg gaa aga gag agc ttc ctt gcc 112
Met Val Arg Glu Arg Glu Ser Phe Leu Ala
-20 -15
ccc agc tca ggt gtg cag cct act ctg gcc atg cct aat ata gca gta 160
Pro Ser Ser Gly Val Gln Pro Thr Leu Ala Met Pro Asn Ile Ala Val
-10 -5 1 5
gga cag aat gtg aca gtg aca gaa aga gtt cta gca cct gct tcc act 208
Gly Gln Asn Val Thr Val Thr Glu Arg Val Leu Ala Pro Ala Ser Thr
10 15 20
ctg caa tcc agt tac cag att ccc act gaa aat tct atg acg gct agg 256
Leu Gln Ser Ser Tyr Gln Ile Pro Thr Glu Asn Ser Met Thr Ala Arg
25 30 35
aac acc acg gtg tct gga gct gga gtc cct ggc cct ctg cca gat ttt 304
Asn Thr Thr Val Ser Gly Ala Gly Val Pro Gly Pro Leu Pro Asp Phe

40 45 50
 ggt tta gag gaa tct ggt cat tct aat tct acc ata acc aca tct tcc 352
 Gly Leu Glu Glu Ser Gly His Ser Asn Ser Thr Ile Thr Thr Ser Ser
 55 60 65 70
 acc aga gtt acc aag cat agc act gta cag cat tct ta 390
 Thr Arg Val Thr Lys His Ser Thr Val Gln His Ser
 75 80

<210> 617
 <211> 233
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 46..231

<221> sig_peptide
 <222> 46..180
 <223> score 3.9
 seq SLLTESSASRVHA/IX

<400> 617 57
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 Met Cys Phe Arg
 -45
 ctt aga ctt ttt att gcc ccc ccc ccc ttt ttt ttt gar acg gag tct 105
 Leu Arg Leu Phe Ile Ala Pro Pro Pro Phe Phe Phe Glu Thr Glu Ser
 -40 -35 -30
 cgc tct gac gca cag gct gga kts cag tgg cyc cga tct ctg ctc act 153
 Arg Ser Asp Ala Gln Ala Gly Xaa Gln Trp Xaa Arg Ser Leu Leu Thr
 -25 -20 -15 -10
 gaa agc tcc gcc tcc cgg gtt cat gcc att cyc ctg cct cag cct cct 201
 Glu Ser Ser Ala Ser Arg Val His Ala Ile Xaa Leu Pro Gln Pro Pro
 -5 1 5
 gag tas ctg gga cta cag gcg ccc acc akt gc 233
 Glu Xaa Leu Gly Leu Gln Ala Pro Thr Xaa
 10 15

<210> 618
 <211> 260
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 103..258

<221> sig_peptide
 <222> 103..156
 <223> score 7.2
 seq LFFLLRIALASWA/LF

<400> 618
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114
ttggttactg tagtcttgta gtatagttta aagtcagata gc atg atg act cta
Met Met Thr Leu
-15
gct ttg ttc ttt ttg ctt agg att gct ttg gct agt tgg gct ctc ttt 162
Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser Trp Ala Leu Phe
-10 -5 1
tgg atc cat atg aat ttt aga aga gct ttt ttc cac tta cgg tgg ttt 210
Trp Ile His Met Asn Phe Arg Arg Ala Phe Phe His Leu Arg Trp Phe
5 10 15
gat atc aat agc act gaa tct gta aat tgc ttt ggg cag tat ggc cta 258
Asp Ile Asn Ser Thr Glu Ser Val Asn Cys Phe Gly Gln Tyr Gly Leu
20 25 30
gc 260

<210> 619
<211> 326
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 72..326
<221> sig_peptide
<222> 72..206
<223> score 6.7
seq PMLGLAAFRWIWS/RE

<400> 619
aaagcggacc cgcggacggt ggcgttaagg gaacgctgag gtcccgcgct ccccgaccga 60
110
ggtatatctc c atg aat aac cta aat gat ccc cca aat tgg aat atc cgg
Met Asn Asn Leu Asn Asp Pro Pro Asn Trp Asn Ile Arg
-45 -40 -35
cct aat tcc agg gcg gat ggt ggt gat gga agc agg tgg aat tat gcc 158
Pro Asn Ser Arg Ala Asp Gly Gly Asp Gly Ser Arg Trp Asn Tyr Ala
-30 -25 -20
ctg ttg gtt cca atg ctg gga ttg gct gct ttt cgt tgg att tgg tct 206
Leu Leu Val Pro Met Leu Gly Leu Ala Ala Phe Arg Trp Ile Trp Ser
-15 -10 -5
agg gag tcc cag aaa gaa gta gaa aaa gag aga gaa gcc tac cgt cgg 254
Arg Glu Ser Gln Lys Glu Val Glu Lys Glu Arg Glu Ala Tyr Arg Arg
1 5 10 15
aga act gct gct ttt caa cag gat ctg gaa gcc aag tac cac gcc atg 302
Arg Thr Ala Ala Phe Gln Gln Asp Leu Glu Ala Lys Tyr His Ala Met
20 25 30
atc tca gam aat cgg cgt gct gtc 326
Ile Ser Xaa Asn Arg Arg Ala Val
35 40

<210> 620

<211> 316
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..316

<221> sig_peptide
 <222> 62..121
 <223> score 9.6
 seq LLALLLCGRPGRG/QT

<400> 620
 accgcagctc cagagccctg cgggaggact cagagtcagg gacacagcag cgtccggcga 60
 g atg aag gcg ctc ggg gct gtc ctg ctt gcb ctc ttg ctg tgc ggg cgg 109
 Met Lys Ala Leu Gly Ala Val Leu Leu Ala Leu Leu Leu Cys Gly Arg
 -20 -15 -10 -5
 cca ggg aga ggg cag aca cag cag gag gaa gag gaa gag gac gag gac 157
 Pro Gly Arg Gly Gln Thr Gln Gln Glu Glu Glu Glu Glu Asp Glu Asp
 1 5 10
 cac ggg cca gat gac tac gac gag gaa gat gag gat gag gtt gaa gag 205
 His Gly Pro Asp Asp Tyr Asp Glu Glu Asp Glu Asp Glu Val Glu Glu
 15 20 25
 gag gag acc aac agg ctc cct ggt ggc agg agc aga gtg ctg ctg cgg 253
 Glu Glu Thr Asn Arg Leu Pro Gly Gly Arg Ser Arg Val Leu Leu Arg
 30 35 40
 tgc tac acc tnk nag tcc ctg ccc agg gac gag cgc tgc aac ctg acg 301
 Cys Tyr Thr Xaa Xaa Ser Leu Pro Arg Asp Glu Arg Cys Asn Leu Thr
 45 50 55 60
 cag aac tgc tca cat 316
 Gln Asn Cys Ser His
 65

<210> 621
 <211> 308
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 67..306

<221> sig_peptide
 <222> 67..123
 <223> score 7.2
 seq VSIMLLLVTVSDC/AV

<400> 621
 aaggctgagc gggaggaagc gagaggcatc taagcaggca gtgttttgcc ttcaccccaa 60
 gtgacc atg aga ggt gcc acg cga gtc tca atc atg ctc cta gta 108
 Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val

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-15          -10
act gtg tct gac tgt gct gtg atc aca ggg gcc tgt gag cgg gat gtc 156
Thr Val Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val
-5          1          5          10
cag tgt ggg gca ggc acc tgc tgt gcc atc agc ctg tgg ctt cga ggg 204
Gln Cys Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly
15          20          25
ctg cgg atg tgc acc ccg ctg ggg cgg gaa ggc gag gag tgc cac ccc 252
Leu Arg Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro
30          35          40
ggc agc cac aag atc ccc ttc ttc agg aaa cgc aag cac cac acc tgt 300
Gly Ser His Lys Ile Pro Phe Phe Arg Lys Arg Lys His His Thr Cys
45          50          55
cct tgc tt
Pro Cys
60

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<210> 622
 <211> 408
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 93..407

<221> sig_peptide
 <222> 93..152
 <223> score 10
 seq SLLLXLLVASGDA/DM

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<400> 622
aatccagcgt ctccctgggcc tagattcccc agctgctgtt ctctggaggg agatgctgcc 60
cccaccccct taggcccgag ggatcaggag ct atg gga cca gag gcc ctg tca 113
Met Gly Pro Glu Ala Leu Ser
-20          -15
tct tta ctg ctg mtg ctc ttg gtg gca agt gga gat gct gac atg aag 161
Ser Leu Leu Leu Xaa Leu Leu Val Ala Ser Gly Asp Ala Asp Met Lys
-10          -5          1
gga cat ttt gat cct gcc dvg tgc cgc tat gcc ctg ggc atg cag gac 209
Gly His Phe Asp Pro Ala Xaa Cys Arg Tyr Ala Leu Gly Met Gln Asp
5          10          15
cgg acc atc cca gac agt gac atc tct gct tcc agc tcc tgg tca gat 257
Arg Thr Ile Pro Asp Ser Asp Ile Ser Ala Ser Ser Ser Trp Ser Asp
20          25          30          35
tcc act gcc gcc mrm cac agc agg ttg gag agc agt gac ggg gat gnn 305
Ser Thr Ala Ala Xaa His Ser Arg Leu Glu Ser Ser Asp Gly Asp Xaa
40          45          50
gcc tgg tgc mcg cag gtn cgg tgt ttc ndn gga gga gga gta ctt gca 353
Ala Trp Cys Xaa Gln Val Arg Cys Phe Xaa Gly Gly Gly Val Leu Ala
55          60          65
ggg gga tct aca acg act gca cct ggt ggc tct ggt ggg cac cca ggg 401
Gly Gly Ser Thr Thr Thr Ala Pro Gly Gly Ser Gly Gly His Pro Gly

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70
acg gca t
Thr Ala
85

75

80

408

<210> 623
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 146..349

<221> sig_peptide
<222> 146..223
<223> score 10
seq FFLMLLAMGLSSA/IG

<400> 623
gcctaacggt atcgagcgag ccggttgtag acgtggtcca ggtttctgca caggaatata 60
gagagcgtca tgaacccgag ctatagagaa aggagatgag gctagcgagg gcccaaagtt 120
tgcattcctg tcctttgttg aagcc atg tcc ttc ctt cct ccg tct gtc ttc 172
Met Ser Phe Leu Pro Pro Ser Val Phe
-25 -20
tgg tct ttt atc ttc ttc ctg atg ttg ctg gcc atg ggg ctg agc agc 220
Trp Ser Phe Ile Phe Phe Leu Met Leu Leu Ala Met Gly Leu Ser Ser
-15 -10 -5
gca ata ggg att atg cag ggc atc att act cca ctc cag gac acc ttc 268
Ala Ile Gly Ile Met Gln Gly Ile Ile Thr Pro Leu Gln Asp Thr Phe
1 5 10 15
tct ttc ttc agg aaa cat aca aag ctg ctc ata gtg gga gtc ttt ttg 316
Ser Phe Phe Arg Lys His Thr Lys Leu Leu Ile Val Gly Val Phe Leu
20 25 30
ctc atg ttc gtg tgc ggc ctc ttc ttc act cga 349
Leu Met Phe Val Cys Gly Leu Phe Phe Thr Arg
35 40

<210> 624
<211> 379
<212> DNA
<213> Homo sapiens

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<221> sig_peptide
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<223> score 3.7
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aagtaacagg acctctttct agctctcaga aaagtctgag aagaaaggag ccctgcgttc      180
ccctaag atg gtg ctc ctg gcc agg tgc gag ggg cac tgc agc cag gcg      229
      Met Val Leu Leu Ala Arg Cys Glu Gly His Cys Ser Gln Ala
              -10
tca cgc tcc gag cct ttg gtg tgc nsc agc act gtc ctc aag caa ccc      277
Ser Arg Ser Glu Pro Leu Val Ser Xaa Ser Thr Val Leu Lys Gln Pro
1              5              10              15
ttc cgt tcc tcc tgt cac tgc tgc cgg ccc cag act tcc aag ctg aag      325
Phe Arg Ser Ser Cys His Cys Cys Arg Pro Gln Thr Ser Lys Leu Lys
              20              25              30
gca ctg cgg ctg cga tgc tca ggg ggc atg cga ctc act gcc acc tac      373
Ala Leu Arg Leu Arg Cys Ser Gly Gly Met Arg Leu Thr Ala Thr Tyr
              35              40              45
cgg tac      379
Arg Tyr
50

<210> 625
<211> 402
<212> DNA
<213> Homo sapiens

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<221> sig_peptide
<222> 128..190
<223> score 9.6
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agagccgggg tctcacaatc cgcttggtcg gggagtcac tgaggttctt gcacctgaa      120
gcaaacc atg gag agc tgg tgg gga ctt ccc tgt ctt gcg ttc ctg tgt      169
      Met Glu Ser Trp Trp Gly Leu Pro Cys Leu Ala Phe Leu Cys
              -20              -15              -10
ttt cta atg cac gcc cga ggt caa aga gac ttt gat ttg gca gat gcc      217
Phe Leu Met His Ala Arg Gly Gln Arg Asp Phe Asp Leu Ala Asp Ala
              -5              1              5
ctt gat gac cct gaa ccc acc aag aag cca aac tca gat atc tac cca      265
Leu Asp Asp Pro Glu Pro Thr Lys Lys Pro Asn Ser Asp Ile Tyr Pro
10              15              20              25
aag cca aaa cca cct tac tac cca cag ccc gag aat ccc gac agc ggt      313
Lys Pro Lys Pro Pro Tyr Tyr Pro Gln Pro Glu Asn Pro Asp Ser Gly
              30              35              40
gga aat aky tac cca agg cca aag cca cgc cct caa ccc cag cct ggc      361
Gly Asn Xaa Tyr Pro Arg Pro Lys Pro Arg Pro Gln Pro Gln Pro Gly
              45              50              55
aat tcc ggc aac agt gga ggt wct tca atg atg tgg acc gt      402

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Asn Ser Gly Asn Ser Gly Gly Xaa Ser Met Met Trp Thr
 60 65 70

<210> 626
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 <212> DNA
 <213> Homo sapiens

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 <222> 12..380

<221> sig_peptide
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 <223> score 5.2
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 -40 -35 -30
 gac tgc atc acc aca ggg tac gcc tac act cag gga ctg agt ggt tcc 98
 Asp Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly Leu Ser Gly Ser
 -25 -20 -15
 atc ctc agt att ttg atg gga gca tca gct ata act gga ata atg gga 146
 Ile Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr Gly Ile Met Gly
 -10 -5 1
 act gta gct ttt act tgg cta cgt cga aaa tgt ggt ttg gtt cgg aca 194
 Thr Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly Leu Val Arg Thr
 5 10 15
 ggt ctg atc tca gga ttg gca cag ctt tcc tgt ttg atc ttg tgt gtg 242
 Gly Leu Ile Ser Gly Leu Ala Gln Leu Ser Cys Leu Ile Leu Cys Val
 20 25 30 35
 atc tct gta ttc atg cct gga agc ccc ctg gac ttg tcc gtt tct cct 290
 Ile Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu Ser Val Ser Pro
 40 45 50
 ttt gad gat atc cga tca agg ttc att caa gga gag tca att aca cct 338
 Phe Xaa Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu Ser Ile Thr Pro
 55 60 65
 acc aag ata cct gan att aca act gab ata tac atg tct aat 380
 Thr Lys Ile Pro Xaa Ile Thr Thr Xaa Ile Tyr Met Ser Asn
 70 75 80

<210> 627
 <211> 370
 <212> DNA
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<220>
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 <222> 182..370

<221> sig_peptide

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<222> 182..259
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 tggtcctcac aatgtccaag tggctgcagt gggtggcatt ggccttgat atcaagggac 120
 agctcacaga catactgcag aagtcctggt ggctgagata ggacggcctc ctggtcctga 180
 a atg gaa tac tgc act gac aga gag tca tac tcc tta gct gct ggc ttg 229
 Met Glu Tyr Cys Thr Asp Arg Glu Ser Tyr Ser Leu Ala Ala Gly Leu
 -25 -20 -15
 gcc ctg ggc atg ctc tgc ttg ggg cat ggc agc aat ttg ata ggt atg 277
 Ala Leu Gly Met Leu Cys Leu Gly His Gly Ser Asn Leu Ile Gly Met
 -10 -5 1 5
 tct gat ctc aat gtg cct gag cag ctc tat cag twc atg gtt gga gga 325
 Ser Asp Leu Asn Val Pro Glu Gln Leu Tyr Gln Xaa Met Val Gly Gly
 10 15 20
 cat agg cgc ttt caa aca gga atg cat agg gag aaa cat aaa tca 370
 His Arg Arg Phe Gln Thr Gly Met His Arg Glu Lys His Lys Ser
 25 30 35

<210> 628
 <211> 347
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 24..347

<221> sig_peptide
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 <223> score 8.5
 seq ALLLLATLAVATG/PA

<400> 628
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 Met Arg Thr Ala Leu Leu Leu Ala Thr
 -15 -10
 ctg gct gtg gct aca ggg cca gcc ctt acc ctg cgc tgc cac gtg tgc 101
 Leu Ala Val Ala Thr Gly Pro Ala Leu Thr Leu Arg Cys His Val Cys
 -5 1 5 10
 acc agc tcc agc aac tgc aag cat tct gtg gtc tgc ccg gcc agc tct 149
 Thr Ser Ser Ser Asn Cys Lys His Ser Val Val Cys Pro Ala Ser Ser
 15 20 25
 cgc ttc tgc aag acc acg aac aca gtg gag cct ctg agg ggg aat ctg 197
 Arg Phe Cys Lys Thr Thr Asn Thr Val Glu Pro Leu Arg Gly Asn Leu
 30 35 40
 gtg aag aag gac tgt gcg gag tgc tgc aca ccc agc tac acc ctg caa 245
 Val Lys Lys Asp Cys Ala Glu Ser Cys Thr Pro Ser Tyr Thr Leu Gln
 45 50 55
 ggc cag gtc agc agc ggc acc agc tcc acc cag tgc tgc cag gag gac 293

Gly	Gln	Val	Ser	Ser	Gly	Thr	Ser	Ser	Thr	Gln	Cys	Cys	Gln	Glu	Asp	
60					65					70						
ctg	tgc	aat	gag	aag	ctg	cac	aac	gct	gca	ccc	acc	cgc	acc	gcc	ctc	341
Leu	Cys	Asn	Glu	Lys	Leu	His	Asn	Ala	Ala	Pro	Thr	Arg	Thr	Ala	Leu	
75					80					85					90	
gcc	caa															347
Ala	Gln															

<210> 629
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 133..288

<221> sig_peptide
 <222> 133..273
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gtaatgcaag	tcccctaact	ccctgggttg	taacattaac	ttccttaagt	aataatcaat											171
gaaagavatt	ct atg cat	ggt ttt	gaa ata	ata tcc	ttg aaa	gag gaa	tca									
	Met His	Gly Phe	Glu Ile	Ile Ser	Leu Lys	Glu Glu	Ser									
		-45		-40		-35										
cca tta	gga aag	gtg agt	cag ggt	cct ttg	ttt aat	gtg act	agt ggc									219
Pro Leu	Gly Lys	Val Ser	Gln Gly	Pro Leu	Phe Asn	Val Thr	Ser Gly									
		-30		-25		-20										
tca tca	tca cca	gtg acc	tgg ttg	ggc cta	ctc tcc	ttc cag	aac ctg									267
Ser Ser	Ser Pro	Val Thr	Trp Leu	Gly Leu	Leu Ser	Phe Gln	Asn Leu									
		-15		-10		-5										
cat tgc	ttc cca	gac ctc	ccc													288
His Cys	Phe Pro	Asp Leu	Pro													
	1		5													

<210> 630
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 31..225

<221> sig_peptide
 <222> 31..126
 <223> score 5.4
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Met Leu Ile Gln Gln Phe Arg Tyr
-25
-30
gac aac tac cga cta cac cag ctg gga aac aat tct gtg ttc acc ctc 102
Asp Asn Tyr Arg Leu His Gln Leu Gly Asn Asn Ser Val Phe Thr Leu
-10
-15
-20
acc ctg cag gcc ggc ctc tca gcc atc aag aca cca cag tgc tac aag 150
Thr Leu Gln Ala Gly Leu Ser Ala Ile Lys Thr Pro Gln Cys Tyr Lys
-5
1
5
gag gac ggc agc tcc aag agc cct gac tgc cct gtg tgc agc cgc tcc 198
Glu Asp Gly Ser Ser Lys Ser Pro Asp Cys Pro Val Cys Ser Arg Ser
10 15 20
ctg aac aag ctg gcg cac ccc tgc cca ta 227
Leu Asn Lys Leu Ala His Pro Cys Pro
25 30

<210> 631
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 183..371
<221> sig_peptide
<222> 183..287
<223> score 3.6
seq ITSLLLLFPAGE/FP

<400> 631
accagagccc cgtgggctgg aacgcgccgg aatctgagga ctgggagttt tcacaccttt 60
gaataagaac tcgacaacag agtgggaact ttctgtcttg tgatccattg cctggtgagt 120
cacagctcac accatggatt taacctgaga gcttcaactt ctgctttggc cctggagttc 180
cc atg ccc tgg tgt ctt cta cca gtt ctt agg ttc tct gtc att ttt 227
Met Pro Trp Cys Leu Leu Pro Val Leu Arg Phe Ser Val Ile Phe
-35 -30 -25
tta ttc ttc ggt gct gtg atc atc aca tca gtt ctg ttg ctt ttc ccg 275
Leu Phe Phe Gly Ala Val Ile Ile Thr Ser Val Leu Leu Leu Phe Pro
-20 -15 -10 -5
cga gct ggt gaa ttc cca gcc cca gaa gtg gaa gtt aag att gtg gat 323
Arg Ala Gly Glu Phe Pro Ala Pro Glu Val Glu Val Lys Ile Val Asp
1 5 10
gac ttt ttc att ggc cgc tat gtc ctg ctg gct ttc ctt agt gcc acc t 372
Asp Phe Phe Ile Gly Arg Tyr Val Leu Leu Ala Phe Leu Ser Ala Thr
15 20 25

<210> 632
<211> 300
<212> DNA
<213> Homo sapiens

<220>
 <221> CDS
 <222> 12..299

<221> sig_peptide
 <222> 12..74
 <223> score 5.8
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 Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe Phe
 -20 -15 -10
 ctt ttg cta gaa gga ggc aaa aca gag caa gta aaa cat tca gag aca 98
 Leu Leu Leu Glu Gly Gly Lys Thr Glu Gln Val Lys His Ser Glu Thr
 -5 1 5
 tat tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg cat 146
 Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His
 10 15 20
 cct tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc tgc 194
 Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys
 25 30 35 40
 tca gag aat ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat gtt 242
 Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn Val
 45 50 55
 cat tgc ctt tct cct gtg cat att cct cat ctg tgc tgc cct cgc tgc 290
 His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys
 60 65 70
 cca gaa gag t 300
 Pro Glu Glu
 75

<210> 633
 <211> 268
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 78..266

<221> sig_peptide
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 <223> score 7
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 ctctcccctc cctttga atg aga gaa act amc ccg ctt ccg aag ccc ctg 110
 Met Arg Glu Thr Xaa Pro Leu Pro Lys Pro Leu
 -40 -35
 aaa gac act gct cct tcc tct cat gga gtt ggc tcc gac agc ccg tct 158

Lys Asp Thr Ala Pro Ser Ser His Gly Val Gly Ser Asp Ser Pro Ser
 -30 -25 -20
 gcc acc agg cca tgg ttc ctt gcc cca tgg tgt cct ggg acc cag agc 206
 Ala Thr Arg Pro Trp Phe Leu Ala Pro Trp Cys Pro Gly Thr Gln Ser
 -15 -10 -5
 aac agg atc tgt cac cca cct ctc tct tct ccc cca gat caa gcg acg 254
 Asn Arg Ile Cys His Pro Pro Leu Ser Ser Pro Pro Asp Gln Ala Thr
 1 5 10 15
 tgc ctc aga ggc tt 268
 Cys Leu Arg Gly
 20

<210> 634
 <211> 381
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 99..380
 <221> sig_peptide
 <222> 99..236
 <223> score 7.8
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 ctaatcccta ctgaattgta gcttggtgtt gtttctga atg gtt ttt gga tat tgg 116
 Met Val Phe Gly Tyr Trp
 -45
 aag cag ccg ctg att acc ctt gca aag aaa tct gta aaa tgt gca cgt 164
 Lys Gln Pro Leu Ile Thr Leu Ala Lys Lys Ser Val Lys Cys Ala Arg
 -40 -35 -30 -25
 gaa tgt ctg aga tgc tct ctc agg cct cta gtc ctt ctg tat ctt tcc 212
 Glu Cys Leu Arg Cys Ser Leu Arg Pro Leu Val Leu Leu Tyr Leu Ser
 -20 -15 -10
 ttt gca gcc ctg ggt gta gta gca ctc agg agt gtt gaa tca ccc ctg 260
 Phe Ala Ala Leu Gly Val Val Ala Leu Arg Ser Val Glu Ser Pro Leu
 -5 1 5
 gcc gag acc cac tcc tgc tgg ctc agc ctg ggc atg tgt gtg ctc cag 308
 Ala Glu Thr His Ser Cys Trp Leu Ser Leu Gly Met Cys Val Leu Gln
 10 15 20
 tgt gaa cag cag tgg gtt cca acc cca gtc tcc ttt ctc tgt ggc ctc 356
 Cys Glu Gln Gln Trp Val Pro Thr Pro Val Ser Phe Leu Cys Gly Leu
 25 30 35 40
 tct ggc tcc agc acc atc atc gtt a 381
 Ser Gly Ser Ser Thr Ile Ile Val
 45

<210> 635
 <211> 254
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 49..252

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<223> score 5.9

seq LLILWFHLDVCSS/IL

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Met Glu Lys
-20

aat cct ttg gca gcc cca tta cta atc ctc tgg ttt cat ctt gac tgc 105
Asn Pro Leu Ala Ala Pro Leu Leu Ile Leu Trp Phe His Leu Asp Cys
-15 -10 -5

gtg agc agc ata ctg aac gtg gaa caa agt cct cag tca ctg cat gtt 153
Val Ser Ser Ile Leu Asn Val Glu Gln Ser Pro Gln Ser Leu His Val
1 5 10

cag gag gga gac agc acc aat ttc acc tgc agc ttc cct tcc agc aat 201
Gln Glu Gly Asp Ser Thr Asn Phe Thr Cys Ser Phe Pro Ser Ser Asn
15 20 25

ttt tat gcc tta cac tgg tac aga tgg gaa act gca aaa agc ccc gag 249
Phe Tyr Ala Leu His Trp Tyr Arg Trp Glu Thr Ala Lys Ser Pro Glu
30 35 40 45

gcc gt 254
Ala

<210> 636

<211> 297

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 22..297

<221> sig_peptide

<222> 22..75

<223> score 5

seq SLSVFGSLPASLG/TW

<400> 636

agtgaggctt ggaaaggcgt c atg gac aga cct ggg tcg ctt tct gtc ttc 51
Met Asp Arg Pro Gly Ser Leu Ser Val Phe
-15 -10

ggg tcc ctc ccg gct tcg ctc ggg acc tgg ctc tca agc cca gct tgg 99
Gly Ser Leu Pro Ala Ser Leu Gly Thr Trp Leu Ser Ser Pro Ala Trp
-5 1 5

ctg gtg gac aga ccg gtg cgc tct gca cac ccg agt gcg aat tcc acc 147

004220"666T560

Leu Val Asp Arg Pro Val Arg Ser Ala His Pro Ser Ala Asn Ser Thr
 10 15 20
 ggc gtg aga atg agc gtg ctc gtg gtc ctg gcc ctg agg tcc ctg ggt 195
 Gly Val Arg Met Ser Val Leu Val Val Leu Ala Leu Arg Ser Leu Gly
 25 30 35 40
 cgc agc tgt tcc ctc tcc cag gct gcc ccc tcc agg tgg acg cgg tca 243
 Arg Ser Cys Ser Leu Ser Gln Ala Ala Pro Ser Arg Trp Thr Arg Ser
 45 50 55
 aac gat gcc ccg cag cct cct ggg tct cag cac ata ttc cac acc tah 291
 Asn Asp Ala Pro Gln Pro Pro Gly Ser Gln His Ile Phe His Thr Xaa
 60 65 70
 gts ccc 297
 Val Pro

<210> 637
 <211> 280
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 72..278
 <221> sig_peptide
 <222> 72..158
 <223> score 4.4
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 gcttttaaagg cctggccagg ggaggagcac agatattttc ctgtataatt ccagaatgtc 60
 ttcagagagc c atg cat gga ttg ctt cat tac ctt ttc cat acg aga aac 110
 Met His Gly Leu Leu His Tyr Leu Phe His Thr Arg Asn
 -25 -20
 cac acc ttc att gtc ctg cac ctg gtc ttg caa ggg atg gtt tat act 158
 His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr Thr
 -15 -10 -5
 gag tac acc tgg gaa gta ttt ggc tac tgt cag gag ctg gag ttg tcc 206
 Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu Ser
 1 5 10 15
 ttg cat tac ctt ctt ctg ccc tat ctg ctg cta ggt gta aac ctg ttt 254
 Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu Phe
 20 25 30
 ttt ttc acc ctg act tgt gga acc aa 280
 Phe Phe Thr Leu Thr Cys Gly Thr
 35 40

<210> 638
 <211> 403
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> 243..401

<221> sig_peptide

<222> 243..380

<223> score 5.2

seq LLTFLVFTXKLSS/LN

<400> 638

cactgaaatc aatctgttca atagcattat accatatttg acataccata gccatgttaa 60
tctgatattg tagaatagca tagtakaata ataataactc ctaactcaag gatgttgwgw 120
kcctttataa ccagcaatcc atgttarata ttagcacagt gcctaaaaca tattaagcat 180
tcaataaatg atcgctacta tttttactaa catcctacag atttggaat tgagtcttag 240
aa atg tta atg tgt aaa atg cta aag agc caa aaa aac tgc cag gaa 287
Met Leu Met Cys Lys Met Leu Lys Ser Gln Lys Asn Cys Gln Glu

-45 -40 -35
aat atr ara att aaa atc att tta ttt ctg aaa ccc atg tgt tcc ccc 335
Asn Xaa Xaa Ile Lys Ile Ile Leu Phe Leu Lys Pro Met Cys Ser Pro
-30 -25 -20
caa tat ctt cta aca ttt cta gta ttt aca gra aaa ctt tca agt ctc 383
Gln Tyr Leu Leu Thr Phe Leu Val Phe Thr Xaa Lys Leu Ser Ser Leu
-15 -10 -5 1
aat atc rga aag ttt cat aa 403
Asn Ile Xaa Lys Phe His
5

<210> 639

<211> 255

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 51..254

<221> sig_peptide

<222> 51..89

<223> score 4.2

seq MTDLLSASPWALT/IV

<400> 639

ccaagtttga gcacctggaa aggggtttatg ctgacatccc ctttctgttg atg acg 56
Met Thr
gac ctc tta agt gcc tca ccc tgg gcc ctc act att gtt tcc agt gag 104
Asp Leu Leu Ser Ala Ser Pro Trp Ala Leu Thr Ile Val Ser Ser Glu
-10 -5 1 5
ctc cac ctt gct cca tcc atg acc aca gtg gac cag ctc gag tct caa 152
Leu His Leu Ala Pro Ser Met Thr Thr Val Asp Gln Leu Glu Ser Gln
10 15 20
gtg gac aat gtc atc tta cag act gga gag agt gct agt gaa tgc ttt 200
Val Asp Asn Val Ile Leu Gln Thr Gly Glu Ser Ala Ser Glu Cys Phe
25 30 35
tgt ctt caa tgc cca tct ctt gga aat att gaa ggt gga gta gca acc 248

Cys Leu Gln Cys Pro Ser Leu Gly Asn Ile Glu Gly Gly Val Ala Thr
 40 45 50

255

ggg cay h
 Gly His
 55

<210> 640
 <211> 325
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 2..325

<221> sig_peptide
 <222> 2..127
 <223> score 5.5
 seq ILGLLFYCFLLCC/FP

<400> 640
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 Met Arg Ile Asp Asn Lys Tyr Phe Tyr Tyr Asn Ser Ala His Thr Tyr
 -40 -35 -30
 ata cta tgt atg cag tgc atc tgc ata gaa cag ttc ctt atc ctt ggc 97
 Ile Leu Cys Met Gln Cys Ile Cys Ile Glu Gln Phe Leu Ile Leu Gly
 -25 -20 -15
 ctt ctg ttt tat tgt ttt ttt ctt tgc tgt ttt ccc ttt gct tct aat 145
 Leu Leu Phe Tyr Cys Phe Phe Leu Cys Cys Phe Pro Phe Ala Ser Asn
 -10 -5 1 5
 att aca gtt ttg tat ttt gta aac aaa aat caa ata atg cat atc aga 193
 Ile Thr Val Leu Tyr Phe Val Asn Lys Asn Gln Ile Met His Ile Arg
 10 15 20
 atc ttt ata tgg aag aaa tcc ttt aht gcc ttt cct ttg ttt cct tgt 241
 Ile Phe Ile Trp Lys Lys Ser Phe Xaa Ala Phe Pro Leu Phe Pro Cys
 25 30 35
 aaa ggc acc htg ttc tgt tat ggt ttt tca tta tat aaa att att ata 289
 Lys Gly Thr Xaa Phe Cys Tyr Gly Phe Ser Leu Tyr Lys Ile Ile Ile
 40 45 50
 tct tat atg aca tat gct aaa att tct tgg aga gtg 325
 Ser Tyr Met Thr Tyr Ala Lys Ile Ser Trp Arg Val
 55 60 65

<210> 641
 <211> 352
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 50..352

<221> sig_peptide

004220"666T560

<222> 50..136
 <223> score 5.7
 seq FIYYLFFLRWSLS/LS

<400> 641
 acagttttgt gaaatccacg atgtatacaa tgagaaaagt aatccttgt atg tta ata 58
 Met Leu Ile
 att gac cca caa act tca act ttt tgt ctt ttt tat tta ttt att tat 106
 Ile Asp Pro Gln Thr Ser Thr Phe Cys Leu Phe Tyr Leu Phe Ile Tyr
 -25 -20 -15
 tat tta ttt ttt ttg aga tgg agt ctc tct ttg tcg ccc agg ctg gag 154
 Tyr Leu Phe Phe Leu Arg Trp Ser Leu Ser Leu Ser Pro Arg Leu Glu
 -10 -5 1 5
 tgc agt ggc aca atc ttg gct cac tgc aag ctc tgc ctc ccg agt tca 202
 Cys Ser Gly Thr Ile Leu Ala His Cys Lys Leu Cys Leu Pro Ser Ser
 10 15 20
 cac cat tct cct acc tca gcc tcc caa gtg gct ggg act aca ggc gcc 250
 His His Ser Pro Thr Ser Ala Ser Gln Val Ala Gly Thr Thr Gly Ala
 25 30 35
 cgc cac cac gcc tgg cta att ttt ttt ttt kgw att ttt agt aga gac 298
 Arg His His Ala Trp Leu Ile Phe Phe Phe Xaa Ile Phe Ser Arg Asp
 40 45 50
 agg gtt tca ccg tgt wag cca gga tgg tct cga tgt cct gac ctc gtr 346
 Arg Val Ser Pro Cys Xaa Pro Gly Trp Ser Arg Cys Pro Asp Leu Val
 55 60 65 70
 atc ccc
 Ile Pro 352

<210> 642
 <211> 267
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 14..265

<221> sig_peptide
 <222> 14..136
 <223> score 5.6
 seq LFLFLTSIAEXCS/TP

<400> 642
 ccctgtkctt ktc atg gtt dtc tgg ctc gtc tta ttt gct ctt cag att 49
 Met Val Xaa Trp Leu Val Leu Phe Ala Leu Gln Ile
 -40 -35 -30
 tac tcc tat kky agt act cga gat cag cct gca tca cgt gak agg ctt 97
 Tyr Ser Tyr Xaa Ser Thr Arg Asp Gln Pro Ala Ser Arg Xaa Arg Leu
 -25 -20 -15
 ctt ttc ctt ttt ctg aca agt att gcg gaa ttc tgc agc act cct tac 145
 Leu Phe Leu Phe Leu Thr Ser Ile Ala Glu Xaa Cys Ser Thr Pro Tyr
 -10 -5 1

004220"66ET560

tct ctt ttg ggt ttk gtc ttc acg gtt tct ttt gtt gcc ttg ggt gtt	193
Ser Leu Leu Gly Xaa Val Phe Thr Val Ser Phe Val Ala Leu Gly Val	
5 10 15	
ctc aca ctc tgc aag ttt tac ttg cag ggt tat cga gct ttc atg aat	241
Leu Thr Leu Cys Lys Phe Tyr Leu Gln Gly Tyr Arg Ala Phe Met Asn	
20 25 30 35	
gat cct gcc atg aat cgg gga ggt gc	267
Asp Pro Ala Met Asn Arg Gly Gly	
40	

<210> 643
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 65..241

<221> sig_peptide
 <222> 65..148
 <223> score 6.1
 seq LYLFSGFWTFXLG/KF

<400> 643	
cacttgartt ggggttaagt tgaagaacag acaaacttag acacaaagct atgcaaaaat	60
tgtg atg aac aag gaa raa gta agt ttn gaa agg ara gca cag gtc aga	109
Met Asn Lys Glu Xaa Val Ser Xaa Glu Arg Xaa Ala Gln Val Arg	
-25 -20 -15	
tta tat tta ttc tca gga ttt tgg act ttt kta tta ggg aaa ttt aaa	157
Leu Tyr Leu Phe Ser Gly Phe Trp Thr Phe Xaa Leu Gly Lys Phe Lys	
-10 -5 1	
caa ggg gaa tgr tct tat atk kgt att cta gaa aga tta ctg tgg cag	205
Gln Gly Glu Xaa Ser Tyr Xaa Xaa Ile Leu Glu Arg Leu Leu Trp Gln	
5 10 15	
cag cag tat gwa gga tgg ctt gta ggr gat aag aga	241
Gln Gln Tyr Xaa Gly Trp Leu Val Gly Asp Lys Arg	
20 25 30	

<210> 644
 <211> 234
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 74..232

<221> sig_peptide
 <222> 74..196
 <223> score 7.7
 seq LLCLGQLHHPGLG/RV

<400> 644
aagtttggtc cccgagttcg gaggcttagga gcccccgcg gctgcggcgc aggtgccctc 60
ggccttagtc ggg atg gag ctg cct gck gtg aac ctt gaa agt gat tct 109
Met Glu Leu Pro Ala Val Asn Leu Glu Ser Asp Ser
-40 -35 -30
cct agg tca ctg gct gct gac aac ctg ggg ctg cat tgt att ctc agg 157
Pro Arg Ser Leu Ala Ala Asp Asn Leu Gly Leu His Cys Ile Leu Arg
-25 -20 -15
ctc cta tgc ctg ggc caa ctt cac cat cct ggc ctt ggg cgt gtg ggc 205
Leu Leu Cys Leu Gly Gln Leu His His Pro Gly Leu Gly Arg Val Gly
-10 -5 1
tgt ggc tca gcg gga ctc cat cga cgc cg 234
Cys Gly Ser Ala Gly Leu His Arg Arg
5 10

<210> 645
<211> 253
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..252

<221> sig_peptide
<222> 40..111
<223> score 4.4
seq FVFLFWGVFETRS/LS

<400> 645
acttggttctt ttacttaac atgtcttgaa catctttgt atg aca gta cat ata 54
Met Thr Val His Ile
-20
gaa cta cct ctt ctt tgt ttt gtt ttt ttg ttt tgg ggg gtt ttt gag 102
Glu Leu Pro Leu Leu Cys Phe Val Phe Leu Phe Trp Gly Val Phe Glu
-15 -10 -5
aca cgg tct ctc tcc ctg tca ccc agg ctg gar tks aag ttg gta gaa 150
Thr Arg Ser Leu Ser Leu Ser Pro Arg Leu Glu Xaa Lys Leu Val Glu
1 5 10
ktc atg mct cac tgt agc atc aaa ctc ctg ggc tca agc gac cct ccc 198
Xaa Met Xaa His Cys Ser Ile Lys Leu Leu Gly Ser Ser Asp Pro Pro
15 20 25
gcc tca gcc ttc ttg gta gct ggt act aca ggc aca tgc cac gac acc 246
Ala Ser Ala Phe Leu Val Ala Gly Thr Thr Gly Thr Cys His Asp Thr
30 35 40 45
cag ccc a 253
Gln Pro

<210> 646
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..167

<221> sig_peptide
<222> 6..131
<223> score 4.6
seq LLTCLCLHLKCVS/YR

<400> 646
tggga atg ggg aat act aaa atg aaa aga tat cct gac tcc caa agt gct 50
Met Gly Asn Thr Lys Met Lys Arg Tyr Pro Asp Ser Gln Ser Ala
-40 -35 -30
ggg att aca ggt gtg agc cac cgt gcc cgg cca ttc cat tta ctt ttg 98
Gly Ile Thr Gly Val Ser His Arg Ala Arg Pro Phe His Leu Leu Leu
-25 -20 -15
acc tgt ttg tgt ctt cac tta aag tgt gtt tct tac aga cac ctt gtg 146
Thr Cys Leu Cys Leu His Leu Lys Cys Val Ser Tyr Arg His Leu Val
-10 -5 1 5
ttt act ttt cta tcc gtg cta at 169
Phe Thr Phe Leu Ser Val Leu
10

<210> 647
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 49..282

<221> sig_peptide
<222> 49..126
<223> score 3.7
seq RLLEARSSRPAAW/XT

<400> 647
cattatitttg ctattcaaag acatttatat ggccaggtgt ggtggctt atg cct gta 57
Met Pro Val
-25
atc cta gca ctt tgg gag gcc aag gtg ggc aga ttg ctt gag gcc agg 105
Ile Leu Ala Leu Trp Glu Ala Lys Val Gly Arg Leu Leu Glu Ala Arg
-20 -15 -10
agt tcg aga cca gcc tgg gca awh acg gtg ars ccc caa ttt tca adt 153
Ser Ser Arg Pro Ala Trp Ala Xaa Thr Val Xaa Pro Gln Phe Ser Xaa
-5 1 5
kat tdm aaa aas ata vha ata aaa gaa ata tat tta gaa aan maa aaa 201
Xaa Xaa Lys Xaa Ile Xaa Ile Lys Glu Ile Tyr Leu Glu Xaa Xaa Lys
10 15 20 25
gva ata tat tca ggc cgg gca cgg tgg ctc atg cct gta atc cca aca 249

004220" 656ET 560

Xaa Ile Tyr Ser Gly Arg Ala Arg Trp Leu Met Pro Val Ile Pro Thr
30 35 40
ctg gga cgc caa ggc ggg agg atc gcc tgm ggt ca
Leu Gly Arg Gln Gly Gly Arg Ile Ala Xaa Gly
45 50

284

<210> 648
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 159..440

<221> sig_peptide
<222> 159..221
<223> score 5.3
seq ALTLVLLIKESGA/WS

<400> 648
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tgataccac ctgagagatc ctgtgtttga acaactgctd cccaaaacgg aaagtatttt 120
caagcctaaa cctttgggtg aaaagaactc ttgaagtc atg att gct tca cag ttt 176
Met Ile Ala Ser Gln Phe
-20
ctc tca gct ctc act ttg gtg ctt ctc att aaa gag agt gga gcc tgg 224
Leu Ser Ala Leu Thr Leu Val Leu Leu Ile Lys Glu Ser Gly Ala Trp 1
-15 -10 -5
tct tac aac acc tcc acg gaa gct atg act tat gat gag gcc agt gct 272
Ser Tyr Asn Thr Ser Thr Glu Ala Met Thr Tyr Asp Glu Ala Ser Ala 15
5 10
tat tgt cag caa agg tac aca cac ctg gtt gca att caa aac aaa gaa 320
Tyr Cys Gln Gln Arg Tyr Thr His Leu Val Ala Ile Gln Asn Lys Glu 30
20 25
gag att gag tac cta aac tcc ata ttg aag cta ttc abc aag tta tta 368
Glu Ile Glu Tyr Leu Asn Ser Ile Leu Lys Leu Phe Xaa Lys Leu Leu 45
35 40
ctg gat tgg aat cag aaa agt caa caa tgt gtg ggt ctg ggt agg aam 416
Leu Asp Trp Asn Gln Lys Ser Gln Gln Cys Val Gly Leu Gly Arg Xaa 60 65
50
cca gaa acc tct gac aga aga agc c
Pro Glu Thr Ser Asp Arg Arg Ser 70

<210> 649
<211> 341
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..339

<221> sig_peptide
 <222> 133..246
 <223> score 8.2
 seq LLLIFLSFPYTLC/IL

<400> 649
 gcctttcact tgcacaaaca ctgttattat gatcacttat ccaactgaca tttttcagac 60
 cttttaactt caactgttct tttttcctgt aaatcttaat tttctttttt tttctccaa 120
 tttttctcct ac atg tct gga ctc ttc cca gtt cct gtc aga gta aat gtt 171
 Met Ser Gly Leu Phe Pro Val Pro Val Arg Val Asn Val
 -35 -30
 gat att gcc cag aac ata act tgc tct tcc ttt tct ctc ctt ctc att 219
 Asp Ile Ala Gln Asn Ile Thr Cys Ser Ser Phe Ser Leu Leu Leu Ile
 -25 -20 -15 -10
 ttt ctt tct ttc ccc tac acc ctc tgt ata ctc tat aga gta aaa tca 267
 Phe Leu Ser Phe Pro Tyr Thr Leu Cys Ile Leu Tyr Arg Val Lys Ser
 -5 1 5
 tat aca ccc acg gag tca ata act gcc ttt aat cta aca att ggg wga 315
 Tyr Thr Pro Thr Glu Ser Ile Thr Ala Phe Asn Leu Thr Ile Gly Xaa
 10 15 20
 ttc cca tat ctt taw wtt tcw acc cc 341
 Phe Pro Tyr Leu Xaa Xaa Ser Thr
 25 30

<210> 650
 <211> 220
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 22..219

<221> sig_peptide
 <222> 22..60
 <223> score 5.7
 seq MIVLLVMLGDILA/GL

<400> 650
 taaagttgta ttttactga a atg att gtt ttg ctg gtt atg ctt ggt gat 51
 Met Ile Val Leu Leu Val Met Leu Gly Asp
 -10 -5
 att tta gcg ggc tta ttt ttg aaa ggc atc tgt tac ttc agt ggc ata 99
 Ile Leu Ala Gly Leu Phe Leu Lys Gly Ile Cys Tyr Phe Ser Gly Ile
 1 5 10
 aag tgc cct cac act gct gtg agc cat cam cmm cat ttc atc tcm aga 147
 Lys Cys Pro His Thr Ala Val Ser His Xaa Xaa His Phe Ile Ser Arg
 15 20 25
 att kgt tct cag tcc caa act gaa act ata cca ttc aaa caa cag cgc 195
 Ile Xaa Ser Gln Ser Gln Thr Glu Thr Ile Pro Phe Lys Gln Gln Arg
 30 35 40 45

tcc cca ttt ccc cct ccc ccg aag c
 Ser Pro Phe Pro Pro Pro Pro Lys
 50

220

<210> 651
 <211> 268
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 80..268

<221> sig_peptide
 <222> 80..136
 <223> score 7.4
 seq LGFLXXSLESTLS/IX

<400> 651
 aatctctatt tccaagacct ttggccagtc ctattgatct ggactcctgg ataggcagct 60
 ggaccaacgg acggacgcc atg agg gct ctg ctg ctc ctg ggg ttc ctg mtr 112
 Met Arg Ala Leu Leu Leu Leu Gly Phe Leu Xaa
 -15 -10
 rtg agc ttg gag tca aca ctt tgc att cma cct tgg gaa gcc ccc aag 160
 Xaa Ser Leu Glu Ser Thr Leu Ser Ile Xaa Pro Trp Glu Ala Pro Lys
 -5 1 5
 gag cat aag tac aaa gct gaa gag cac aca gtc gtt ctc act gtc acc 208
 Glu His Lys Tyr Lys Ala Glu Glu His Thr Val Val Leu Thr Val Thr
 10 15 20
 ggg gag ccc tgc cac ttc ccc ttc cag tac cac cgg cag ctg tac cac 256
 Gly Glu Pro Cys His Phe Pro Phe Gln Tyr His Arg Gln Leu Tyr His
 25 30 35 40
 aaa tgt acc cac 268
 Lys Cys Thr His

<210> 652
 <211> 354
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 143..352

<221> sig_peptide
 <222> 143..226
 <223> score 4.5
 seq LRWSLTLLPRLEC/GF

<400> 652
 cagttacatg ttttttgttt tgagacaggg ttttgctctg tgccccaggg tggcttgca 60
 tgatgcgatc gtggctcact gcagcctcga cctcccatgc tcaagcgatc ctcccatctc 120

agcctcttga gtagctggga cc atg gca tgc acg tca tgc ctg gct gat tta 172
Met Ala Cys Thr Ser Cys Leu Ala Asp Leu
-25 -20
aaa aaa att ttt ttt ttg aga tgg agt ctc act ctg ttg ccc agg ctg 220
Lys Lys Ile Phe Phe Leu Arg Trp Ser Leu Thr Leu Leu Pro Arg Leu
-15 -10 -5
gaa tgc ggt ttc atg atc ttg gcc tac ttg caa cct mcg cht gct ggg 268
Glu Cys Gly Phe Met Ile Leu Ala Tyr Leu Gln Pro Xaa Xaa Ala Gly
1 5 10
ttc aag caa ttc ttc tgc ctc agc ctc ccg agt agc tgg gat tam agg 316
Phe Lys Gln Phe Phe Cys Leu Ser Leu Pro Ser Ser Trp Asp Xaa Arg
15 20 25 30
cgt ggc cca gct aat ttt bgd att ttt agt aga gac ag 354
Arg Gly Pro Ala Asn Phe Xaa Ile Phe Ser Arg Asp
35 40

<210> 653
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..282

<400> 653
tctttgcgtc tgcgtagttc gctcacctcc ctttctaact ccgctgccgc c atg gct 57
Met Ala
1
cct gtg aaa aag ctt gtg gtg aag ggg ggc aaa aaa aag aag caa gtt 105
Pro Val Lys Lys Leu Val Val Lys Gly Gly Lys Lys Lys Lys Gln Val
5 10 15
ctg aag ttc act ctt gat tgc acc cac cct gta gaa gat gga atc atg 153
Leu Lys Phe Thr Leu Asp Cys Thr His Pro Val Glu Asp Gly Ile Met
20 25 30
gat gct gcc aat ttt gag cag ttt ttg caa gaa agg atc aaa gtg aac 201
Asp Ala Ala Asn Phe Glu Gln Phe Leu Gln Glu Arg Ile Lys Val Asn
35 40 45 50
gga aaa gct ggg aac ctt ggt gga ggg gtg gtg acc atc gaa agg agc 249
Gly Lys Ala Gly Asn Leu Gly Gly Gly Val Val Thr Ile Glu Arg Ser
55 60 65
aag agc aag atc acc tcc tcc acc atc tcc cca gc 284
Lys Ser Lys Ile Thr Ser Ser Thr Ile Ser Pro
70 75

<210> 654
<211> 466
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 281..466

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<400> 654
agggagcgat ctccgagcga ggcggcaaga tggacgcggg atttttccgc ggaacaagtg      60
cagaacagga taatcggttc agcaacaaac agaagaaact actgaagcag ctgaaatttg      120
cagaatgcct wgraaamaaa ggtgrmcatg argcamagta annttggmgg ttataaagcc      180
ttggataaca aaaagagtaa cggaaatcct tgggtttgaa gatgatgttg tgattgagtt      240
tatattcaac cagctggaag tgaagaatcc agactccaaa atg atg caa atc aan      295
                                     Met Met Gln Ile Xaa
                                     1           5

nng act gga ttt ttg aat gga aaa aat gct cga gaa ttt atg gga gaa      343
Xaa Thr Gly Phe Leu Asn Gly Lys Asn Ala Arg Glu Phe Met Gly Glu
                                     10           15           20

ctg tgg ccc ctg ctg cta agt gca caa gaa aac atc gcg gga atc cct      391
Leu Trp Pro Leu Leu Leu Ser Ala Gln Glu Asn Ile Ala Gly Ile Pro
                                     25           30           35

tct gct ttc cta gaa ctg aag aaa gaa gam ata aaa caa aga cag att      439
Ser Ala Phe Leu Glu Leu Lys Lys Glu Xaa Ile Lys Gln Arg Gln Ile
                                     40           45           50

gaa caa gaa aaa ctg gca tct atg aaa      466
Glu Gln Glu Lys Leu Ala Ser Met Lys
                                     55           60

<210> 655
<211> 482
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..482

<400> 655
ctttttacag ctagacctgt gtgctgcaag gagctaaggc cttcagtgtc cccttcctta      60
cccaggtttc tcacaga atg gat tcc cag cgg gaa ctt gca gag gaa ctg      110
                                     Met Asp Ser Gln Arg Glu Leu Ala Glu Glu Leu
                                     1           5           10

cgg ctt tac caa tcc acc ctt ctt cag gat ggt cta aaa gat ctc ctg      158
Arg Leu Tyr Gln Ser Thr Leu Leu Gln Asp Gly Leu Lys Asp Leu Leu
                                     15           20           25

gat gag aaa aaa ttc atc gat tgc acc cta aaa gca ggt gac aaa agt      206
Asp Glu Lys Lys Phe Ile Asp Cys Thr Leu Lys Ala Gly Asp Lys Ser
                                     30           35           40

ctt cct tgc cac aga ttg att ttg tca gct tgt agt cct tac ttc cgt      254
Leu Pro Cys His Arg Leu Ile Leu Ser Ala Cys Ser Pro Tyr Phe Arg
                                     45           50           55

gag tac ttt tta tct gaa att gat gag gcg aaa aaa aag gag gta gtg      302
Glu Tyr Phe Leu Ser Glu Ile Asp Glu Ala Lys Lys Lys Glu Val Val
                                     60           65           70           75

cta gac aat gtg gat cct gct ata ctt gat tta atc atc aaa tac ctg      350
Leu Asp Asn Val Asp Pro Ala Ile Leu Asp Leu Ile Ile Lys Tyr Leu
                                     80           85           90

tac tct gcc agt att gat ctc aat gac gga aat gtg caa gat att ttt      398

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Tyr Ser Ala Ser Ile Asp Leu Asn Asp Gly Asn Val Gln Asp Ile Phe
 95 100 105
 gca ttg gcc agc cgc ttt cag atc ccc tca gtg ttt act gtc tgc gtt 446
 Ala Leu Ala Ser Arg Phe Gln Ile Pro Ser Val Phe Thr Val Cys Val
 110 115 120
 tct tat ctt cag aaa aga ctt gct cct ggt aac tgt 482
 Ser Tyr Leu Gln Lys Arg Leu Ala Pro Gly Asn Cys
 125 130 135

<210> 656
 <211> 788
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 126..788

<400> 656
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 atagatacta tggtgaagaa gatgtcagca taaaaaaaag tggtaggaaa actctaaaac 120
 ctcga atg tca gta agt gct gat gaa aga ggt ggt tta gag aat atg agg 170
 Met Ser Val Ser Ala Asp Glu Arg Gly Gly Leu Glu Asn Met Arg
 1 5 10 15
 ccc cct aac aac agc agt cca gta caa gag gat gct gaa aat gca tct 218
 Pro Pro Asn Asn Ser Ser Pro Val Gln Glu Asp Ala Glu Asn Ala Ser
 20 25 30
 tgt gag ctg tgt gga ctt aca ata acc gag gag gac ctg tca tct cat 266
 Cys Glu Leu Cys Gly Leu Thr Ile Thr Glu Glu Asp Leu Ser Ser His
 35 40 45
 tac tta gcc aaa cac att gaa aat atc tgt gca tgt ggt aaa tgt gga 314
 Tyr Leu Ala Lys His Ile Glu Asn Ile Cys Ala Cys Gly Lys Cys Gly
 50 55 60
 caa ata ctt gta aag ggt agg cag ctt cag gaa cat gct caa cra tgt 362
 Gln Ile Leu Val Lys Gly Arg Gln Leu Gln Glu His Ala Gln Xaa Cys
 65 70 75
 ggc gag ccc caa gat ctg acc atg aat ggg tta gga aat act gag gag 410
 Gly Glu Pro Gln Asp Leu Thr Met Asn Gly Leu Gly Asn Thr Glu Glu
 80 85 90 95
 aaa atg gac ttg gaa gag aat cct gat gag cag tcc gaa ata aga gat 458
 Lys Met Asp Leu Glu Glu Asn Pro Asp Glu Gln Ser Glu Ile Arg Asp
 100 105 110
 atg ttt gtt gaa atg ctg gat gat ttt agg gac aat cat tac cag ata 506
 Met Phe Val Glu Met Leu Asp Asp Phe Arg Asp Asn His Tyr Gln Ile
 115 120 125
 aac agt atc caa aaa aag cag tta ttt aaa cat tct gcc tgc cct ttt 554
 Asn Ser Ile Gln Lys Lys Gln Leu Phe Lys His Ser Ala Cys Pro Phe
 130 135 140
 cga tgt cct aat tgt ggc cag cgt ttt gaa act gaa aat cta gtg gtt 602
 Arg Cys Pro Asn Cys Gly Gln Arg Phe Glu Thr Glu Asn Leu Val Val
 145 150 155
 gaa cat atg tct agc tgc tta gat caa gat atg ttt aag agt gcc atc 650
 Glu His Met Ser Ser Cys Leu Asp Gln Asp Met Phe Lys Ser Ala Ile

160		165		170		175	
atg gaa gaa aat gaa aga gat cac aga cga aag cat ttt tgt aat ctg							698
Met Glu Glu Asn Glu Arg Asp His Arg Arg Lys His Phe Cys Asn Leu							
	180		185		190		
tgt gga aaa gga ttt tat cag cgg tgt cac tta aga gaa cac tat act							746
Cys Gly Lys Gly Phe Tyr Gln Arg Cys His Leu Arg Glu His Tyr Thr							
	195		200		205		
gtt cat act aag gaa aaa cag ttt gtt tgt caa aca tgt gga							788
Val His Thr Lys Glu Lys Gln Phe Val Cys Gln Thr Cys Gly							
	210		215		220		

<210> 657
 <211> 348
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 35..346

<400> 657	
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	Met Glu Pro Gln Glu Arg
	1 5
gaa acg cag gtt gct gcg tgg tta aaa aaa ata ttt gga gat cat cct	103
Glu Thr Gln Val Ala Ala Trp Leu Lys Lys Ile Phe Gly Asp His Pro	
	10 15 20
att cca cag tat gag gtg aac cca cgg acc aca gag att tta cat cac	151
Ile Pro Gln Tyr Glu Val Asn Pro Arg Thr Thr Glu Ile Leu His His	
	25 30 35
ctt tca gaa cgc aac agg gtc cgg gac agg gat gtc tac ctg gta ata	199
Leu Ser Glu Arg Asn Arg Val Arg Asp Arg Val Tyr Leu Val Ile	
	40 45 50 55
gag gac ttg aag cag aaa gca agt gaa tac gag tca gaa gcc aag tat	247
Glu Asp Leu Lys Gln Lys Ala Ser Glu Tyr Glu Ser Glu Ala Lys Tyr	
	60 65 70
ctt caa gac ctt ctc atg gag agt gtg aat ttt tcc ccc gcc aat ctc	295
Leu Gln Asp Leu Leu Met Glu Ser Val Asn Phe Ser Pro Ala Asn Leu	
	75 80 85
tct agc act ggt tcc agg tat ctg aat gct ttg gtt gac agt gcg gtg	343
Ser Ser Thr Gly Ser Arg Tyr Leu Asn Ala Leu Val Asp Ser Ala Val	
	90 95 100
gcc tt	348
Ala	

<210> 658
 <211> 285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 67..285

<400> 658
 acagccagag ctgggcggtg gcgggcgctg ctgaaggagt ctcgctgagc tcgaggaggt 60
 ggcgcg atg gag gga ctg gaa gag aat gga ggt gtt gtc caa gtt gga 108
 Met Glu Gly Leu Glu Glu Asn Gly Gly Val Val Gln Val Gly
 1 5 10
 gaa ttg tta cct tgc aag att tgt gga aga aca ttc ttt cca gta gca 156
 Glu Leu Leu Pro Cys Lys Ile Cys Gly Arg Thr Phe Phe Pro Val Ala
 15 20 25 30
 tta aaa aaa cat gga ccc att tgc cag aag act gca act aaa aaa cgg 204
 Leu Lys Lys His Gly Pro Ile Cys Gln Lys Thr Ala Thr Lys Lys Arg
 35 40 45
 aag act ttt gat tca agc aga cag aga gct gaa gga act gat att cca 252
 Lys Thr Phe Asp Ser Ser Arg Gln Arg Ala Glu Gly Thr Asp Ile Pro
 50 55 60
 aca gta aaa cct ctc aaa ccg agg cca gaa cca 285
 Thr Val Lys Pro Leu Lys Pro Arg Pro Glu Pro
 65 70

 <210> 659
 <211> 420
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 148..420

 <400> 659
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 atagtcacatc tccagagtct tcctccacaa actgggattc atccccgctg aaaaagcaca 120
 atctaacagc aagggaacaa aaaaacc atg cta tca cat aat act atg atg aag 174
 Met Leu Ser His Asn Thr Met Met Lys
 1 5
 cag aga aaa cag caa gca aca gcc atc atg aag gaa gtc cat gga aat 222
 Gln Arg Lys Gln Gln Ala Thr Ala Ile Met Lys Glu Val His Gly Asn
 10 15 20 25
 gat gtt gat ggc atg gac ctg ggc aaa aag gtc agc atc ccc aga gac 270
 Asp Val Asp Gly Met Asp Leu Gly Lys Lys Val Ser Ile Pro Arg Asp
 30 35 40
 atc atg ttg gaa gaa tta tcc cat ctc agt aac cgt ggt gcc agg cta 318
 Ile Met Leu Glu Glu Leu Ser His Leu Ser Asn Arg Gly Ala Arg Leu
 45 50 55
 ttt aag atg cgt caa aga aga tct gac aaa tac aca ttt gaa aat ttc 366
 Phe Lys Met Arg Gln Arg Arg Ser Asp Lys Tyr Thr Phe Glu Asn Phe
 60 65 70
 cag tat caa tct aga gca caa ata aat cac agt att gct atg cag aat 414
 Gln Tyr Gln Ser Arg Ala Gln Ile Asn His Ser Ile Ala Met Gln Asn
 75 80 85
 ggg aag 420
 Gly Lys
 90

<210> 660
 <211> 468
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 267..467

<400> 660
 gctgggacgt agtgagtgtg atggccgccg cgaggccggg aaggtgaagt caggactggg 60
 ggagtcaaca cagtcaatca atagccaacc tcaacctgag acaggacaga agagaactca 120
 gaatcttttt gtcttttggg cttcagccat gtccatgatg cctaccctgt gaagatctct 180
 caccatccaa aaaattgtgc cagcagacga tccgtggatc catTTtattt tccctgctag 240
 gagttgctgt acataacact ggcgca atg tcc ctg ctc ttc act cga tgc aac 293
 Met Ser Leu Leu Phe Thr Arg Cys Asn
 1 5
 tct atc gtc aca gtc aag aaa aat aag aga cac atn kct gag gtg aat 341
 Ser Ile Val Thr Val Lys Lys Asn Lys Arg His Xaa Xaa Glu Val Asn
 10 15 20 25
 gca tcc cca ctn aag cac ttt gtc act gcc aag aag aag atc aat ggc 389
 Ala Ser Pro Leu Lys His Phe Val Thr Ala Lys Lys Lys Ile Asn Gly
 30 35 40
 att ttt gag cag ctg ggg gcc tac atc cag gag agc gcc acc ttc ctt 437
 Ile Phe Glu Gln Leu Gly Ala Tyr Ile Gln Glu Ser Ala Thr Phe Leu
 45 50 55
 gaa gac acg tac agg aat gca gaa ctg gac c 468
 Glu Asp Thr Tyr Arg Asn Ala Glu Leu Asp
 60 65

<210> 661
 <211> 544
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 321..542

<400> 661
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 cccctgagtg acagaaccgt ggacagcaac atttcccaca ggacacgaag tttgtcggcc 120
 cttgccttgg cagagctgag taagaaaaat caccaagaat attatttttg gtatttggaa 180
 ttgaatttgc caggaatgca agcactgcta cctaactaaa gaccttggct ttggaaacat 240
 cttacccctt ggcagctctc cagagtttag acttggcagc atcaaagaca caacgcaagc 300
 aggcattttg gagatcaaag atg ggt aga aaa gat gct gyt act ata aaa ctt 353
 Met Gly Arg Lys Asp Ala Xaa Thr Ile Lys Leu
 1 5 10
 cct gtt gat cag tac aga aaa caa att ggt aaa cag gat tat aaa aaa 401
 Pro Val Asp Gln Tyr Arg Lys Gln Ile Gly Lys Gln Asp Tyr Lys Lys
 15 20 25

act aaa cct att tta cga gca acc aaa tta aaa gca gaa gca aag aaa 449
 Thr Lys Pro Ile Leu Arg Ala Thr Lys Leu Lys Ala Glu Ala Lys Lys
 30 35 40
 aca gca ata ggc ata aag ttg gcc ttg tac ttg cag cta tat tgg cac 497
 Thr Ala Ile Gly Ile Lys Leu Ala Leu Tyr Leu Gln Leu Tyr Trp His
 45 50 55
 tac tac tgg ctt tct atg ctt tcw nwt atc tca gac tca cca cgg at 544
 Tyr Tyr Trp Leu Ser Met Leu Ser Xaa Ile Ser Asp Ser Pro Arg
 60 65 70

<210> 662
 <211> 386
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 159..386

<400> 662
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 cccctgagtg acagaaccgt ggacagcaac atttcccaca ggacacgaag tttgtcggcc 120
 cttgccttgg cagagctgag gcatttttga gatcaaaw atg ggt aga aaa gat gct 176
 Met Gly Arg Lys Asp Ala
 1 5
 gct act ata aaa ctt ccw rtt gat cag tac aga aaa caa att ggt aaa 224
 Ala Thr Ile Lys Leu Pro Xaa Asp Gln Tyr Arg Lys Gln Ile Gly Lys
 10 15 20
 cag gat tat aaa aaa act aaa cct att tta cga gca acc aaa tta aaa 272
 Gln Asp Tyr Lys Lys Thr Lys Pro Ile Leu Arg Ala Thr Lys Leu Lys
 25 30 35
 gca gaa gca aag aaa aca gca ata ggc ata aag gaa gtt ggc ctt gta 320
 Ala Glu Ala Lys Lys Thr Ala Ile Gly Ile Lys Glu Val Gly Leu Val
 40 45 50
 ctt gca gct ata ttg gca cta cta ctg gct ttc tat gct ttc wnw tat 368
 Leu Ala Ala Ile Leu Ala Leu Leu Leu Ala Phe Tyr Ala Phe Xaa Tyr
 55 60 65 70
 ctc aga ctc acc acg gat 386
 Leu Arg Leu Thr Thr Asp
 75

<210> 663
 <211> 482
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 136..480

<400> 663
 gtgtgtcact tccggcctcc ctttagctgc catcttgcgt cccgcgtgt gtgcgcctaa 60

tctcaggtgg tccacccgag accccttgag caccaaccct agtccccgc gcggccctt	120
attcgctccg acaag atg aaa gaa aca atc atg aac cag gaa aaa ctc gcc	171
Met Lys Glu Thr Ile Met Asn Gln Glu Lys Leu Ala	
1 5 10	
aaa ctg cag gca caa gtg cgc att ggt ggg aaa gga act gct cgc aga	219
Lys Leu Gln Ala Gln Val Arg Ile Gly Gly Lys Gly Thr Ala Arg Arg	
15 20 25	
aag aag aag gtg gtt cat aga aca gcc aca gca gat gac aaa aaa ctt	267
Lys Lys Lys Val Val His Arg Thr Ala Thr Ala Asp Asp Lys Lys Leu	
30 35 40	
cag ttc tcc tta aag aag tta ggg gta aac aat atc tct ggt att gaa	315
Gln Phe Ser Leu Lys Lys Leu Gly Val Asn Asn Ile Ser Gly Ile Glu	
45 50 55 60	
gag gtg aat atg ttt aca aac caa gga aca gtg atc cac ttt aac aac	363
Glu Val Asn Met Phe Thr Asn Gln Gly Thr Val Ile His Phe Asn Asn	
65 70 75	
cct aaa gtt cag gca tct ctg gca gcg aac act ttc acc att aca ggc	411
Pro Lys Val Gln Ala Ser Leu Ala Ala Asn Thr Phe Thr Ile Thr Gly	
80 85 90	
cat gct gag aca aag cag ctg aca gaa atg cta ccc agc atc tta aac	459
His Ala Glu Thr Lys Gln Leu Thr Glu Met Leu Pro Ser Ile Leu Asn	
95 100 105	
cag ctt ggt gcg gat agt ctg ac	482
Gln Leu Gly Ala Asp Ser Leu	
110 115	
<210> 664	
<211> 426	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> 60..425	
<400> 664	
aagaaagcag gcgagcctgg gccggcgcgg ggccttggtg gagggcttaa ggaagtaaa	59
atg gcg gac ctg gcg aac gaa gaa aag cct gcc att gct ccg ccc gtc	107
Met Ala Asp Leu Ala Asn Glu Glu Lys Pro Ala Ile Ala Pro Pro Val	
1 5 10 15	
ttt gtg ttt cag aag gat aaa gga caa aag agg tca gct ggc ggc tcc	155
Phe Val Phe Gln Lys Asp Lys Gly Gln Lys Arg Ser Ala Gly Gly Ser	
20 25 30	
agt cct gaa ggc gga gaa gat tct gac aga gaa gat gga aat tac tgc	203
Ser Pro Glu Gly Gly Glu Asp Ser Asp Arg Glu Asp Gly Asn Tyr Cys	
35 40 45	
cct cct gtc aag cga gaa aga aca tcc tct tta acc cag ttc cca ccc	251
Pro Pro Val Lys Arg Glu Arg Thr Ser Ser Leu Thr Gln Phe Pro Pro	
50 55 60	
tca cag tca gag gaa agg agc agt ggc ttc cgg ttg aag cca cca acg	299
Ser Gln Ser Glu Glu Arg Ser Ser Gly Phe Arg Leu Lys Pro Pro Thr	
65 70 75 80	
ctg atc cac ggc caa scc ccc agc gca ggt ctg cca agc cag aag ccc	347

Leu Ile His Gly Gln Xaa Pro Ser Ala Gly Leu Pro Ser Gln Lys Pro
85 90 95
aag gag cag cag cgg acg kgg ctt cgc ccg gca gtg tta caa gct ccg 395
Lys Glu Gln Gln Arg Thr Xaa Leu Arg Pro Ala Val Leu Gln Ala Pro
100 105 110
cag cca aag gcg ctg tcc cag amt gtc ccc a 426
Gln Pro Lys Ala Leu Ser Gln Xaa Val Pro
115 120

<210> 665
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 177..359

<400> 665
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ggtctcgctg ggggccgctc gggaccaatt ttgaagaggt acttggccac gacttatttt 120
cacctccgac ctttccttcc aggcgggtgag actctggact gagagtggct ttcaca atg 179
Met
1
gaa ggg atc agt aat ttc aag aca cca agc aaa tta tca gaa aaa aag 227
Glu Gly Ile Ser Asn Phe Lys Thr Pro Ser Lys Leu Ser Glu Lys Lys
5 10 15
aaa tct gta tta tgt tca act cca act ata aat atc ccg gcc tct ccg 275
Lys Ser Val Leu Cys Ser Thr Pro Thr Ile Asn Ile Pro Ala Ser Pro
20 25 30
ttt atg cag aag ctt ggc ttt ggt act ggg gwa aat gtn gta nct aat 323
Phe Met Gln Lys Leu Gly Phe Gly Thr Gly Xaa Asn Val Val Xaa Asn
35 40 45
gaa aag atc tcc aag agg ttt gtc tca ttc tcc ttg g 360
Glu Lys Ile Ser Lys Arg Phe Val Ser Phe Ser Leu
50 55 60

<210> 666
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 321..500

<400> 666
ctcatttttc tactgctcgt ggatttacgc gcacgttgga accgaagaga gctctgttgt 60
tgcaacatgg cggastgacg gtggagggtc gcggctctaa cggggctttc tacaagggat 120
ttatcaaaga tggtcatgaa gactccctta cagttgtttt tgaaaataat tggcaaccag 180
aacgccaggt tccatttaat gaagttagat taccaccacc acctgatata aaaaaagaaa 240
ttagtgaagg agatgaagta gaggtatatt caagagcaaa tgaccaagag ccatgtgggt 300

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ggtggttggc taaagttcgg atg atg aaa gga gaa ttt tat gtc att gaa tat      353
      Met Met Lys Gly Glu Phe Tyr Val Ile Glu Tyr
      1          5          10
gct gct tgt gac gct act tac aat gaa ata gtc aca ttt gaa cga ctt      401
Ala Ala Cys Asp Ala Thr Tyr Asn Glu Ile Val Thr Phe Glu Arg Leu
      15          20          25
cgg cct gtc aat caa aat aaa act gtc aaa aaa aat acc ttc ttt aaa      449
Arg Pro Val Asn Gln Asn Lys Thr Val Lys Lys Asn Thr Phe Phe Lys
      30          35          40
tgc aca gtg gat gtt cct gag gat ttg aga gag gcg tgt gct aat gaa      497
Cys Thr Val Asp Val Pro Glu Asp Leu Arg Glu Ala Cys Ala Asn Glu
      45          50          55
aat g      501
Asn
60

<210> 667
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 164..439

<400> 667
acagtcgtga tgtctttcaa gaggggaagga gacgattgga gtcaactcaa tgtgctcaaa      60
gtaagcgtga ggnnagagga tctggagccg cttcagtcgc tccctgaaga aaagaagagt      120
cgggggacctc ctagccagtt acattccaga ggatgaggcg ctg atg ctt cgg gat      175
      Met Leu Arg Asp
      1
gga cgc ttt gct tgt gcc atc tgc ccc cat cga ccg gta ctg gac acc      223
Gly Arg Phe Ala Cys Ala Ile Cys Pro His Arg Pro Val Leu Asp Thr
      10          15          20
ctg gcc atg ctg act gcc cac cgt gca ggc aag aaa cat ctg tcc agc      271
Leu Ala Met Leu Thr Ala His Arg Ala Gly Lys Lys His Leu Ser Ser
      25          30          35
ttg cag ctt ttc tat ggc aag aag cag ccg gga aag gaa aga aag cag      319
Leu Gln Leu Phe Tyr Gly Lys Lys Gln Pro Gly Lys Glu Arg Lys Gln
      40          45          50
aat cca aaa cat cag aat gaa ttg aga agg gaa gaa acc aaa gct gar      367
Asn Pro Lys His Gln Asn Glu Leu Arg Arg Glu Glu Thr Lys Ala Glu
      55          60          65
gct cct ctg cta act cag aca cga ctt atc acc cag agt gct ctg cac      415
Ala Pro Leu Leu Thr Gln Thr Arg Leu Ile Thr Gln Ser Ala Leu His
      70          75          80
aga gct ccc cac tat aac agt tgc tg      441
Arg Ala Pro His Tyr Asn Ser Cys
85          90

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<210> 668
 <211> 484
 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 126..482

<400> 668
aagtacggag gccgacagga agagaaggaa aaaagagaag gcgctgtccc gctcttgcta 60
cggtggcctg gaggagtggc gaaaccggaa cagagaatctt atcacttctg ggactcacag 120
tcgtg atg tct ttc aag agg gaa gga gac gat tgg agt caa ctc aat gtg 170
Met Ser Phe Lys Arg Glu Gly Asp Asp Trp Ser Gln Leu Asn Val
1 5 10 15
ctc aaa aaa aga aga gtc ggg gac ctc cta gcc agt tac att cca gag 218
Leu Lys Lys Arg Arg Val Gly Asp Leu Leu Ala Ser Tyr Ile Pro Glu
20 25 30
gat gag gcg ctg atg ctt cgg gat gga cgc ttt gct tgt gcc atc tgc 266
Asp Glu Ala Leu Met Leu Arg Asp Gly Arg Phe Ala Cys Ala Ile Cys
35 40 45
ccc cat cga ccg gta ctg gac acc ctg gcc atg ctg act gcc cac cgt 314
Pro His Arg Pro Val Leu Asp Thr Leu Ala Met Leu Thr Ala His Arg
50 55 60
gca ggc aag aaa cat ctg tcc agc ttg cag ctt ttc tat ggc aag aag 362
Ala Gly Lys Lys His Leu Ser Ser Leu Gln Leu Phe Tyr Gly Lys Lys
65 70 75
cag ccg gga aag gaa aga aag cag aat cca aaa cat cag aat gaa ttg 410
Gln Pro Gly Lys Glu Arg Lys Gln Asn Pro Lys His Gln Asn Glu Leu
80 85 90 95
aga agg gaa gaa acc aaa gct gag gct cct ctg cta act cag aca cga 458
Arg Arg Glu Glu Thr Lys Ala Glu Ala Pro Leu Leu Thr Gln Thr Arg
100 105 110
ctt aty acc cag agt gct ctg cac ag 484
Leu Ile Thr Gln Ser Ala Leu His
115

<210> 669

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 118..342

<400> 669
agcgaccggt tgccatggcg actatgtaca cagccaggca gccccgcgtg gggagtgcag 60
gtggtttcgg ttgcggcagt cgcgtcccg gagcgtcgct gcctggtgaa cgctaga 117
atg ggt act agg aaa aaa gtt cat gca ttt gtc cgk gtc aaa ccc acc 165
Met Gly Thr Arg Lys Lys Val His Ala Phe Val Arg Val Lys Pro Thr
1 5 10 15
gat gac ttt gct cat gaa atg atc aga tac gga gat gac aaa aga agc 213
Asp Asp Phe Ala His Glu Met Ile Arg Tyr Gly Asp Asp Lys Arg Ser
20 25 30

att gat att cac tta aaa aaa gac att cgg aga gga gtt gtc aat aac	261
Ile Asp Ile His Leu Lys Lys Asp Ile Arg Arg Gly Val Val Asn Asn	
35 40 45	
caa cag aca gac tgg tcg ttt aag ttg gat gga gtt ctt cac gat gcc	309
Gln Gln Thr Asp Trp Ser Phe Lys Leu Asp Gly Val Leu His Asp Ala	
50 55 60	
tcc cag gac ttg gtt tat gag aca gtt gca aag	342
Ser Gln Asp Leu Val Tyr Glu Thr Val Ala Lys	
65 70 75	

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<220>  
<221> CDS  
<222> 115..453
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<400> 670																60	
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cacagcgctt		cagaaaagag		tgggacaggg		acaagcatat		ctaagaggct		gaac atg						117	
																Met	
																1	
aat	cca	cag	atc	aga	aac	ccg	atg	aag	gca	atg	tat	cca	ggc	aca	ttc	165	
Asn	Pro	Gln	Ile	Arg	Asn	Pro	Met	Lys	Ala	Met	Tyr	Pro	Gly	Thr	Phe		
																10	
																15	
tac	ttc	caa	ttt	aaa	aac	cta	tgg	gaa	gcc	aac	gat	cgg	aac	gaa	act	213	
Tyr	Phe	Gln	Phe	Lys	Asn	Leu	Trp	Glu	Ala	Asn	Asp	Arg	Asn	Glu	Thr		
																20	
																25	
																30	
tgg	ctg	tgc	ttc	acc	gtg	gaa	ggg	ata	aag	cgc	cgc	tca	ggt	gtc	tcc	261	
Trp	Leu	Cys	Phe	Thr	Val	Glu	Gly	Ile	Lys	Arg	Arg	Ser	Val	Val	Ser		
																35	
																40	
																45	
tgg	aag	acg	ggc	gtc	ttc	cga	aac	cag	gtg	gat	tct	gag	acc	cat	tgt	309	
Trp	Lys	Thr	Gly	Val	Phe	Arg	Asn	Gln	Val	Asp	Ser	Glu	Thr	His	Cys		
																50	
																55	
																60	
cat	gca	gaa	agg	tgc	ttc	ctc	tct	tgg	ttc	tgc	gac	gac	ata	ctg	tct	357	
His	Ala	Glu	Arg	Cys	Phe	Leu	Ser	Trp	Phe	Cys	Asp	Asp	Ile	Leu	Ser		
																70	
																75	
																80	
cct	aac	aca	aag	tac	cag	gtc	acc	tgg	tac	aca	tct	tgg	agc	cct	tgc	405	
Pro	Asn	Thr	Lys	Tyr	Gln	Val	Thr	Trp	Tyr	Thr	Ser	Trp	Ser	Pro	Cys		
																85	
																90	
																95	
cca	gac	tgt	gca	ggg	gag	gtg	gcc	gag	ttc	ctg	gcc	agg	cac	agc	aac	g	454
Pro	Asp	Cys	Ala	Gly	Glu	Val	Ala	Glu	Phe	Leu	Ala	Arg	His	Ser	Asn		
																100	
																105	
																110	

<220>
<221> CDS

<222> 44..484

<400> 671

agagcgcaga gctgcagccg ccgagccgga cgtgtccgcg aag atg gcg ggc cgg 55
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1
agc atg caa gcg gca aga tgt cct aca gat gaa tta tct tta acc aat 103
Ser Met Gln Ala Ala Arg Cys Pro Thr Asp Glu Leu Ser Leu Thr Asn
5 10 15 20
tgt gca gtt gtg aat gaa aag gat ttc cag tct ggc cag cat gtg att 151
Cys Ala Val Val Asn Glu Lys Asp Phe Gln Ser Gly Gln His Val Ile
25 30 35
gtg agg acc tct ccc aat cac agg tac aca ttt aca ctg aag aca cat 199
Val Arg Thr Ser Pro Asn His Arg Tyr Thr Phe Thr Leu Lys Thr His
40 45 50
cca tcg gtg gtt cca ggg agc att gca ttc agt tta cct cag aga aaa 247
Pro Ser Val Val Pro Gly Ser Ile Ala Phe Ser Leu Pro Gln Arg Lys
55 60 65
tgg gct ggg ctt tct att ggg caa gaa ata gaa gtc tcc tta tat aca 295
Trp Ala Gly Leu Ser Ile Gly Gln Glu Ile Glu Val Ser Leu Tyr Thr
70 75 80
ttt gac aaa gcc aaa cag tgt att ggc aca atg acc atc gag att gat 343
Phe Asp Lys Ala Lys Gln Cys Ile Gly Thr Met Thr Ile Glu Ile Asp
85 90 95 100
ttc ctg cag aaa aaa agc att gac tcc aac cct tat gac acc gac aag 391
Phe Leu Gln Lys Lys Ser Ile Asp Ser Asn Pro Tyr Asp Thr Asp Lys
105 110 115
atg gca gca gaa ttt att cag caa tca aca acc agg cct tct cag tgg 439
Met Ala Ala Glu Phe Ile Gln Gln Ser Thr Thr Arg Pro Ser Gln Trp
120 125 130
gac aac agc ttg tct tcc agt cca agt tct gaa ttt tac cct ttc c 485
Asp Asn Ser Leu Ser Ser Ser Pro Ser Ser Glu Phe Tyr Pro Phe
135 140 145

<210> 672

<211> 487

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 44..487

<400> 672

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Met Ala Gly Arg
1
agc atg caa gcg gca aga tgt cct aca gat gaa tta tct tta acc aat 103
Ser Met Gln Ala Ala Arg Cys Pro Thr Asp Glu Leu Ser Leu Thr Asn
5 10 15 20
tgt gca gtt gtg aat gaa aag gat ttc cag tct ggc cag cat gtg att 151
Cys Ala Val Val Asn Glu Lys Asp Phe Gln Ser Gly Gln His Val Ile

	25	30	35	
gtg agg acc tct ccc aat cac agg tac aca ttt aca ctg aag aca cat				199
Val Arg Thr Ser Pro Asn His Arg Tyr Thr Phe Thr Leu Lys Thr His				
	40	45	50	
cca tcg gtg gtt cca ggg agc att gca ttc agt tta cct cag aga aaa				247
Pro Ser Val Val Pro Gly Ser Ile Ala Phe Ser Leu Pro Gln Arg Lys				
	55	60	65	
tgg gct ggg ctt tct att ggg caa gaa ata gaa gtc tcc tta tat aca				295
Trp Ala Gly Leu Ser Ile Gly Gln Glu Ile Glu Val Ser Leu Tyr Thr				
	70	75	80	
ttt gac aaa gcc aaa cag tgt att ggc aca atg acc atc gag att gat				343
Phe Asp Lys Ala Lys Gln Cys Ile Gly Thr Met Thr Ile Glu Ile Asp				
	85	90	95	
ttc ctg cag aaa aaa agc att gac tcc aac cct tat gac acc gac aag				391
Phe Leu Gln Lys Lys Ser Ile Asp Ser Asn Pro Tyr Asp Thr Asp Lys				
	105	110	115	
atg gca gca gwa ttt att cag caa ttc aac aac cag gcc ttc tca gtg				439
Met Ala Ala Xaa Phe Ile Gln Gln Phe Asn Asn Gln Ala Phe Ser Val				
	120	125	130	
gga caa cag ctt gtc ttt agc ttc aat gaa aag ctt ttt ggc tta ctg				487
Gly Gln Gln Leu Val Phe Ser Phe Asn Glu Lys Leu Phe Gly Leu Leu				
	135	140	145	

<210> 673
 <211> 502
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> 159..500

 <400> 673
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 ttaaccactg ttacacttcc aggggctccc cactcagtc ccagtcattct atcgacagtg 120
 agctgagtac ttcagaattg gaggatgatt ctatctcc atg gga tat aaa tta cag 176
 Met Gly Tyr Lys Leu Gln
 1 5
 gac ctc act gat gtt cag atc atg gct cgt ctg caa gaa gaa agt ctc 224
 Asp Leu Thr Asp Val Gln Ile Met Ala Arg Leu Gln Glu Glu Ser Leu
 10 15 20
 agg caa gat tat gct tct act tca gca tct gta tca aga cat agt tcc 272
 Arg Gln Asp Tyr Ala Ser Thr Ser Ala Ser Val Ser Arg His Ser Ser
 25 30 35
 agt gtg tca ttg agt tca gga aaa aaa ggg aca tgt agt gat caa gaa 320
 Ser Val Ser Leu Ser Ser Gly Lys Lys Gly Thr Cys Ser Asp Gln Glu
 40 45 50
 tat gac caa tac agt ctg gag gat gaa gag gaa ttt gat cat ttg cca 368
 Tyr Asp Gln Tyr Ser Leu Glu Asp Glu Glu Glu Phe Asp His Leu Pro
 55 60 65 70
 cca cct cag cct cgt ctt cca aga tgt tcc cct ttc caa aga gga att 416
 Pro Pro Gln Pro Arg Leu Pro Arg Cys Ser Pro Phe Gln Arg Gly Ile
 75 80 85

ccc cat tca cag act ttc tcc agc att cgg gag tgt agg agg agc ccc 464
 Pro His Ser Gln Thr Phe Ser Ser Ile Arg Glu Cys Arg Arg Ser Pro
 90 95 100
 agt tcc cag tat ttt cct tca aat aat tac cag cag ca 502
 Ser Ser Gln Tyr Phe Pro Ser Asn Asn Tyr Gln Gln
 105 110

<210> 674
 <211> 307
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 63..305

<400> 674
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 at atg aaa agg cct aag tta aag aaa gca agt aaa cgc atg acc tgc 107
 Met Lys Arg Pro Lys Leu Lys Lys Ala Ser Lys Arg Met Thr Cys
 1 5 10 15
 cat aag cgg tat aaa atc caa aaa aag gtt cga gaa cat cat cga aaa 155
 His Lys Arg Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys
 20 25 30
 tta aga aag gag gct aaa aag crg ggt cac aag aag cct agg aaa gac 203
 Leu Arg Lys Glu Ala Lys Lys Xaa Gly His Lys Lys Pro Arg Lys Asp
 35 40 45
 cca gga gtt cca aac agt gct ccc ttt aag gag gct ctt ctt agg gaa 251
 Pro Gly Val Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Arg Glu
 50 55 60
 gct gag cta agg aaa cag agg ctt gaw gaa cta awa cag cag cag awa 299
 Ala Glu Leu Arg Lys Gln Arg Leu Xaa Glu Leu Xaa Gln Gln Gln Xaa
 65 70 75
 ctt gac ag 307
 Leu Asp
 80

<210> 675
 <211> 404
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 104..403

<400> 675
 cttaactgga gttcatcaag ttcccactga gmmgtgtgcag gtgcatttca cagagaggtc 60
 atttgatctt ttggtaaaga atctaaatgg gaagagttac tcc atg att gtg aac 115
 Met Ile Val Asn
 1
 aat ctc ttg aaa ccc atc tct gtg gaa ggc agt tca aaa aaa gtc aag 163

0044220" 656E553

Asn	Leu	Leu	Lys	Pro	Ile	Ser	Val	Glu	Gly	Ser	Ser	Lys	Lys	Val	Lys		
5					10					15					20		
act	gat	aca	gtt	ctt	ata	ttg	tgt	aga	aag	aaa	gtg	gaa	aac	aca	agg	211	
Thr	Asp	Thr	Val	Leu	Ile	Leu	Cys	Arg	Lys	Lys	Val	Glu	Asn	Thr	Arg		
				25					30					35			
tgg	gat	tac	ctg	acc	cag	gtt	gaa	aag	gag	tgc	aaa	gaa	aaa	gag	aag	259	
Trp	Asp	Tyr	Leu	Thr	Gln	Val	Glu	Lys	Glu	Cys	Lys	Glu	Lys	Glu	Lys		
			40					45					50				
ccc	tcc	tat	gac	act	gaa	aca	gat	cct	agt	gag	gga	ttg	atg	aat	gtt	307	
Pro	Ser	Tyr	Asp	Thr	Glu	Thr	Asp	Pro	Ser	Glu	Gly	Leu	Met	Asn	Val		
		55					60					65					
cta	aag	aaa	att	tat	gaa	gat	gga	gac	gat	gat	atg	aag	cga	acc	att	355	
Leu	Lys	Lys	Ile	Tyr	Glu	Asp	Gly	Asp	Asp	Asp	Met	Lys	Arg	Thr	Ile		
		70				75					80						
aat	aaa	gcc	tgg	gtg	gaa	tca	aga	gag	aag	caa	gcc	aaa	gga	gac	acg g	404	
Asn	Lys	Ala	Trp	Val	Glu	Ser	Arg	Glu	Lys	Gln	Ala	Lys	Gly	Asp	Thr		
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 <211> 392
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 84..392

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gacaaaccgg	accgcgaacc	acc atg aac agc aaa ggt caa tat cca aca cag														113	
		Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln															
		1		5													
cca acc tac cct gtg cag cct cct ggg aat cca gta tac cct cag acc																161	
Pro Thr Tyr Pro Val Gln Pro Pro Gly Asn Pro Val Tyr Pro Gln Thr																	
		15		20											25		
ttg cat ctt cct cag gct cca ccc tat acc gat gct cca cct gcc tac																209	
Leu His Leu Pro Gln Ala Pro Pro Tyr Thr Asp Ala Pro Pro Ala Tyr																	
		30		35											40		
tca gag ctc tat cgt ccg agc ttt gtg cac cca ggg gct gcc aca gtc																257	
Ser Glu Leu Tyr Arg Pro Ser Phe Val His Pro Gly Ala Ala Thr Val																	
		45		50											55		
ccc acc atg tca gcc gca ttt cct gga gcc tct ctg tat ctt ccc atg																305	
Pro Thr Met Ser Ala Ala Phe Pro Gly Ala Ser Leu Tyr Leu Pro Met																	
		60		65											70		
gcc cag tct gtg gct gtt ggg cct tta ggt tcc aca atc ccc atg gct																353	
Ala Gln Ser Val Ala Val Gly Pro Leu Gly Ser Thr Ile Pro Met Ala																	
		75		80											85		
tat tat cca gtc ggt ccc atc tat cca nct ggc tcc aca																392	
Tyr Tyr Pro Val Gly Pro Ile Tyr Pro Xaa Gly Ser Thr																	
				95											100		

<210> 677
 <211> 446

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..444

<400> 677
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Met Ala Ser Leu Lys Cys Ser Thr Val Val Cys Val Ile Cys
1 5 10
ttg gag aag ccc aaa tac cgc tgt cca gcc tgc cgc gtg ccc tac tgc 99
Leu Glu Lys Pro Lys Tyr Arg Cys Pro Ala Cys Arg Val Pro Tyr Cys
15 20 25 30
tcg gta gtc tgc ttc cgg aag cac aaa gaa cag tgc aac cct gaa act 147
Ser Val Val Cys Phe Arg Lys His Lys Glu Gln Cys Asn Pro Glu Thr
35 40 45
cgt cct gtt gag aaa aaa ata aga tca gct ctt cct acc aaa acc gta 195
Arg Pro Val Glu Lys Lys Ile Arg Ser Ala Leu Pro Thr Lys Thr Val
50 55 60
aag cct gtg gaa aac aaa gat gat gat gac tct ata gct gat ttt ctc 243
Lys Pro Val Glu Asn Lys Asp Asp Asp Ser Ile Ala Asp Phe Leu
65 70 75
aat agt gat gag gaa gaa gac aga gtt tct ttg cag aat tta aag aat 291
Asn Ser Asp Glu Glu Glu Asp Arg Val Ser Leu Gln Asn Leu Lys Asn
80 85 90
tta gat gga ctc tcg tcc tgt cac cca ggc tgg agt gca gcg gcg caa 339
Leu Asp Gly Leu Ser Ser Cys His Pro Gly Trp Ser Ala Ala Ala Gln
95 100 105 110
tct cgg ctc act gca acc tct ccc tcc cag att cra gca att ctc atg 387
Ser Arg Leu Thr Ala Thr Ser Pro Ser Gln Ile Xaa Ala Ile Leu Met
115 120 125
cct cag cct ccc gag cag ctg gga cta cag gmg cct gcs act acg ccc 435
Pro Gln Pro Pro Glu Gln Leu Gly Leu Gln Xaa Pro Ala Thr Thr Pro
130 135 140
aac caa ttt tt 446
Asn Gln Phe
145

<210> 678
<211> 619
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 326..619

<400> 678
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gggtggacaa ggggggggta gcagctgggc tgcgaccgtt agggaggggc tcaaggtgtg 120
catgtgtgag ggaagagaga gagagagaag ggcgcctcag aggtgacttt cagcctgcga 180

gccttcttcc cggggcgcca taaacgcccc caatttccca gctgctaaag gaagaggaag 240
 attcaaccct atgaaaagat aaaggccagg ggcttgcttg ataatatatc ttccgtgttg 300
 aacaaactag tgggtgtgaa actca atg gtg gtt tgg gaa cca gca tgg ggc 352
 Met Val Val Trp Glu Pro Ala Trp Gly
 1 5
 tgc aaa ggc cct aaa agt ctg att ggt gtg agg aat gag aat acc ttt 400
 Cys Lys Gly Pro Lys Ser Leu Ile Gly Val Arg Asn Glu Asn Thr Phe
 10 15 20 25
 ctg gat ctg act gtt cag caa att gaa cat ttg aat aaa acc tac aat 448
 Leu Asp Leu Thr Val Gln Gln Ile Glu His Leu Asn Lys Thr Tyr Asn
 30 35 40
 aca gat gtt cct ctt gtt tta atg aac tct ttt aac acg gat gaa gat 496
 Thr Asp Val Pro Leu Val Leu Met Asn Ser Phe Asn Thr Asp Glu Asp
 45 50 55
 acc aaa aaa ata cta cag aag tac aat cat tgt cgt gtg aaa atc tac 544
 Thr Lys Lys Ile Leu Gln Lys Tyr Asn His Cys Arg Val Lys Ile Tyr
 60 65 70
 act ttc aat caa agc agg tac ccg agg att aat aaa gaa tct tta ctt 592
 Thr Phe Asn Gln Ser Arg Tyr Pro Arg Ile Asn Lys Glu Ser Leu Leu
 75 80 85
 cct gta gca aag gac gtg tct tac tca 619
 Pro Val Ala Lys Asp Val Ser Tyr Ser
 90 95
 <210> 679
 <211> 426
 <212> DNA
 <213> Homo sapiens
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 <221> CDS
 <222> 267..425
 <400> 679
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 gaacaaagct tatcattaca gataaacaac ttgatgcaga tgtttcccc aagccacta 120
 tttttcttcc ttcaattgct gaaacaaagc tccagaaggc tggaacatac ctttgtcttc 180
 ttgagaaatt tttccctgat gttattaaga tacattggca agaaaagaag agcaacacga 240
 ttctgggatc ccaggagggg aacacc atg aag act aac gac aca tac atg aaa 293
 Met Lys Thr Asn Asp Thr Tyr Met Lys
 1 5
 ttt agc tgg tta acg gtg cca gaa aag tca ctg gac aaa gaa cac aga 341
 Phe Ser Trp Leu Thr Val Pro Glu Lys Ser Leu Asp Lys Glu His Arg
 10 15 20 25
 tgt atc gtc aga cat gag aat aat aaa aac gga gtt gat caa gaa att 389
 Cys Ile Val Arg His Glu Asn Asn Lys Asn Gly Val Asp Gln Glu Ile
 30 35 40
 atc ttt cct cca ata aag aca gat gtc atc aca atg g 426
 Ile Phe Pro Pro Ile Lys Thr Asp Val Ile Thr Met
 45 50
 <210> 680
 <211> 359

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 159..359

<400> 680
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ggcatctttt tgcgtactag tgttttgggt aataactacc cagtgggtgcc tgggttctat 120
ttttaaagtc attggtagaa attcatcttt acttgaac atg gca gta aga ctt ttg 176
Met Ala Val Arg Leu Leu
1 5
tgk tca ctc ata aaa aaa tcc aat cag agt gct tat ctg agg tca cag 224
Xaa Ser Leu Ile Lys Lys Ser Asn Gln Ser Ala Tyr Leu Arg Ser Gln
10 15 20
agc aga act tcc tct aac agc ttt cct cct gta tct cac cta gtt gta 272
Ser Arg Thr Ser Ser Asn Ser Phe Pro Pro Val Ser His Leu Val Val
25 30 35
gcc ctt cat ctg tct ggg ttt tat tgc cgc ata cac tta tcc agc agt 320
Ala Leu His Leu Ser Gly Phe Tyr Cys Arg Ile His Leu Ser Ser Ser
40 45 50
ttt tca ttt ggc ttg aac tca aaa cag tcc ccc gat gct 359
Phe Ser Phe Gly Leu Asn Ser Lys Gln Ser Pro Asp Ala
55 60 65

<210> 681
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..315

<400> 681
actgcgaaga ttcaaaagct ccaaaaacct actgtagaca tcgaagaacc aatatatata 60
atg ggc caa caa tcc agt gtc cgc agg ctg aag agg agc gtc ccc tgt 108
Met Gly Gln Gln Ser Ser Val Arg Arg Leu Lys Arg Ser Val Pro Cys
1 5 10 15
gaa tcc aac gag gcc aac gag gcc aat gag gcc aac aag acg atg ccg 156
Glu Ser Asn Glu Ala Asn Glu Ala Asn Lys Thr Met Pro
20 25 30
gag acc cca act ggg gac tca gac ccg caa cct gct cct aaa aaa atg 204
Glu Thr Pro Thr Gly Asp Ser Asp Pro Gln Pro Ala Pro Lys Lys Met
35 40 45
aaa aca tct gag tcc tcg acc ata cta gtg gtt cgc tac agg agg aac 252
Lys Thr Ser Glu Ser Ser Thr Ile Leu Val Val Arg Tyr Arg Arg Asn
50 55 60
gtg aaa aga aca tct cca gag gaa ctg gtg aat gac cac gcc cga gag 300
Val Lys Arg Thr Ser Pro Glu Glu Leu Val Asn Asp His Ala Arg Glu
65 70 75 80

aac aga atc aac ccc g
Asn Arg Ile Asn Pro
85

316

<210> 682
<211> 443
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..443

<400> 682
gcgagagagc gagtsagcaa gcgagcagaa aagaggtgga gaggggggga ataagaaaga 60
gagagaagga aaggagagaa ggcaggaaga aggcaaggga cgagacaacc atg ctg 116
Met Leu
1
tgc tgt atg aga aga acc aaa cag gtt gaa aaa aat gat gac gac caa 164
Cys Cys Met Arg Arg Thr Lys Gln Val Glu Lys Asn Asp Asp Asp Gln
5 10 15
aag att gaa caa gat ggt atc aaa cca gaa gat aaa gct cat aag gcc 212
Lys Ile Glu Gln Asp Gly Ile Lys Pro Glu Asp Lys Ala His Lys Ala
20 25 30
gca acc aaa att cag gct agc ttc cgt gga cac ata aca agg aaa aag 260
Ala Thr Lys Ile Gln Ala Ser Phe Arg Gly His Ile Thr Arg Lys Lys
35 40 45 50
ctc aaa gga gag aag aag gat gat gtc caa gct gct gag gct gaa gct 308
Leu Lys Gly Glu Lys Lys Asp Asp Val Gln Ala Ala Glu Ala Glu Ala
55 60 65
aat aag aag gat gaa gcc cct gtt gcc gat ggg gtg gag aag aag gga 356
Asn Lys Lys Asp Glu Ala Pro Val Ala Asp Gly Val Glu Lys Lys Gly
70 75 80
gaa ggc acc act act gcc gaa gca gcc cca gcc ant ggc tcc aag cct 404
Glu Gly Thr Thr Thr Ala Glu Ala Ala Pro Ala Xaa Gly Ser Lys Pro
85 90 95
gat gag ccc ggm aaa gcr gga aaa wct cct tcc gag gag 443
Asp Glu Pro Gly Lys Ala Gly Lys Xaa Pro Ser Glu Glu
100 105 110

<210> 683
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 194..478

<400> 683
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gtagatctcg gctctggcct gctttattta tttatattttt ggtttggttt ctttggtcct 120

<213> Homo sapiens

<220>

<221> CDS

<222> 74..433

<400> 685
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 ggccgtagga gcc atg gcg ccc agc cgg aat ggc atg gtc ttg aag ccc 109
 Met Ala Pro Ser Arg Asn Gly Met Val Leu Lys Pro
 1 5 10
 cac ttc cac aag gac tgg cag cgg cgc gtg gcc acg tgg ttc aac cag 157
 His Phe His Lys Asp Trp Gln Arg Arg Val Ala Thr Trp Phe Asn Gln
 15 20 25
 ccg gcc cgg aag atc cgc aga cgt aag gcc cgg caa gcc aag gcg cgc 205
 Pro Ala Arg Lys Ile Arg Arg Arg Lys Ala Arg Gln Ala Lys Ala Arg
 30 35 40
 cgc atc gct ccg cgc ccc gcg tgc ggt ccc atc cgg ccc atc gtg cgc 253
 Arg Ile Ala Pro Arg Pro Ala Ser Gly Pro Ile Arg Pro Ile Val Arg
 45 50 55 60
 tgc ccc acg gtt cgg tac cac acg aag gtg cgc gcc ggc cgc ggc ttc 301
 Cys Pro Thr Val Arg Tyr His Thr Lys Val Arg Ala Gly Arg Gly Phe
 65 70 75
 agc ctg gag gag ctc agg gtg gcc ggc att cac aag aag gtg gcc cgg 349
 Ser Leu Glu Glu Leu Arg Val Ala Gly Ile His Lys Lys Val Ala Arg
 80 85 90
 acc atc ggc att tct gtg gat ccg agg agg cgg aac aag tcc acg gag 397
 Thr Ile Gly Ile Ser Val Asp Pro Arg Arg Arg Asn Lys Ser Thr Glu
 95 100 105
 tcc ctg cag gcc aac gtg cag cgg ctg aag gag tac cg 435
 Ser Leu Gln Ala Asn Val Gln Arg Leu Lys Glu Tyr
 110 115 120

<210> 686

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 67..426

<400> 686
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 ggagcc atg gcg ccc agc cgg aat ggc atg gtc ttg aag ccc cac ttc 108
 Met Ala Pro Ser Arg Asn Gly Met Val Leu Lys Pro His Phe
 1 5 10
 cac aag gac tgg cag cgg cgc gtg gcc acg tgg ttc aac cag ccg gcc 156
 His Lys Asp Trp Gln Arg Arg Val Ala Thr Trp Phe Asn Gln Pro Ala
 15 20 25 30
 cgg aag atc cgc aga cgt aag gcc cgg caa gcc aag gcg cgc cgc atc 204
 Arg Lys Ile Arg Arg Arg Lys Ala Arg Gln Ala Lys Ala Arg Arg Ile

<221> CDS
<222> 102..401

<400> 688
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tgtctacttc ctctgcttc cccgccgccg ccgccgccat c atg agg gaa atc gtg 116
Met Arg Glu Ile Val
1 5
cac ttg cag gcc ggg cag tgc ggc aac caa atc ggc gcc aag ttt tgg 164
His Leu Gln Ala Gly Gln Cys Gly Asn Gln Ile Gly Ala Lys Phe Trp
10 15 20
gag gtg atc agc gat gag cac ggc atc gac ccc acg ggc acc tac cac 212
Glu Val Ile Ser Asp Glu His Gly Ile Asp Pro Thr Gly Thr Tyr His
25 30 35
ggg gac agc gac ctg cag ctg gaa cgc atc aac gtg tac tac aat gag 260
Gly Asp Ser Asp Leu Gln Leu Glu Arg Ile Asn Val Tyr Tyr Asn Glu
40 45 50
gcc acc ggc ggc aag tac gtg ccc cgc gcc gtg ctc gtg gat ctg gag 308
Ala Thr Gly Gly Lys Tyr Val Pro Arg Ala Val Leu Val Asp Leu Glu
55 60 65
ccc ggc acc atg gac tcc gtg cgc tgc ggg ccc ttc ggg cag atc ttc 356
Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro Phe Gly Gln Ile Phe
70 75 80 85
cgg ccg gac aac ttc gtt ttc ggt cag agt ggt gct ggg aac aac tg 403
Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly Ala Gly Asn Asn
90 95 100

<210> 689
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 190..381

<400> 689
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aggacggaca gacccagacg ccgccggacc aggaggacgc tgacgaggca ccatgcgtga 120
gatcgtgcac atccaggcgg gccagrtgcg gcaaccagat cggcgccaag ttttgggagg 180
tcatcagtg atg agc atg gga ttg acc cca ctg gca gtt acc atg gag aca 231
Met Ser Met Gly Leu Thr Pro Leu Ala Val Thr Met Glu Thr
1 5 10
gtg att tgc agc tgg aga gaa tca atg ttt tac tac aat gaa gcc act 279
Val Ile Cys Ser Trp Arg Glu Ser Met Phe Tyr Tyr Asn Glu Ala Thr
15 20 25 30
ggw aac aaa tat gtt cct cgg gcc aay cct cag tgg atc tgg aag cca 327
Gly Asn Lys Tyr Val Pro Arg Ala Asn Pro Gln Trp Ile Trp Lys Pro
35 40 45
ggc acg atg gat ycg gtt mng tct gga cca ttc ggc crn mtc ttc aga 375
Gly Thr Met Asp Xaa Val Xaa Ser Gly Pro Phe Gly Xaa Xaa Phe Arg
50 55 60

cca aga ca
Pro Arg

383

<210> 690
<211> 498
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 165..497

<400> 690
cctttctccc tctcagaacc ttctgcccgt cgcgtttgca cctcgctgct ccagcctctg 60
gggcgcattc caaccttcca gcctgcgacc tgcggagaaaa aaaaattact tattttcttg 120
ccccatacat accttgaggc gagcaaaaaa attaaatttt aacc atg agg gaa atc 176
Met Arg Glu Ile
1
gtg cac atc cag gct ggt cag tgt ggc aac cag atc ggt gcc aag ttc 224
Val His Ile Gln Ala Gly Gln Cys Gly Asn Gln Ile Gly Ala Lys Phe
5 10 15 20
tgg gag gtg atc agt gat gaa cat ggc atc gac ccc acc ggc acc tac 272
Trp Glu Val Ile Ser Asp Glu His Gly Ile Asp Pro Thr Gly Thr Tyr
25 30 35
cac ggg gac agc gac ctg cag ctg gac cgc atc tct gtg tac tac aat 320
His Gly Asp Ser Asp Leu Gln Leu Asp Arg Ile Ser Val Tyr Tyr Asn
40 45 50
gaa gcc aca ggt ggc aaa tat gtt cct cgt gcc atc ctg gtg gat cta 368
Glu Ala Thr Gly Gly Lys Tyr Val Pro Arg Ala Ile Leu Val Asp Leu
55 60 65
gaa cct ggg acc atg gac tct gtt cgc tca ggt cct ttt ggc cag atc 416
Glu Pro Gly Thr Met Asp Ser Val Arg Ser Gly Pro Phe Gly Gln Ile
70 75 80
ttt aga cca gac aac ttt gta ttt ggt cag tct ggg gca ggt aac aac 464
Phe Arg Pro Asp Asn Phe Val Phe Gly Gln Ser Gly Ala Gly Asn Asn
85 90 95 100
tgg gcc aaa ggc act aca cag agg gcg cga gct g 498
Trp Ala Lys Gly Thr Thr Gln Arg Ala Arg Ala
105 110

<210> 691
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 92..391

<400> 691
ggatgtgggg gccagccctc ggaaacggaa gtgagcggcg gggtcgactg acggtaacgg 60
ggcagagagg ctgttcgcag agctgcggaa g atg aat gcc aga gga ctt gga 112

	Met	Asn	Ala	Arg	Gly	Leu	Gly	
	1				5			
tct gag cta aag gac agt att cca gtt act gaa ctt tca gca agt gga								160
Ser Glu Leu Lys Asp Ser Ile Pro Val Thr Glu Leu Ser Ala Ser Gly								
10 15 20								
cct ttt gaa agt cat gat ctt ctt cgg aaa ggt ttt tct tgt gtg aaa								208
Pro Phe Glu Ser His Asp Leu Leu Arg Lys Gly Phe Ser Cys Val Lys								
25 30 35								
aat gaa ctt ttg cct agt cat ccc ctt gaa tta tca gaa aaa aat ttc								256
Asn Glu Leu Leu Pro Ser His Pro Leu Glu Leu Ser Glu Lys Asn Phe								
40 45 50 55								
cag ctc aac caa gat aaa atg aat ttt tcc aca ctg aga aac att cag								304
Gln Leu Asn Gln Asp Lys Met Asn Phe Ser Thr Leu Arg Asn Ile Gln								
60 65 70								
ggt cta ttt gct ccg cta aaa tta cag atg gnw ttc aag gca gtg cag								352
Gly Leu Phe Ala Pro Leu Lys Leu Gln Met Xaa Phe Lys Ala Val Gln								
75 80 85								
cag aca gga ctt ggc cct gca gag cat ctc cca tgg gca g								392
Gln Thr Gly Leu Gly Pro Ala Glu His Leu Pro Trp Ala								
90 95 100								
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aaaatgaact taatctttca tgagaaactg aggatagaga tgtcaataag cagccactgt								180
ttccacctcc ccacctaag agctaggagg acaactacaa agagcctgac tgccttctcg								240
gaatgaggag agaggaaaac agcaacagta tcagttttca ag atg gca gca tct								294
					Met	Ala	Ala	Ser
					1			
atg cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga								342
Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg								
5 10 15 20								
cca atg gtc ata gaa atc ata gan aaa aat ttt gac tat ctt aga aaa								390
Pro Met Val Ile Glu Ile Ile Xaa Lys Asn Phe Asp Tyr Leu Arg Lys								
25 30 35								
gaa atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct								438
Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala								
40 45 50								
ggt ttc tct gga ata ttc tca aac ttc ctg ttc aga cgc tgc ttc aag								486
Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys								
55 60 65								
ggt aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca								534
Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro								
70 75 80								

ttt ttg tct act gtt gtt act gac aag ctt ttt gta att gat gct ttg	582
Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu	
85 90 95 100	
tat tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg	630
Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu	
105 110 115	
att ggc ata gtt tgt ggw gtt ttc tat ccc agt tct ntg gct ttt act a	679
Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Xaa Ala Phe Thr	
120 125 130	

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 <222> 115..405

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aaactgaatt ccgatataaa tttacttgtg gttaaataaa tcttctacct aatt atg	117
Met	
1	
agt ttc att tta ata aat gna cca gtc ttt tta ttt tta ttt att tat	165
Ser Phe Ile Leu Ile Asn Xaa Pro Val Phe Leu Phe Leu Phe Ile Tyr	
5 10 15	
ttt gag aca ggg tct cac ttt gtc acc caa gct gga ggg aag tgg cgt	213
Phe Glu Thr Gly Ser His Phe Val Thr Gln Ala Gly Gly Lys Trp Arg	
20 25 30	
ggg ctg ggc tcg ctg caa cct ctg cct ccc ggg ttt agg cga tcc tcc	261
Gly Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Phe Arg Arg Ser Ser	
35 40 45	
tgc ctc agc ctc ctg agt ggc tgg gat tgc ggg ctt gcg cca cca cgc	309
Cys Leu Ser Leu Leu Ser Gly Trp Asp Cys Gly Leu Ala Pro Pro Arg	
50 55 60 65	
tcg gct aat ttt tgt att ttt agt gga gat ggg gtt tcg ccg tgt tgg	357
Ser Ala Asn Phe Cys Ile Phe Ser Gly Asp Gly Val Ser Pro Cys Trp	
70 75 80	
sca gac tgg tct tca act cct ggc ttc agg tgg tcc amc ctc ctc ggc c	406
Xaa Asp Trp Ser Ser Thr Pro Gly Phe Arg Trp Ser Xaa Leu Leu Gly	
85 90 95	

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 <222> 123..278

001399-022400

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taccttctct gccttcggcg cgcttctcag cggggccgcc gacccaaagg agccgtccga 120
ct atg tct aac atg gag aaa cac ctg ttc aac ctg aag ttc gcg gcc 167
Met Ser Asn Met Glu Lys His Leu Phe Asn Leu Lys Phe Ala Ala
1 5 10 15
aaa gaa ctg agt agg agt gcc aaa aaa tgc gat aag gag gaa aag gcc 215
Lys Glu Leu Ser Arg Ser Ala Lys Lys Cys Asp Lys Glu Glu Lys Ala
20 25 30
gaa aag gcc aaa att aaa aag gcc att cag aag ggc aac atg gaa gtt 263
Glu Lys Ala Lys Ile Lys Lys Ala Ile Gln Lys Gly Asn Met Glu Val
35 40 45
gcg agg ata crc gcc g 279
Ala Arg Ile Xaa Ala
50

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<211> 445
<212> DNA
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Met Asp Gly Ser Arg Lys Glu Glu Glu
1 5
gaa gac agc aca ttc acc aac att tct ctt gca gat gac ata grc cat 101
Glu Asp Ser Thr Phe Thr Asn Ile Ser Leu Ala Asp Asp Ile Xaa His
10 15 20 25
tcc tca aga att ttg tat cca agg ccc aaa agt ttg tta ccc aag atg 149
Ser Ser Arg Ile Leu Tyr Pro Arg Pro Lys Ser Leu Leu Pro Lys Met
30 35 40
atg aat gct gac atg gat gca gtt gat kct gaa aat caa gtg gaa ctg 197
Met Asn Ala Asp Met Asp Ala Val Asp Xaa Glu Asn Gln Val Glu Leu
45 50 55
gag gaa aaa aca aga ctt att aat caa gtg ttg gaa ctc caa cac aca 245
Glu Glu Lys Thr Arg Leu Ile Asn Gln Val Leu Glu Leu Gln His Thr
60 65 70
ctt gaa gat ctc tct gca aga gta gat gca gtt aag gaa gaa aat ctg 293
Leu Glu Asp Leu Ser Ala Arg Val Asp Ala Val Lys Glu Glu Asn Leu
75 80 85
aag cta aaa tca gaa aac caa gtt ctt gga caa tat ata gaa aat ctc 341
Lys Leu Lys Ser Glu Asn Gln Val Leu Gly Gln Tyr Ile Glu Asn Leu
90 95 100 105
atg tca gct tct agt gtt ttt caa aca act gac aca aaa agc aaa aga 389
Met Ser Ala Ser Ser Val Phe Gln Thr Thr Asp Thr Lys Ser Lys Arg
110 115 120
agt aag gga ttg aca ccc ttc tgt ttt atg gaa ttg ctg ctg atc att 437
Ser Lys Gly Leu Thr Pro Phe Cys Phe Met Glu Leu Leu Leu Ile Ile
125 130 135

ttt tct tt
Phe Ser

445

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<211> 384
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<220>
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<222> 26..382

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Met Ser Ala Gln Phe Arg Ser Leu His
1 5
cag tat gct gcc cag agg atc atc agt tta ttt tct ttg ctg tct aaa 100
Gln Tyr Ala Ala Gln Arg Ile Ile Ser Leu Phe Ser Leu Leu Ser Lys
10 15 20 25
aaa cac aac aaa gtt ctg gaa caa gcc aca mag tyc ttg ara ggt tgc 148
Lys His Asn Lys Val Leu Glu Gln Ala Thr Xaa Xaa Leu Xaa Gly Ser
30 35 40
ctg agt tct aat gat gtt cct cta cca gat tat gca caa gac cta aat 196
Leu Ser Ser Asn Asp Val Pro Leu Pro Asp Tyr Ala Gln Asp Leu Asn
45 50 55
gtc att gaa gaa gtg att cga atg atg tta gag atc atc aac tcc tgc 244
Val Ile Glu Glu Val Ile Arg Met Met Leu Glu Ile Ile Asn Ser Cys
60 65 70
ctg aca aat tcc ctt cac cac aac cca aac ttg gta tac gcc ctg ctt 292
Leu Thr Asn Ser Leu His His Asn Pro Asn Leu Val Tyr Ala Leu Leu
75 80 85
tac aaa cgc gat ctc ttt gaa caa ttt cga act cat cct tca ttt cag 340
Tyr Lys Arg Asp Leu Phe Glu Gln Phe Arg Thr His Pro Ser Phe Gln
90 95 100 105
gat ata atg caa aat att gat ctg gtg atc tcc ttc ttt agc tc 384
Asp Ile Met Gln Asn Ile Asp Leu Val Ile Ser Phe Phe Ser
110 115

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<222> 30..365

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Met Gln Arg Glu Glu Lys Gln Leu
1 5
gag gca tca tta gat gca ctg ctg agt caa gtg gct gat ctg aag aac 101

Glu	Ala	Ser	Leu	Asp	Ala	Leu	Leu	Ser	Gln	Val	Ala	Asp	Leu	Lys	Asn		
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tct	ctg	ggg	agt	ttc	att	tgc	aag	ttg	gar	amc	gag	tat	ggc	cgg	ctg	149	
Ser	Leu	Gly	Ser	Phe	Ile	Cys	Lys	Leu	Glu	Xaa	Glu	Tyr	Gly	Arg	Leu		
25					30					35					40		
acc	tgg	cca	tct	gtc	ctg	gac	agc	ttt	gcc	ttg	ctt	tct	gga	cag	ctg	197	
Thr	Trp	Pro	Ser	Val	Leu	Asp	Ser	Phe	Ala	Leu	Leu	Ser	Gly	Gln	Leu		
				45					50					55			
aac	act	ctg	aac	aag	gtc	ttg	aag	cat	gaa	aaa	aca	ccg	ctg	ttc	cgt	245	
Asn	Thr	Leu	Asn	Lys	Val	Leu	Lys	His	Glu	Lys	Thr	Pro	Leu	Phe	Arg		
			60					65					70				
aac	cag	gtc	atc	att	cct	ctg	gtg	ttg	tct	cca	gac	cga	gat	gaa	gat	293	
Asn	Gln	Val	Ile	Ile	Pro	Leu	Val	Leu	Ser	Pro	Asp	Arg	Asp	Glu	Asp		
		75					80					85					
ctc	atg	cgg	cag	act	gaa	gga	cgg	gtg	cct	gtt	ttc	agc	cat	gag	gta	341	
Leu	Met	Arg	Gln	Thr	Glu	Gly	Arg	Val	Pro	Val	Phe	Ser	His	Glu	Val		
	90					95					100						
gtc	cct	gac	cat	ctg	aga	acc	aag	c								366	
Val	Pro	Asp	His	Leu	Arg	Thr	Lys										
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agaaatccat	tctgtatgat	gagcgaagtg	tacacaaagt	agaaccaatt	accaagcata											240	
taggtttggt	gtacagtggc	atg ggc ccc	gat tac aga	gtg ctt	gtg cac	aga										293	
		Met Gly	Pro Asp	Tyr Arg	Val Leu	Val His	Arg										
		1		5		10											
gct cga	aaa cta	gct caa	caa tac	tat ctt	gtg tac	caa gaa	ccc att									341	
Ala Arg	Lys Leu	Ala Gln	Gln Tyr	Tyr Leu	Val Tyr	Gln Glu	Pro Ile										
	15			20		25											
cct aca	gct cag	ctg gta	cag aga	gta gct	tct gtg	atg caa	gaa tat									389	
Pro Thr	Ala Gln	Leu Val	Gln Arg	Val Ala	Ser Val	Met Gln	Glu Tyr										
	30			35		40											
act cag	tca ggt	ggt gtt	cgt cca	ttt gga	gtt tct	tta ctt	att tgt									437	
Thr Gln	Ser Gly	Gly Val	Arg Pro	Phe Gly	Val Ser	Leu Leu	Ile Cys										
	45			50		55											
ggt tgg	aat gag	gga cga	cca tat	tta ttt	cag tca	gat c										477	
Gly Trp	Asn Glu	Gly Arg	Pro Tyr	Leu Phe	Gln Ser	Asp											
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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 578..787

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gatcctgatt gcagaacctt ccctgattac agaatcttgg atacctgcct ttctttctag 180
gttgatcttc ccacttcacc cttctagacc atcccagaag atctataaga tttcatctgg 240
gaaatcacta ggagttcttg gaagggaaag aaggaagatt gttggttggg ataaaaacag 300
ggttggagga acggcagtgta tcacacgtcg gctgctggga agatctggat tctcgtttca 360
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tgcagaacct tccctgatta cagaatcttg ggttgatctt ccacttcac ccttctagac 480
catcccagaa gatctataag atttcatctg ggaaatcact aggagttctt ggaagggaaa 540
gaaggaagat tgttggttgg aataaaaaaca gggttga atg agt tcc aga aag cag 595
Met Ser Ser Arg Lys Gln
1 5
ggt tct caa cct cgt gga cag caa tct gca gaa gaa gag aac ttc aaa 643
Gly Ser Gln Pro Arg Gly Gln Gln Ser Ala Glu Glu Glu Asn Phe Lys
10 15 20
aaa cca act aga agc aac atg cag aga agt aaa atg aga ggg gcc tcc 691
Lys Pro Thr Arg Ser Asn Met Gln Arg Ser Lys Met Arg Gly Ala Ser
25 30 35
tca gga aag aag aca gct ggt cca cag cag aaa aat ctt gaa cca gct 739
Ser Gly Lys Lys Thr Ala Gly Pro Gln Gln Lys Asn Leu Glu Pro Ala
40 45 50
ctc cca gga aga tgg ggt ggt cgc tct gca gag aac ccc cct tca gga 787
Leu Pro Gly Arg Trp Gly Gly Arg Ser Ala Glu Asn Pro Pro Ser Gly
55 60 65 70
tc 789

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<211> 549
<212> DNA
<213> Homo sapiens

<220>
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<222> 338..547

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gatcctgatt gcagaacctt ccctgattac agaatcttgg atgatttcac aaaagttcat 180
cttcattgca gatacctgcc tttctttcta ggttgatctt ccacttcac ccttctagac 240
catcccagaa gatctataag atttcatctg ggaaatcact aggagttctt ggaagggaaa 300
gaaggaagat tgttggttgg aataaaaaaca gggttga atg agt tcc aga aag cag 355
Met Ser Ser Arg Lys Gln
1 5

ggt tct caa cct cgt gga cag caa tct gca gaa gaa gag aac ttc aaa	403
Gly Ser Gln Pro Arg Gly Gln Gln Ser Ala Glu Glu Glu Asn Phe Lys	
10 15 20	
aaa cca act aga agc aac atg cag aga agt aaa atg aga ggg gcc tcc	451
Lys Pro Thr Arg Ser Asn Met Gln Arg Ser Lys Met Arg Gly Ala Ser	
25 30 35	
tca gga aag aag aca gct ggt cca cag cag aaa aat ctt gaa cca gct	499
Ser Gly Lys Lys Thr Ala Gly Pro Gln Gln Lys Asn Leu Glu Pro Ala	
40 45 50	
ctc cca gga aga tgg ggt ggt cgc tct gca gag aac ccc cct tca gga	547
Leu Pro Gly Arg Trp Gly Gly Arg Ser Ala Glu Asn Pro Pro Ser Gly	
55 60 65 70	
tc	549

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<400> 701	
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gatactgatt gcagaacctt ccctgattac agaattcttg gattgttgag aggattacat	180
gtaaagtacc aggacagtgc atggcacata tgatttcaca aaagttcatc ttcattgcag	240
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atctataaga tttcatctgg gaaatcacta ggagttcttg gaagggaag aaggaagatt	360
gttggttgga ataaaaacag gggtga atg agt tcc aga aag cag ggt tct caa	413
Met Ser Ser Arg Lys Gln Gly Ser Gln	
1 5	
cct cgt gga cag caa tct gca gaa gaa gag aac ttc aaa aaa cca act	461
Pro Arg Gly Gln Gln Ser Ala Glu Glu Glu Asn Phe Lys Lys Pro Thr	
10 15 20 25	
aga agc aac atg cag aga agt aaa atg aga ggg gcc tcc tca gga aag	509
Arg Ser Asn Met Gln Arg Ser Lys Met Arg Gly Ala Ser Ser Gly Lys	
30 35 40	
aag aca gct ggt cca cag cag aaa aat ctt gaa cca gct ctc cca gga	557
Lys Thr Ala Gly Pro Gln Gln Lys Asn Leu Glu Pro Ala Leu Pro Gly	
45 50 55	
aga tgg ggt ggt cgc tct gca gag aac ccc cct tca gga tc	598
Arg Trp Gly Gly Arg Ser Ala Glu Asn Pro Pro Ser Gly	
60 65 70	

<210> 702
 <211> 869
 <212> DNA
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<220>
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<222> 658..867

<400> 702

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gaccttgatt gcagaacctt ccctgattac agaattcttg gattgttgag aggattacat 180
gtaaagtacc aggacagtgc atggcacata tgatttcaca aaagtccatc ttcattgcag 240
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gttggttgga ataaaaacag ggttgaggga acggcagtga tcacacgtcg gctgctggga 420
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cccacttcac ctttctagac catcccagaa gatctataag atttcatctg ggaaatcact 600
aggagttctt ggaagggaag gaaggaagat tgttggttg aataaaaaaca ggggtga 657
atg agt tcc aga aag cag ggt tct caa cct cgt gga cag caa tct gca 705
Met Ser Ser Arg Lys Gln Gly Ser Gln Pro Arg Gly Gln Gln Ser Ala
1 5 10 15
gaa gaa gag aac ttc aaa aaa cca act aga agc aac atg cag aga agt 753
Glu Glu Glu Asn Phe Lys Lys Pro Thr Arg Ser Asn Met Gln Arg Ser
20 25 30
aaa atg aga ggg gcc tcc tca gga aag aag aca gct ggt cca cag cag 801
Lys Met Arg Gly Ala Ser Ser Gly Lys Lys Thr Ala Gly Pro Gln Gln
35 40 45
aaa aat ctt gaa cca gct ctc cca gga aga tgg ggt ggt cgc tct gca 849
Lys Asn Leu Glu Pro Ala Leu Pro Gly Arg Trp Gly Gly Arg Ser Ala
50 55 60
gag aac ccc cct tca gga tc 869
Glu Asn Pro Pro Ser Gly
65 70

<210> 703

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 185..394

<400> 703

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gaccttgatt gcagaacctt ccctgattac agaattcttg tgggtggaat aaaaacaggg 180
ttga atg agt tcc aga aag cag ggt tct caa cct cgt gga cag caa tct 229
Met Ser Ser Arg Lys Gln Gly Ser Gln Pro Arg Gly Gln Gln Ser
1 5 10 15
gca gaa gaa gag aac ttc aaa aaa cca act aga agc aac atg cag aga 277
Ala Glu Glu Glu Asn Phe Lys Lys Pro Thr Arg Ser Asn Met Gln Arg
20 25 30
agt aaa atg aga ggg gcc tcc tca gga aag aag aca gct ggt cca cag 325
Ser Lys Met Arg Gly Ala Ser Ser Gly Lys Lys Thr Ala Gly Pro Gln
35 40 45

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 atg ggg ttc ctg aaa ctg att gag att gag aac ttt aag tcg tac aag 107
 Met Gly Phe Leu Lys Leu Ile Glu Ile Glu Asn Phe Lys Ser Tyr Lys
 1 5 10 15
 ggt cga cag att atc gga cca ttt cag agg ttc acc gcc atc att gga 155
 Gly Arg Gln Ile Ile Gly Pro Phe Gln Arg Phe Thr Ala Ile Ile Gly
 20 25 30
 ccc aat ggc tct ggt aag tca aat ctc atg gat gcc atc agc ttt gtg 203
 Pro Asn Gly Ser Gly Lys Ser Asn Leu Met Asp Ala Ile Ser Phe Val
 35 40 45
 cta ggt gaa aaa acc agc aac ctg cgg gta aag acc ctg cgg gac ctg 251
 Leu Gly Glu Lys Thr Ser Asn Leu Arg Val Lys Thr Leu Arg Asp Leu
 50 55 60
 atc cat gga gct cct gtg ggc aag cca gct gcc aac cgg gcc ttt gtc 299
 Ile His Gly Ala Pro Val Gly Lys Pro Ala Ala Asn Arg Ala Phe Val
 65 70 75 80
 agc atg gtc tac tct gag gag ggt gct gag gac 332
 Ser Met Val Tyr Ser Glu Glu Gly Ala Glu Asp
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<210> 706
 <211> 204
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 29..202

<400> 706
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 Met Ala Gly Glu Lys Val Glu Lys
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 Pro Asp Thr Lys Glu Lys Lys Pro Glu Ala Lys Lys Val Asp Ala Gly
 10 15 20
 ggc aag gtg aaa aag ggt aac ctc aaa gct aaa aag ccc aag aag ggg 148
 Gly Lys Val Lys Lys Gly Asn Leu Lys Ala Lys Lys Pro Lys Lys Gly
 25 30 35 40
 aag ccc ctt rcc ttc atg gac gac tca gwg gtg gag tcg acc gcc agc 196
 Lys Pro Leu Xaa Phe Met Asp Asp Ser Xaa Val Glu Ser Thr Ala Ser
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 atc ttg gc 204
 Ile Leu

<210> 707
 <211> 318
 <212> DNA
 <213> Homo sapiens

[illegible]

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Met Ala Gly Glu Lys Val Glu Lys
1 5

cca gat act aaa gag aag aaa ccc gaa gcc aag aag gtt gat gct ggt 100
Pro Asp Thr Lys Glu Lys Lys Pro Glu Ala Lys Lys Val Asp Ala Gly
10 15 20

ggc aag gtg aaa aag ggt aac ctc aaa gct aaa aag ccc aag aag ggg 148
 Gly Lys Val Lys Lys Gly Asn Leu Lys Ala Lys Lys Pro Lys Lys Gly
 25 30 35 40

aag ccc cat tgc agc cgc aac cct gtc ctt gtc aga gga att ggc agg 196
Lys Pro His Cys Ser Arg Asn Pro Val Leu Val Arg Gly Ile Gly Arg
45 50 55

tat	tcc	cga	tct	gcc	atg	tat	tcc	aga	aag	gcc	atg	aaa	gag	aaa	gac	244
Tyr	Ser	Arg	Ser	Ala	Met	Tyr	Ser	Arg	Lys	Ala	Met	Lys	Glu	Lys	Asp	
			60					65					70			

agg gaa aag gag aga gag agg gra aag gra cgt gaa aaa gaa aag gya 292
Arg Glu Lys Glu Arg Glu Arg Xaa Lys Xaa Arg Glu Lys Glu Lys Xaa
75 80 85

cgg ggt aaa aac mma grc cgg gac aa
 Arg Gly Lys Asn Xaa Xaa Arg Asp
 90 95

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<220>  
<221> CDS  
<222> 29..316
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accttaattc tctttcccat cttgcaag atg gcg ggt gaa aaa gtt gag aag 52
Met Ala Gly Glu Lys Val Glu Lys
1 5

cca gat act aaa gag aag aaa ccc gaa gcc aag aag gtt gat gct ggt 100
Pro Asp Thr Lys Glu Lys Lys Pro Glu Ala Lys Lys Val Asp Ala Gly
10 15 20

ggc aag gtg aaa aag ggt aac ctc aaa gct aaa aag ccc aag aag ggg 148
Gly Lys Val Lys Lys Gly Asn Leu Lys Ala Lys Lys Pro Lys Lys Gly
25 30 35 40

aag ccc cat tgc agc cgc aac cct gtc ctt gtc aga gga att ggc agg 196
Lys Pro His Cys Ser Arg Asn Pro Val Leu Val Arg Gly Ile Gly Arg
45 50 55

tat tcc cga tct gcc atg tat tcc aga aag gcc atg tac aag agg aag 244
Tyr Ser Arg Ser Ala Met Tyr Ser Arg Lys Ala Met Tyr Lys Arg Lys
60 65 70

<400> 712

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 agccaaaagg tttcgcgtct cccagcgtcc ccgaccggaa gtcgcctctt ggtctttgcg 120
 atctttttct ctggctcaat ttgggctgat tccgtttgtg tccgcaattc ctaaatacgag 180
 tttcttgaaa agagacactg gtcttaaggg ttaagacgaa ag atg gcg ggt gaa 234
 Met Ala Gly Glu

1

aaa gtt gag aag cca gat act aaa gag aag aaa ccc gaa gcc aag aag 282
 Lys Val Glu Lys Pro Asp Thr Lys Glu Lys Lys Pro Glu Ala Lys Lys
 5 10 15 20
 gtt gat gct ggt ggc aag gtg aaa aag ggt aac ctc aaa gct aaa aag 330
 Val Asp Ala Gly Gly Lys Val Lys Lys Gly Asn Leu Lys Ala Lys Lys
 25 30 35
 ccc aag aag ggg aag ccc cat tgc agc cgc aac cct gtc ctt gtc aga 378
 Pro Lys Lys Gly Lys Pro His Cys Ser Arg Asn Pro Val Leu Val Arg
 40 45 50
 gga att ggc agg tat tcc cga tct gcc atg tat tcc aga aag gcc atg 426
 Gly Ile Gly Arg Tyr Ser Arg Ser Ala Met Tyr Ser Arg Lys Ala Met
 55 60 65
 tac aag agg aag cag ctc ctg aag cca aga wwc aga aag tgg aag gca 474
 Tyr Lys Arg Lys Gln Leu Leu Lys Pro Arg Xaa Arg Lys Trp Lys Ala
 70 75 80
 cag aac cga cta cgg ctt tca atc tct ttg ttg gaa 510
 Gln Asn Arg Leu Arg Leu Ser Ile Ser Leu Leu Glu
 85 90 95

<210> 713

<211> 891

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 223..891

<400> 713

gtcctggggt ccagaggatg acactgagcc tgtcgcagcc acgttgggggt tccgcactga 60
 agccaaaagg tttcgcgtct cccagcgtcc ccgaccggaa gtcgcctctt ggtctttgcg 120
 atctttttct ctggctcaat ttgggctgat tccgtttgtg tccgcaattc ctaaatacgag 180
 tttcttgaaa agagacactg gtcttaaggg ttaagacgaa ag atg gcg ggt gaa 234
 Met Ala Gly Glu

1

aaa gtt gag aag cca gat act aaa gag aag aaa ccc gaa gcc aag aag 282
 Lys Val Glu Lys Pro Asp Thr Lys Glu Lys Lys Pro Glu Ala Lys Lys
 5 10 15 20
 gtt gat gct ggt ggc aag gtg aaa aag ggt aac ctc aaa gct aaa aag 330
 Val Asp Ala Gly Gly Lys Val Lys Lys Gly Asn Leu Lys Ala Lys Lys
 25 30 35
 ccc aag aag ggg aag ccc cat tgc agc cgc aac cct gtc ctt gtc aga 378
 Pro Lys Lys Gly Lys Pro His Cys Ser Arg Asn Pro Val Leu Val Arg
 40 45 50

gga att ggc agg tat tcc cga tct gcc atg tat tcc aga aag gcc atg	426
Gly Ile Gly Arg Tyr Ser Arg Ser Ala Met Tyr Ser Arg Lys Ala Met	
55 60 65	
tac aag agg aag tac tca gcc gct aaa tcc aag gtt gaa aag aaa aag	474
Tyr Lys Arg Lys Tyr Ser Ala Ala Lys Ser Lys Val Glu Lys Lys Lys	
70 75 80	
aag gag aag gtt ctc gca act gtt aca aaa cca gtt ggt ggt gac aag	522
Lys Glu Lys Val Leu Ala Thr Val Thr Lys Pro Val Gly Gly Asp Lys	
85 90 95 100	
aac ggc ggt acc cgg gtg gtt aaa ctt cgc aaa atg cct aga tat tat	570
Asn Gly Gly Thr Arg Val Val Lys Leu Arg Lys Met Pro Arg Tyr Tyr	
105 110 115	
cct act gaa gat gtg cct cga aag ctg ttg agc cac ggc aaa aaa ccc	618
Pro Thr Glu Asp Val Pro Arg Lys Leu Leu Ser His Gly Lys Lys Pro	
120 125 130	
ttc agt cag cac gtg aga aaa ctg cga gcc agc att acc ccc ggg acc	666
Phe Ser Gln His Val Arg Lys Leu Arg Ala Ser Ile Thr Pro Gly Thr	
135 140 145	
att ctg atc atc ctc act gga cgc cac agg ggc aag agg gtg gtt ttc	714
Ile Leu Ile Ile Leu Thr Gly Arg His Arg Gly Lys Arg Val Val Phe	
150 155 160	
ctg aag cag ctg gct agt ggc tta tta ctt gtg act gga cct ctg gtc	762
Leu Lys Gln Leu Ala Ser Gly Leu Leu Leu Val Thr Gly Pro Leu Val	
165 170 175 180	
ctc aat cga gtt cct cta cga aga aca cac cag aaa ttt gtc att gcc	810
Leu Asn Arg Val Pro Leu Arg Arg Thr His Gln Lys Phe Val Ile Ala	
185 190 195	
act tca acc aaa atc gat atc agc aat gta aaa atc cca aaa cat ctt	858
Thr Ser Thr Lys Ile Asp Ile Ser Asn Val Lys Ile Pro Lys His Leu	
200 205 210	
act gat gct tac ttc aag aag aag aag ctg cgg	891
Thr Asp Ala Tyr Phe Lys Lys Lys Lys Leu Arg	
215 220	

<210> 714

<211> 476

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> 187..474

<400> 714

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ttcgccatcc gaacctggag ggcattccagt cgacacctac aggggtcggn catgtccaar	120
gctaactgag aggccttcca gacgcttcat ttttggtgtt tgggtttgcg gcagggcaca	180
aagagg atg gcg ggt gaa aaa gtt gag aag cca gat act aaa gag aag	228
Met Ala Gly Glu Lys Val Glu Lys Pro Asp Thr Lys Glu Lys	
1 5 10	
aaa ccc gaa gcc aag aag gtt gat gct ggt ggc aag gtg aaa aag ggt	276
Lys Pro Glu Ala Lys Lys Val Asp Ala Gly Gly Lys Val Lys Lys Gly	
15 20 25 30	

aac ctc aaa gct aaa aag ccc aag aag ggg aag ccc cat tgc agc cgc	324
Asn Leu Lys Ala Lys Lys Pro Lys Lys Gly Lys Pro His Cys Ser Arg	
35 40 45	
aac cct gtc ctt gtc aga gga att ggc agg tat tcc cga tct gcc atg	372
Asn Pro Val Leu Val Arg Gly Ile Gly Arg Tyr Ser Arg Ser Ala Met	
50 55 60	
tat tcc aga aag gcc atg aaa gag aaa gac agg gaa aag gag aga gag	420
Tyr Ser Arg Lys Ala Met Lys Glu Lys Asp Arg Glu Lys Glu Arg Glu	
65 70 75	
agg gra aag gra cgt gaa aaa gaa aag gya cgg ggt aaa aac mma grc	468
Arg Xaa Lys Xaa Arg Glu Lys Glu Lys Xaa Arg Gly Lys Asn Xaa Xaa	
80 85 90	
cgg gac aa	476
Arg Asp	
95	

<210> 715
 <211> 474
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> 187..474

<400> 715	
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ttcgccatcc gaacctggag ggcattccagt cgacacctac aggggtcggc catgtccaar	120
gctaactgag aggccttcca gacgcttcat tttgtgtgtt tgggtttgcg gcagggcaca	180
aagagg atg gcg ggt gaa aaa gtt gag aag cca gat act aaa gag aag	228
Met Ala Gly Glu Lys Val Glu Lys Pro Asp Thr Lys Glu Lys	
1 5 10	
aaa ccc gaa gcc aag aag gtt gat gct ggt ggc aag gtg aaa aag ggt	276
Lys Pro Glu Ala Lys Lys Val Asp Ala Gly Gly Lys Val Lys Lys Gly	
15 20 25 30	
aac ctc aaa gct aaa aag ccc aag aag ggg aag ccc cat tgc agc cgc	324
Asn Leu Lys Ala Lys Lys Pro Lys Lys Gly Lys Pro His Cys Ser Arg	
35 40 45	
aac cct gtc ctt gtc aga gga att ggc agg tat tcc cga tct gcc atg	372
Asn Pro Val Leu Val Arg Gly Ile Gly Arg Tyr Ser Arg Ser Ala Met	
50 55 60	
tat tcc aga aag gcc atg tac aag agg aag cag ctc ctg aag cca aga	420
Tyr Ser Arg Lys Ala Met Tyr Lys Arg Lys Gln Leu Leu Lys Pro Arg	
65 70 75	
wwc aga aag tgg aag gca cag aac cga cta cgg ctt tca atc tct ttg	468
Xaa Arg Lys Trp Lys Ala Gln Asn Arg Leu Arg Leu Ser Ile Ser Leu	
80 85 90	
ttg gaa	474
Leu Glu	
95	

<210> 716
 <211> 855

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 187..855

<400> 716
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ttcgccatcc gaacctggag ggcattccagt cgacacctac aggggtcggg catgtccaar 120
gctaactgag aggccttcca gacgcttcat tttgttggtt tgggtttgcg gcagggcaca 180
aagagg atg gcg ggt gaa aaa gtt gag aag cca gat act aaa gag aag 228
Met Ala Gly Glu Lys Val Glu Lys Pro Asp Thr Lys Glu Lys
1 5 10
aaa ccc gaa gcc aag aag gtt gat gct ggt ggc aag gtg aaa aag ggt 276
Lys Pro Glu Ala Lys Lys Val Asp Ala Gly Gly Lys Val Lys Lys Gly
15 20 25 30
aac ctc aaa gct aaa aag ccc aag aag ggg aag ccc cat tgc agc cgc 324
Asn Leu Lys Ala Lys Lys Pro Lys Lys Gly Lys Pro His Cys Ser Arg
35 40 45
aac cct gtc ctt gtc aga gga att ggc agg tat tcc cga tct gcc atg 372
Asn Pro Val Leu Val Arg Gly Ile Gly Arg Tyr Ser Arg Ser Ala Met
50 55 60
tat tcc aga aag gcc atg tac aag agg aag tac tca gcc gct aaa tcc 420
Tyr Ser Arg Lys Ala Met Tyr Lys Arg Lys Tyr Ser Ala Ala Lys Ser
65 70 75
aag gtt gaa aag aaa aag aag gag aag gtt ctc gca act gtt aca aaa 468
Lys Val Glu Lys Lys Lys Lys Glu Lys Val Leu Ala Thr Val Thr Lys
80 85 90
cca gtt ggt ggt gac aag aac ggc ggt acc cgg gtg gtt aaa ctt cgc 516
Pro Val Gly Gly Asp Lys Asn Gly Gly Thr Arg Val Val Lys Leu Arg
95 100 105 110
aaa atg cct aga tat tat cct act gaa gat gtg cct cga aag ctg ttg 564
Lys Met Pro Arg Tyr Tyr Pro Thr Glu Asp Val Pro Arg Lys Leu Leu
115 120 125
agc cac ggc aaa aaa ccc ttc agt cag cac gtg aga aaa ctg cga gcc 612
Ser His Gly Lys Lys Pro Phe Ser Gln His Val Arg Lys Leu Arg Ala
130 135 140
agc att acc ccc ggg acc att ctg atc atc ctc act gga cgc cac agg 660
Ser Ile Thr Pro Gly Thr Ile Leu Ile Ile Leu Thr Gly Arg His Arg
145 150 155
ggc aag agg gtg gtt ttc ctg aag cag ctg gct agt ggc tta tta ctt 708
Gly Lys Arg Val Val Phe Leu Lys Gln Leu Ala Ser Gly Leu Leu Leu
160 165 170
gtg act gga cct ctg gtc ctc aat cga gtt cct cta cga aga aca cac 756
Val Thr Gly Pro Leu Val Leu Asn Arg Val Pro Leu Arg Arg Thr His
175 180 185 190
cag aaa ttt gtc att gcc act tca acc aaa atc gat atc agc aat gta 804
Gln Lys Phe Val Ile Ala Thr Ser Thr Lys Ile Asp Ile Ser Asn Val
195 200 205
aaa atc cca aaa cat ctt act gat gct tac ttc aag aag aag aag ctg 852
Lys Ile Pro Lys His Leu Thr Asp Ala Tyr Phe Lys Lys Lys Lys Leu
210 215 220

004220"666E550

cgg
Arg

<210> 717
<211> 402
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..402

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cgtgctttgc agcagatgtg tgacctggcg ttcccctgag tgctcggaaa atggccttgt 120
ctccggtcgt tcccgttcag gagcagaatt ttcccactgt aaaaaaccga gcaagtctgg 180
ataagtgagg ctggctcc atg tat cca gaa tca acg acg ggc tcc ccg gct 231
Met Tyr Pro Glu Ser Thr Thr Gly Ser Pro Ala
1 5 10
cgg ctc tgc ctg cgg cag acg ggc tcc ccc ggg atg atc tac agt act 279
Arg Leu Ser Leu Arg Gln Thr Gly Ser Pro Gly Met Ile Tyr Ser Thr
15 20 25
cgg tat ggg agt ccc aaa aga cag ctc cag ttt tac agg aac ctg ggc 327
Arg Tyr Gly Ser Pro Lys Arg Gln Leu Gln Phe Tyr Arg Asn Leu Gly
30 35 40
aag tct ggc ctg cgg gtc tcc tgc ctg gga ctt gga nca tgg gtg acc 375
Lys Ser Gly Leu Arg Val Ser Cys Leu Gly Leu Gly Xaa Trp Val Thr
45 50 55
ttc gga ggc cag atc acc gat gag atg 402
Phe Gly Gly Gln Ile Thr Asp Glu Met
60 65

<210> 718
<211> 332
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..331

<400> 718
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Met Ala Ala Pro Ser Gly Gly Val Asn Cys Glu Glu
1 5 10
ttc gcc gag ttc cag gaa tta ctc aag gtg atg agg aca att gat gac 97
Phe Ala Glu Phe Gln Glu Leu Leu Lys Val Met Arg Thr Ile Asp Asp
15 20 25
aga ata gta cat gaa tta aac act acg gtt cca aca gct tcc ttt gca 145
Arg Ile Val His Glu Leu Asn Thr Thr Val Pro Thr Ala Ser Phe Ala
30 35 40
ggg aaa att gat gcc agc caa acc tgt aaa caa ctt tat gag tct ttg 193

Gly	Lys	Ile	Asp	Ala	Ser	Gln	Thr	Cys	Lys	Gln	Leu	Tyr	Glu	Ser	Leu	
45					50				55					60		
atg	gca	gct	cat	gcc	agt	aga	gac	aga	gtc	ata	aaa	aac	tgt	ata	gcc	241
Met	Ala	Ala	His	Ala	Ser	Arg	Asp	Arg	Val	Ile	Lys	Asn	Cys	Ile	Ala	
			65					70					75			
cag	act	tca	gca	gta	gta	aaa	aac	ctc	cga	gaa	gag	aga	gaa	aag	aat	289
Gln	Thr	Ser	Ala	Val	Val	Lys	Asn	Leu	Arg	Glu	Glu	Arg	Glu	Lys	Asn	
			80					85					90			
ttg	gac	gat	tta	acg	tta	tta	aaa	caa	ctt	aga	aaa	gag	cag	a		332
Leu	Asp	Asp	Leu	Thr	Leu	Leu	Lys	Gln	Leu	Arg	Lys	Glu	Gln			
	95						100					105				

<210> 719
 <211> 445
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 107..445

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ctttgtttgt ccttcctggt agaggcgggt tccctccctc ggcaag atg ccg gag	115
	Met Pro Glu
	1
tgc tgg gat ggg gaa cat gac atc gag aca ccc tac ggc ctt ctg cat	163
Cys Trp Asp Gly Glu His Asp Ile Glu Thr Pro Tyr Gly Leu Leu His	
5 10 15	
gta gtg atc cgg ggc tcc ccc aag ggg aac cgc cca gcc atc ctc acc	211
Val Val Ile Arg Gly Ser Pro Lys Gly Asn Arg Pro Ala Ile Leu Thr	
20 25 30 35	
tac cat gat gtg ggc ctc aac cac aaa cta tgc ttc aac acc ttc ttc	259
Tyr His Asp Val Gly Leu Asn His Lys Leu Cys Phe Asn Thr Phe Phe	
40 45 50	
aac ttc gag gac atg cag gag atc acc aag cac ttt gtg gtg tgt cac	307
Asn Phe Glu Asp Met Gln Glu Ile Thr Lys His Phe Val Val Cys His	
55 60 65	
gtg gan ncs cct gga caa cag gtg ggg gcg tcg cag ttt cct cag ggg	355
Val Xaa Xaa Pro Gly Gln Gln Val Gly Ala Ser Gln Phe Pro Gln Gly	
70 75 80	
tac cag ttc ccc tcc atg gag cag ctg gct gcc atg ctc ccc agc gtg	403
Tyr Gln Phe Pro Ser Met Glu Gln Leu Ala Ala Met Leu Pro Ser Val	
85 90 95	
gtg cag cat ttc ggg ttc aag tat gtg att ggc atc gga gtg	445
Val Gln His Phe Gly Phe Lys Tyr Val Ile Gly Ile Gly Val	
100 105 110	

<210> 720
 <211> 401
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 141..401

<400> 720
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 gcttccgcgg ggcgctgggc cgccagcctc ggcaccgtcc ttccctttct ccctcgcgtt 120
 aggcaggtga cagcaggac atg tct cgg gag atg cag gat gta gac ctc gct 173
 Met Ser Arg Glu Met Gln Asp Val Asp Leu Ala
 1 5 10
 gag gtg aag cct ttg gtg gag aaa ggg gag acc atc acc ggc ctc ctg 221
 Glu Val Lys Pro Leu Val Glu Lys Gly Glu Thr Ile Thr Gly Leu Leu
 15 20 25
 caa gag ttt gat gtc cag gag cag gac atc gag act tta cat ggc tct 269
 Gln Glu Phe Asp Val Gln Glu Gln Asp Ile Glu Thr Leu His Gly Ser
 30 35 40
 gtt cac gtc acg ctg tgt ggg act ccc aag gga aac cgg cct gtc atc 317
 Val His Val Thr Leu Cys Gly Thr Pro Lys Gly Asn Arg Pro Val Ile
 45 50 55
 ctc acc tac cat gac atc ggc atg aac cac aaa acc tgc tac aac ccc 365
 Leu Thr Tyr His Asp Ile Gly Met Asn His Lys Thr Cys Tyr Asn Pro
 60 65 70 75
 ctc ttc aac tac gag gac atg cag gag atc acc cag 401
 Leu Phe Asn Tyr Glu Asp Met Gln Glu Ile Thr Gln
 80 85

<210> 721
 <211> 372
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> 62..370

<400> 721
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 g atg tcg aag cga gga cgt ggt ggg tcc tct ggt gcg aaa ttc cgg att 109
 Met Ser Lys Arg Gly Arg Gly Gly Ser Ser Gly Ala Lys Phe Arg Ile
 1 5 10 15
 tcc ttg ggt ctt ccg gta gga gct gta atc aat tgt gct gac aac aca 157
 Ser Leu Gly Leu Pro Val Gly Ala Val Ile Asn Cys Ala Asp Asn Thr
 20 25 30
 gga gcc aaa aac ctg tat atc atc tcc gtg aag grg atc aag gga cgg 205
 Gly Ala Lys Asn Leu Tyr Ile Ile Ser Val Lys Xaa Ile Lys Gly Arg
 35 40 45
 ctg aac aga ctt ccc gct gct ggt gtg ggt gac atg gtg atg gcc aca 253
 Leu Asn Arg Leu Pro Ala Ala Gly Val Gly Asp Met Val Met Ala Thr
 50 55 60
 gtc aag aaa ggc aaa cca gag ctc aga aaa aag gta cat cca gca gtg 301
 Val Lys Lys Gly Lys Pro Glu Leu Arg Lys Lys Val His Pro Ala Val
 65 70 75 80